

- NT2RM2000577//tRNA synthetases class I
 NT2RM2000594//C-5 cytosine-specific DNA methylases
 NT2RM2000691//Actins
 NT2RM2000735//Zinc finger, C2H2 type
 5 NT2RM2000740//Helicases conserved C-terminal domain
 NT2RM2000951//FGGY family of carbohydrate kinases
 NT2RM2001324//LIM domain containing proteins
 NT2RM2001499//Amino acid permeases
 NT2RM2001547//DnaJ, prokaryotic heat shock protein //Thioredoxins
 10 NT2RM2001613//eubacterial secY protein
 NT2RM2001670//Zinc finger, C2H2 type
 NT2RM2001700//Acyl-CoA dehydrogenases
 NT2RM2001730//Ubiquitin carboxyl-terminal hydrolases family 2
 NT2RM2001813//WD domain, G-beta repeats
 15 NT2RM2001823//Helicases conserved C-terminal domain //SNF2 and others N-terminal domain
 NT2RM2001896//Cytochrome C oxidase subunit II
 NT2RM2001989//RNA recognition motif. (aka RRM, RBD, or RNP domain)
 NT2RM2001997//Thioredoxins
 NT2RM2002088//KH domain family of RNA binding proteins
 20 NT2RM2002100//DEAD and DEAH box helicases //Helicases conserved C-terminal domain
 NT2RM2002109//IG superfamily
 NT2RM4000046//Zinc finger, C3HC4 type (RING finger)
 NT2RM4000104//Zinc finger, C2H2 type
 NT2RM4000167//Kinesin motor domain
 25 NT2RM4000191//DEAD and DEAH box helicases //Helicases conserved C-terminal domain
 NT2RM4000202//Zinc finger, C2H2 type
 NT2RM4000229//PH (pleckstrin homology) domain
 NT2RM4000344//ATPases associated with various cellular activities (AAA)
 NT2RM4000356//Ras family (contains ATP/GTP binding P-loop)
 30 NT2RM4000471//Aminotransferases class-V
 NT2RM4000496//ATPases associated with various cellular activities (AAA)
 NT2RM4000611//WD domain, G-beta repeats
 NT2RM4000657//C2 domain //Phosphatidylinositol-specific phospholipase C, Y domain
 NT2RM4000712//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2
 35 NT2RM4000733//Forkhead-associated (FHA) domain
 NT2RM4000734//Zinc finger, C2H2 type
 NT2RM4000751//Zinc finger, C2H2 type
 NT2RM4000795//Carboxylesterases
 NT2RM4000996//Zinc finger, C2H2 type
 40 NT2RM4001054//eubacterial secY protein
 NT2RM4001140//Homeobox domain
 NT2RM4001178//DEAD and DEAH box helicases
 NT2RM4001200//Zinc finger, C2H2 type
 NT2RM4001313//Phosphatidylinositol 3- and 4-kinases
 45 NT2RM4001316//Acyl-CoA dehydrogenases
 NT2RM4001320//Src homology domain 3
 NT2RM4001411//PH (pleckstrin homology) domain //Src homology domain 2
 NT2RM4001454//PH (pleckstrin homology) domain
 NT2RM4001483//Zinc finger, C2H2 type
 50 NT2RM4001629//Src homology domain 3
 NT2RM4001758//Eukaryotic protein kinase domain
 NT2RM4001810//Zinc finger, C2H2 type
 NT2RM4001813//Lectin C-type domain short and long forms
 NT2RM4001823//Zinc finger, C2H2 type
 55 NT2RM4001828//Zinc finger C2H2 type
 NT2RM4001987//IG superfamily
 NT2RM4002013//WD domain, G-beta repeats

- NT2RM4002073//AMP-binding enzymes
 NT2RM4002093//RNA recognition motif. (aka RRM, RBD, or RNP domain)
 NT2RM4002145//IG superfamily
 NT2RM4002287//Fibronectin type III domain
 5 NT2RM4002527//WD domain, G-beta repeats
 NT2RM4002623//tRNA synthetases class II
 NT2RP1000101//Zinc finger, C2H2 type
 NT2RP1000202//Ank repeat
 NT2RP1000272//RNA recognition motif. (aka RRM, RBD, or RNP domain)
 10 NT2RP1000363//PH (pleckstrin homology) domain
 NT2RP1000376//Ank repeat
 NT2RP1000470//DEAD and DEAH box helicases
 NT2RP1000478//Tubulin
 NT2RP1000522//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2
 15 NT2RP1000677//Kazal-type serine protease inhibitor domain
 NT2RP1000701//WD domain, G-beta repeats
 NT2RP1000733//Elongation factor Tu family (contains ATP/GTP binding P-loop)
 NT2RP1000782//4 transmembrane segments integral membrane proteins
 NT2RP1000833//3'5'-cyclic nucleotide phosphodiesterases
 20 NT2RP1000856//4 transmembrane segments integral membrane proteins
 NT2RP1000947//Ubiquitin-conjugating enzymes
 NT2RP1000959//60s Acidic ribosomal protein
 NT2RP1000966//RNA recognition motif. (aka RRM, RBD, or RNP domain)
 NT2RP1001033//Tubulin
 25 NT2RP1001080//DEAD and DEAH box helicases //Helicases conserved C-terminal domain
 NT2RP1001177//Core histones H2A, H2B, H3 and H4
 NT2RP1001247//Transforming growth factor beta like domain
 NT2RP1001294//WD domain, G-beta repeats
 NT2RP1001302//WD domain, G-beta repeats
 30 NT2RP1001313//Heme-binding domain in cytochrome b5 and oxidoreductases
 NT2RP1001457//WD domain, G-beta repeats
 NT2RP1001546//4 transmembrane segments integral membrane proteins
 NT2RP2000008//Zinc finger, C2H2 type
 NT2RP2000040//C2 domain
 35 NT2RP2000045//DnaJ, prokaryotic heat shock protein
 NT2RP2000054//Zinc finger, C3HC4 type (RING finger)
 NT2RP2000070//Cadherin
 NT2RP2000126//Helicases conserved C-terminal domain //SNF2 and others N-terminal domain
 NT2RP2000153//RNA recognition motif. (aka RRM, RBD, or RNP domain)
 40 NT2RP2000224//PH (pleckstrin, homology) domain
 NT2RP2000257//Mitochondrial carrier proteins
 NT2RP2000329//Adenylate kinases
 NT2RP2000414//RNA recognition motif. (aka RRM, RBD, or RNP domain)
 NT2RP2000448//PH (pleckstrin homology) domain
 45 NT2RP2000660//ATPases associated with various cellular activities (AAA)
 NT2RP2000668//Eukaryotic protein kinase domain
 NT2RP2000710//tRNA synthetases class II
 NT2RP2000764//Aminotransferases class-V
 NT2RP2000842//7 transmembrane receptor (rhodopsin family)
 50 NT2RP2000880//Elongation factor Tu family (contains ATP/GTP binding P-loop)
 NT2RP2000931//RNA recognition motif. (aka RRM, RBD, or RNP domain)
 NT2RP2000932//Ank repeat
 NT2RP2001081//C2 domain
 NT2RP2001174//Zinc finger, C2H2 type
 55 NT2RP2001397//Cyclins
 NT2RP2001597//Zinc finger, C2H2 type (RING finger)
 NT2RP2001740//Ubiquitin carboxyl-terminal hydrolases family 2

- NT2RP2001748//Polyprenyl synthetases
 NT2RP2001756//Zinc finger, C2H2 type
 NT2RP2001839//Eukaryotic protein kinase domain
 NT2RP2001900//Actins
 5 NT2RP2001991//Sodium:neurotransmitter symporter family
 NT2RP2002058//WD domain, G-beta repeats
 NT2RP2002124//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2
 NT2RP2002185//Ubiquitin family
 NT2RP2002208//Zinc finger, C3HC4 type (RING finger)
 10 NT2RP2002256//Cytochrome P450
 NT2RP2002479//ABC transporters
 NT2RP2002503//Zinc finger, C2H2 type
 NT2RP2002520//Ank repeat
 NT2RP2002591//Zinc finger, C2H2 type
 15 NT2RP2002741//Src homology domain 3
 NT2RP2002929//WD domain, G-beta repeats
 NT2RP2002939//Zinc finger, C2H2 type
 NT2RP2002959//Ubiquitin-conjugating enzymes
 NT2RP2002980//Ribosomal protein S10
 20 NT2RP2003137//Ubiquitin family
 NT2RP2003164//Eukaryotic protein kinase domain
 NT2RP2003228//MCM2/3/5 family
 NT2RP2003243//Fibronectin type III domain
 NT2RP2003272//Ubiquitin family
 25 NT2RP2003307//Kinesin light chain repeat
 NT2RP2003401//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases, family 2
 NT2RP2003433//eubacterial secY protein
 NT2RP2003480//Zinc finger, C2H2 type
 NT2RP2003713//Ubiquitin carboxyl-terminal hydrolases family 2
 30 NT2RP2003737//Ubiquitin-conjugating enzymes
 NT2RP2003777//Zinc finger, C3HC4 type (RING finger)
 NT2RP2003840//Ubiquitin-conjugating enzymes
 NT2RP2003857//Ank repeat
 NT2RP2003981//Zinc finger, C3HC4 type (RING finger)
 35 NT2RP2004170//WD domain, G-beta repeats
 NT2RP2004187//Zinc finger, C2H2 type
 NT2RP2004232//Phorbol esters / diacylglycerol binding domain //PH (pleckstrin homology) domain //Eukaryotic protein kinase domain
 NT2RP2004389//Ribosomal protein S9
 40 NT2RP2004538//PH (pleckstrin homology) domain
 NT2RP2004568//DEAD and DEAH box helicases //Helicases conserved C-terminal domain
 NT2RP2004710//WW/rsp5/WWP domain containing proteins
 NT2RP2004768//Eukaryotic protein kinase domain
 NT2RP2004933//Eukaryotic protein kinase domain
 45 NT2RP2004961//Zinc finger, C2H2 type
 NT2RP2005003//Zinc finger, C3HC4 type (RING finger)
 NT2RP2005012//DnaJ, prokaryotic heat shock protein
 NT2RP2005126//DEAD and DEAH box helicases //Helicases conserved C-terminal domain
 NT2RP2005139//Ank repeat
 50 NT2RP2005140//PH (pleckstrin homology) domain
 NT2RP2005239//Aminotransferases class-V
 NT2RP2005288//Regulator of chromosome condensation (RCC1)
 NT2RP2005293//PH (pleckstrin homology) domain
 NT2RP2005325//Homeobox domain //LIM domain containing proteins
 55 NT2RP2005344//E1-E2 ATPases
 NT2RP2005345//M1-M2 ATPases
 NT2RP2005525//Forkhead-associated domain
 NT2RP2005531//Band 4.1 family

- NT2RP2005557//Bacterial mutT protein
 NT2RP2005654//DnaJ, prokaryotic heat shock protein
 NT2RP2005701//Zinc finger, C3HC4 type (RING finger)
 NT2RP2005722//Zinc finger, C2H2 type
 5 NT2RP2005752//TNFR/NGFR cysteine-rich region
 NT2RP2005763//DEAD and DEAH box helicases //Helicases conserved C-terminal domain
 NT2RP2005767//HMG (high mobility group) box
 NT2RP2006312//HMG (high mobility group) box
 NT2RP2006464//HMG (high mobility group) box
 10 NT2RP2006571//Cytochrome P450
 NT2RP3000050//Zinc finger, C2H2 type
 NT2RP3000068//PH (pleckstrin homology) domain
 NT2RP3000085//Biotin-requiring enzymes //Carbamoyl-phosphate synthase (CPSase)
 NT2RP3000299//Src homology domain 3
 15 NT2RP3000359//Adenylate kinases
 NT2RP3000366//Ras family (contains ATP/GTP binding P-loop)
 NT2RP3000403//WW/rsp5/WWP domain containing proteins
 NT2RP3000487//WW/rsp5/WWP domain containing proteins
 NT2RP3000512//Homeobox domain
 20 NT2RP3000527//Zinc finger, C2H2 type
 NT2RP3000531//IG superfamily
 NT2RP3000590//Zinc finger, C3HC4 type (RING finger)
 NT2RP3000603//Helix-loop-helix DNA-binding domain
 NT2RP3000605//Zinc finger, C2H2 type
 25 NT2RP3000632//Zinc finger, C2H2 type
 NT2RP3000742//Phosphatidylinositol-specific phospholipase C, X domain //Phosphatidylinositol-specific phospholipase C, Y domain
 NT2RP3000759//ADP-ribosylation factors (Arf family) (contains ATP/GTP binding P-loop)
 NT2RP3000825//EGF-like domain
 30 NT2RP3000869//ATPases associated with various cellular activities (AAA)
 NT2RP3000994//Double-stranded RNA binding motif
 NT2RP3001057//Zinc finger, C2H2 type
 NT2RP3001084//PH (pleckstrin homology) domain
 NT2RP3001120//Zinc finger, C2H2 type
 35 NT2RP3001140//Thrombospondin type 1 domain
 NT2RP3001150//Forkhead-associated (FHA) domain
 NT2RP3001155//HMG (high mobility group) box
 NT2RP3001214//Zinc finger, C2H2 type
 NT2RP3001268//Zinc finger, C2H2 type
 40 NT2RP3001338//Zinc finger, C2H2 type
 NT2RP3001355//Mitochondrial carrier proteins
 NT2RP3001398//Zinc finger, C2H2 type
 NT2RP3001426//DnaJ, prokaryotic heat shock protein
 NT2RP3001453//ABC transporters
 45 NT2RP3001457//PH (pleckstrin homology) domain
 NT2RP3001472//HMG (high mobility group) box
 NT2RP3001495//Alcohol/other dehydrogenases, short chain type //WW/rsp5/WWP domain containing proteins
 NT2RP3001497//Zinc finger, C3HC4 type (RING finger)
 NT2RP3001724//Helicases conserved C-terminal domain
 50 NT2RP3001792//RNA recognition motif. (aka RRM, RBD, or RNP domain)
 NT2RP3001943//Zinc finger, C3HC4 type (RING finger)
 NT2RP3001944//Zinc finger, C3HC4 type (RING finger)
 NT2RP3002007//ATPases associated with various cellular activities (AAA)
 NT2RP3002054//Low-density lipoprotein receptor domain class A
 55 NT2RP3002151//Elongation factor Tu family (contains ATP/GTP binding P-loop)
 NT2RP3002399//MCM2/3/5/6/7
 NT2RP3002501//Serine/threonine dehydratase
 NT2RP3002602//Thioredoxins

- NT2RP3002628//DnaJ, prokaryotic heat shock protein //Thioredoxins
 NT2RP3002663//PH (pleckstrin homology) domain
 NT2RP3002909//Ank repeat
 NT2RP3002953//Cadherin
 5 NT2RP3002969//AMP-binding enzymes
 NT2RP3003061//Ank repeat
 NT2RP3003145//Zinc carboxypeptidases
 NT2RP3003230//WD domain, G-beta repeats
 NT2RP3003251//Zinc finger, C3HC4 type (RING finger)
 10 NT2RP3003278//Ank repeat //Zinc finger, C2H2 type
 NT2RP3003282//PH (pleckstrin homology) domain
 NT2RP3003311//PH (pleckstrin homology) domain
 NT2RP3003385//Ank repeat //Chaperonins clpA/B
 NT2RP3003589//Ras family (contains ATP/GTP binding P-loop)
 15 NT2RP3003621//CUB domain //Krigle domain
 NT2RP3003701//Thrombospondin type 1 domain
 NT2RP3003716//Fibronectin type III domain
 NT2RP3003809//ATPases associated with various cellular activities (AAA)
 NT2RP3004016//Zinc finger, C3HC4 type (RING finger)
 20 NT2RP3004207//CUB domain //Sushi domain
 NT2RP3004209//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2
 NT2RP3004242//PH (pleckstrin homology) domain
 NT2RP3004262//DnaJ, prokaryotic heat shock protein
 NT2RP3004566//Zinc finger, C2H2 type
 25 NT2RP3004569//Ank repeat
 NT2RP3004594//HMG (high mobility group) box
 NT2RP3004617//Zinc finger, C3HC4 type (RING finger)
 NT2RP4000259//Glutathione peroxidases
 NT2RP4000370//Prokaryotic-type class I peptide chain release factors
 30 NT2RP4000376//WD domain, G-beta repeats
 NT2RP4000398//Zinc finger, C2H2 type
 NT2RP4000455//Forkhead-associated (FHA) domain //Zinc finger, C3HC4 type (RING finger)
 NT2RP4000457//Ubiquitin carboxyl-terminal hydrolases family 2
 NT2RP4000518//DEAD and DEAH box helicases //Helicases conserved C-terminal domain
 35 NT2RP4000588//Actinin-type actin-binding domain containing proteins
 NT2RP4000614//RNA recognition motif. (aka RRM, RBD, or RNP domain)
 NT2RP4000648//Forkhead-associated (FHA) domain //Zinc finger, C3HC4 type (RING finger)
 NT2RP4000837//Zinc finger, C2H2 type
 NT2RP4000839//WD domain, G-beta repeats
 40 NT2RP4000865//Zinc finger, C2H2 type
 NT2RP4000907//Fibronectin type III domain //IG superfamily
 NT2RP4000925//Fibronectin type III domain
 NT2RP4000927//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2
 NT2RP4000973//DnaJ, prokaryotic heat shock protein //Thioredoxins
 45 NT2RP4001079//E1-E2 ATPases
 NT2RP4001080//RNA recognition motif. (aka RRM, RBD, or RNP domain)
 NT2RP4001117//eubacterial secY protein
 NT2RP4001150//Fibronectin type III domain
 NT2RP4001213//Zinc finger, C2H2 type
 50 NT2RP4001219//Thioredoxins
 NT2RP4001235//Zinc finger, CCHC class
 NT2RP4001433//Zinc finger, C2H2 type
 NT2RP4001498//Ank repeat
 NT2RP4001568//Ank repeat
 55 NT2RP4001644//Eukaryotic protein kinase domain
 NT2RP4001735//Zinc finger, C2H2 type
 NT2RP4001790//Zinc finger, C2H2 type

- NT2RP4001822//4 transmembrane segments integral membrane proteins
 NT2RP4001823//Fibrinogen beta and gamma chains, C-terminal globular domain
 NT2RP4001893//Ank repeat
 NT2RP4001896//WD domain, G-beta repeats
 5 NT2RP4001927//WD domain, G-beta repeats
 NT2RP4001938//Zinc finger, C2H2 type
 NT2RP4002047//Elongation factor Tu family (contains ATP/GTP binding P-loop)
 NT2RP4002078//Zinc finger, C2H2 type
 NT2RP4002408//Eukaryotic protein kinase domain
 10 NT2RP4002905//Cyclins
 NT2RP5003477//WD domain, G-beta repeats
 OVARC1000006//Core histones H2A, H2B, H3 and H4
 OVARC1000085//Proteasome A-type and B-type
 OVARC1000148//RNA recognition motif. (aka RRM, RBD, or RNP domain)
 15 OVARC1000556//Eukaryotic protein kinase domain
 OVARC1000649//PH (pleckstrin homology) domain //Src homology domain 2
 OVARC1000746//Double-stranded RNA binding motif
 OVARC1000885//Alcohol/other dehydrogenases, short chain type
 OVARC1000937//Cyclins
 20 OVARC1000999//Ank repeat
 OVARC1001154//Granulins
 OVARC1001180//Ubiquitin family
 OVARC1001306//Helix-loop-helix DNA-binding domain
 OVARC1001577//RNA recognition motif. (aka RRM, RBD, or RNP domain)
 25 OVARC1001731//Tropomyosins
 OVARC1001943//Zinc finger, C2H2 type
 OVARC1002050//Spectrin alpha chain, repeated domain
 OVARC1002112//Core histones H2A, H2B, H3 and H4
 OVARC1002138//ATPases associated with various cellular activities (AAA)
 30 OVARC1002182//WD domain, G-beta repeats
 PLACE1000014//Zinc finger, C3HC4 type (RING finger)
 PLACE1000040//Ras family (contains ATP/GTP binding P-loop)
 PLACE1000050//Zinc finger, C2H2 type
 PLACE1000081//PH (pleckstrin homology) domain
 35 PLACE1000142//Enoyl-CoA hydratase/isomerase
 PLACE1000401//IG superfamily
 PLACE1000406//RNA recognition motif. (aka RRM, RBD, or RNP domain)
 PLACE1000420//Bacterial mutT protein
 PLACE1000706//Bromodomain
 40 PLACE1000769//KH domain family of RNA binding proteins
 PLACE1000786//PH (pleckstrin homology) domain
 PLACE1000863//Ribosomal protein S4
 PLACE1000909//Ank repeat
 PLACE1000972//Src homology domain 3
 45 PLACE1000979//Zinc finger, C2H2 type
 PLACE1001304//Zinc finger, C2H2 type
 PLACE1001387//Src homology domain 3
 PLACE1001632//Zinc finger, C2H2 type
 PLACE1001672//Aminotransferases class-III pyridoxal-phosphate
 50 PLACE1001716//Zinc finger, CCHC class
 PLACE1001739//DEAD and DEAH box helicases //Helicases conserved C-terminal domain
 PLACE1001781//Phosphoglucosyltransferase and phosphomannosyltransferase phosphoserine
 PLACE1001869//FGGY family of carbohydrate kinases
 PLACE1002438//Zinc finger, C2H2 type
 55 PLACE1002450//Zinc finger, C2H2 type
 PLACE1002474//RING finger
 PLACE1002499//Zinc finger, C3HC4 type (RING finger)
 PLACE1002532//Homeobox domain

PLACE1002571//Actins
 PLACE1002685//Src homology domain 2
 PLACE1002722//7 transmembrane receptor (rhodopsin family)
 PLACE1002775//Bromodomain
 5 PLACE1002834//Zinc finger, C2H2 type
 PLACE1003100//Alcohol/other dehydrogenases, short chain type
 PLACE1003174//Ubiquitin-conjugating enzymes
 PLACE1003238//7 transmembrane receptor (rhodopsin family)
 PLACE1003302//Zinc finger, C2H2 type
 10 PLACE1003334//RNA recognition motif. (aka RRM, RBD, or RNP domain)
 PLACE1003366//C2 domain
 PLACE1003394//Ras family (contains ATP/GTP binding P-loop)
 PLACE1003420//Mitochondrial carrier proteins
 PLACE1003493//C1q domain
 15 PLACE1003519//KH domain family of RNA binding-proteins
 PLACE1003723//Src homology domain 2
 PLACE1003738//Zinc finger, C2H2 type
 PLACE1003888//C2 domain //Phosphatidylinositol-specific phospholipase C, X domain //Phosphatidylinositol-specific phospholipase C, Y domain
 20 PLACE1004128//WD domain, G-beta repeats
 PLACE1004358//PH (pleckstrin homology) domain
 PLACE1004428//Acyl-CoA dehydrogenases
 PLACE1004437//Isocitrate and isopropylmalate dehydrogenases
 PLACE1004506//LIM domain containing proteins
 25 PLACE1004674//EF hand
 PLACE1004918//L-lactate dehydrogenases
 PLACE1005243//Eukaryotic protein kinase domain
 PLACE1005305//Adenylate kinases
 PLACE1005327//Src homology domain 3
 30 PLACE1005530//Zinc finger, C3HC4 type (RING finger)
 PLACE1005646//Helicases conserved C-terminal domain
 PLACE1005656//Ribonucleotide reductases
 PLACE1005966//WD domain, G-beta repeats
 PLACE1006157//Sushi domain
 35 PLACE1006196//DEAH and DEAR box helicases //Helicases conserved C-terminal domain
 PLACE1006438//Zinc finger, C2H2 type
 PLACE1006626//Double-stranded RNA binding motif
 PLACE1006754//IG superfamily
 PLACE1006829//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2
 40 PLACE1006917//RNA recognition motif. (aka RRM, RBD, or RNP domain)
 PLACE1006956//ABC transporters
 PLACE1006958//Heat shock hsp70 proteins
 PLACE1007375//C2 domain
 PLACE1007488//PH (pleckstrin homology) domain
 45 PLACE1007511//Intermediate filament proteins
 PLACE1007537//Ank repeat
 PLACE1007544//Zinc finger, C2H2 type
 PLACE1007547//Zinc finger, C3HC4 type (RING finger)
 PLACE1007598//Zinc finger, C2H2 type
 50 PLACE1007697//ABC transporters
 PLACE1007958//3'5'-cyclic nucleotide phosphodiesterases
 PLACE1007969//RNA recognition motif. (aka RRM, RBD, or RNP domain)
 PLACE1008201//Zinc finger, C2H2 type
 PLACE1008429//Ank repeat
 55 PLACE1008465//Zinc finger, C2H2 type
 PLACE1008655//Winged helix domain
 PLACE1009020//Aminotransferases class
 PLACE1009094//von Willebrand factor type C domain

Y79AA1000342//Zinc finger, C2H2 type
 Y79AA1000349//Double-stranded RNA binding motif
 Y79AA1000627//Zinc finger, C2H2 type
 Y79AA1000705//Helicases conserved C-terminal domain
 5 Y79AA1000752//KH domain family of RNA binding proteins
 Y79AA1000833//Tubulin
 Y79AA1001048//Acyl-CoA dehydrogenases
 Y79AA1001391//Homeobox domain
 Y79AA1001394//ATPases associated with various cellular activities (AAA)
 10 Y79AA1001493//Ubiquitin-conjugating enzymes
 Y79AA1001613//Zinc finger, C2H2 type
 Y79AA1001874//TNFR/NGFR cysteine-rich region
 Y79AA1002027//Ubiquitin-conjugating enzymes
 Y79AA1002139//DnaJ, prokaryotic heat shock protein
 15 Y79AA1002208//Ank repeat
 Y79AA1002246//C2 domain
 Y79AA1002307//Fibronectin type III domain
 Y79AA1002472//Zinc finger, C2H2 type
 HEMBA1003538//CUB domain HEMBA1003645//WD domain, G-beta repeats //Src homology domain 3
 20 HEMBA1005206//Glutathione S-transferases.
 HEMBA1006521//Alcohol/other dehydrogenases, short chain type
 HEMBB1001482//Zinc finger, C2H2 type HEMBB1001915//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2 HEMBB1002044//Cadherin MAMMA1000183//Zinc finger, C2H2 type
 MAMMA1000897//von Willebrand factor type A domain MAMMA1001080//IG superfamily MAMMA1002498//IG
 25 superfamily MAMMA1002573//KH domain family of RNA binding proteins MAMMA1002617//Zinc finger, C2H2 type
 NT2RM1000833//eubacterial secY protein NT2RM2001797//Zinc finger, C2H2 type
 NT2RP1001013//Zinc finger, C2H2 type NT2RP2001233//Zinc finger, C2H2 type
 NT2RP2001440//14-3-3 proteins NT2RP2002105//7 transmembrane receptor (rhodopsin family)
 NT2RP3001723//Laminin G domain NT2RP3001938//Eukaryotic protein kinase domain NT2RP3002330//Elongation factor Tu family (contains ATP/GTP binding P-loop) NT2RP3003133//Zinc finger, C2H2 type
 30 NT2RP3003500//Eukaryotic protein kinase domain NT2RP3003799//C2 domain
 NT2RP3003800//Eukaryotic protein kinase domain NT2RP3004013//Double-stranded RNA binding motif
 NT2RP3004125//Zinc finger, C2H2 type
 OVARC1001244//Bromodomain OVARC1001496//D-isomer specific 2-hydroxyacid dehydrogenases
 35 PLACE1000007//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2
 PLACE1001118//Zinc finger, C2H2 type PLACE1010310//Zinc finger, C2H2 type PLACE1011896//wnt family of developmental signaling proteins PLACE3000124//Src homology domain 2
 PLACE4000100//D-isomer specific 2-hydroxyacid dehydrogenases
 PLACE4000259//Helicases conserved C-terminal domain PLACE4000261//Bromodomain SKNMC1000013//ABC
 40 transporters SKNMC1000091//Basic region plus leucine zipper transcription factors THYRO1000343//Src homology domain 3 THYRO1000569//Zinc finger, C2H2 type THYRO1001189//Zinc finger, C2H2 type Y79AA1002103//
 Zinc finger, C2H2 type PLACE3000350//Eukaryotic protein kinase domain
 PLACE4000156//Zinc finger, C2H2 type

45 EXAMPLE 18

Classification of cDNA clones into functional categories based on the full-length nucleotide sequences

[0257] Prediction of functions of proteins encoded by the clones and the categorization thereof were performed based
 50 on the results of homology search (see Homology search results 6, 12, 13 and 14) of the databases, GenBank, Swiss-Prot and UniGene, for the full-length nucleotide sequences of 4997 clones and based on the results of domain search (see Example 17) of the deduced amino acid sequences encoded by the full-length nucleotide sequences. The target 4997 clones are listed below:

HEMBA1000005,	HEMBA1000012,	HEMBA1000020,	HEMBA1000030,	HEMBA1000042,	HEMBA1000046,
55 HEMBA1000050,	HEMBA1000076	HEMBA1000129	HEMBA1000141	HEMBA1000150	HEMBA1000156
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HEMBA1000216,	HEMBA1000226	HEMBA1000236	HEMBA1000246	HEMBA1000256	HEMBA1000266
HEMBA1000264,	HEMBA1000280	HEMBA1000282,	HEMBA1000288,	HEMBA1000290,	HEMBA1000302,

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	HEMBA1000303,	HEMBA1000304,	HEMBA1000307,	HEMBA1000327,	HEMBA1000333,	HEMBA1000338,
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	HEMBA1000392,	HEMBA1000396,	HEMBA1000411,	HEMBA1000428,	HEMBA1000442,	HEMBA1000456,
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5	HEMBA1000501,	HEMBA1000504,	HEMBA1000505,	HEMBA1000508,	HEMBA1000518,	HEMBA1000519,
	HEMBA1000520,	HEMBA1000523,	HEMBA1000531,	HEMBA1000534,	HEMBA1000542,	HEMBA1000545,
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	HEMBA1000986,	HEMBA1000991,	HEMBA1001008,	HEMBA1001009,	HEMBA1001019,	HEMBA1001020,
	HEMBA1001022,	HEMBA1001024,	HEMBA1001026,	HEMBA1001043,	HEMBA1001051,	HEMBA1001052,
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	HEMBA1001088,	HEMBA1001094,	HEMBA1001099,	HEMBA1001109,	HEMBA1001121,	HEMBA1001122,
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	THYRO1000092,	THYRO1000107,	THYRO1000111,	THYRO1000121,	THYRO1000124,	THYRO1000132,
	THYRO1000156,	THYRO1000173,	THYRO1000186,	THYRO1000187,	THYRO1000197,	THYRO1000199,
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35	THYRO1000381,	THYRO1000387,	THYRO1000394,	THYRO1000395,	THYRO1000401,	THYRO1000452,
	THYRO1000471,	THYRO1000484,	THYRO1000488,	THYRO1000501,	THYRO1000502,	THYRO1000505,
	THYRO1000558,	THYRO1000569,	THYRO1000570,	THYRO1000585,	THYRO1000596,	THYRO1000605,
	THYRO1000625,	THYRO1000637,	THYRO1000662,	THYRO1000666,	THYRO1000676,	THYRO1000684,
	THYRO1000712,	THYRO1000715,	THYRO1000734,	THYRO1000748,	THYRO1000756,	THYRO1000777,
40	THYRO1000783,	THYRO1000787,	THYRO1000793,	THYRO1000796,	THYRO1000805,	THYRO1000815,
	THYRO1000843,	THYRO1000852,	THYRO1000855,	THYRO1000865,	THYRO1000895,	THYRO1000916,
	THYRO1000926,	THYRO1000934,	THYRO1000951,	THYRO1000952,	THYRO1000983,	THYRO1000988,
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	THYRO1001133,	THYRO1001134,	THYRO1001142,	THYRO1001173,	THYRO1001189,	THYRO1001204,
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	THYRO1001321,	THYRO1001322,	THYRO1001347,	THYRO1001363,	THYRO1001365,	THYRO1001374,
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	THYRO1001434,	THYRO1001458,	THYRO1001480,	THYRO1001487,	THYRO1001534,	THYRO1001537,
	THYRO1001541,	THYRO1001559,	THYRO1001570,	THYRO1001584,	THYRO1001595,	THYRO1001602,
50	THYRO1001605,	THYRO1001617,	THYRO1001637,	THYRO1001656,	THYRO1001661,	THYRO1001671,
	THYRO1001673,	THYRO1001703,	THYRO1001706,	THYRO1001721,	THYRO1001738,	THYRO1001745,
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	Y79AA1000059,	Y79AA1000065,	Y79AA1000131,	Y79AA1000181,	Y79AA1000202,	Y79AA1000214,
55	Y79AA1000230,	Y79AA1000231,	Y79AA1000258,	Y79AA1000268,	Y79AA1000313,	Y79AA1000328,
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	Y79AA1000574,	Y79AA1000589,	Y79AA1000627,	Y79AA1000705,	Y79AA1000734,	Y79AA1000748,

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 15 Y79AA1002246, Y79AA1002258, Y79AA1002298, Y79AA1002307, Y79AA1002311, Y79AA1002351,
 Y79AA1002361, Y79AA1002399, Y79AA1002407, Y79AA1002416, Y79AA1002431, Y79AA1002433,
 Y79AA1002472, Y79AA1002482, Y79AA1002487,

[0258] Among the 4997 clones, there are 2189 clones that presumably encode proteins belonging to any of the categories of secretory or membrane proteins, glycoprotein-associated proteins, signal transduction-associated proteins, transcription-associated proteins, disease-associated proteins, enzymes and/or metabolism-associated proteins, ATP- and/or GTP-binding proteins, nuclear proteins, DNA- and/or RNA-binding proteins, RNA synthesis-associated proteins, protein synthesis- and/or protein transport-associated proteins, cytoskeleton-associated proteins, cell division- and/or cell proliferation-associated proteins, embryogenesis- and/or development-associated proteins, or cellular defense-associated proteins.

25 [0259] The clones that presumably encode proteins belonging to the category of secretory or membrane proteins are those which matched the full-length sequences of Swiss-Prot database with the keywords "growth factor", "cytokine", "hormone", "signal", "transmembrane", "membrane", "extracellular matrix", "receptor", "G-protein coupled receptor", "ionic channel", "voltage-gated channel", "calcium channel", "cell adhesion", "collagen", or "connective tissue"; those which matched the data, suggesting that the proteins are secretory or membrane proteins; or those which
 30 matched the full-length sequences of GenBank or UniGene database with similar description; and, further, those predicted to have an N-terminal signal sequence or a transmembrane region as a result of domain search for the amino acid sequences deduced from the full-length nucleotide sequences.

[0260] The clones that presumably encode proteins belonging to the category of glycoprotein-associated proteins are those which matched the full-length sequences of Swiss-Prot database with the keywords "glycoprotein"; those
 35 which matched the data, suggesting that the proteins are glycoprotein; or those which matched the full-length sequences of GenBank or UniGene database with similar description.

[0261] The clones that presumably encode proteins belonging to the category of signal transduction-associated proteins are those which matched the full-length sequences of Swiss-Prot database with the keywords "serine/threonine-protein kinase", "tyrosine-protein kinase", or "SH3 domain"; those which matched the data, suggesting that the proteins
 40 are signal transduction-associated proteins (for example, "ADP-ribosylation factor"); or those which matched the full-length sequences of GenBank or UniGene database with similar description.

[0262] The clones that presumably encode proteins belonging to the category of transcription-associated proteins are those which matched the full-length sequences of Swiss-Prot database with the keywords "transcription regulation", "zinc finger", or "homeobox"; those which matched the data, suggesting that the proteins are transcription-associated
 45 proteins; or those which matched the full-length sequences of GenBank or UniGene database with similar description.

[0263] The clones that presumably encode proteins belonging to the category of disease-associated proteins are those which matched the full-length sequences of Swiss-Prot database with the keywords "disease mutation" or "syndrome"; those which matched the data, suggesting that the proteins are disease-associated proteins; or those which
 50 matched the full-length sequences of Swiss-Prot database and GenBank or UniGene database where the matched sequences of genes or proteins which had been registered in the database of Online Mendelian Inheritance in Man (OMIM) (<http://www.ncbi.nlm.nih.gov/Omim/>), which is a database of human genes and diseases.

[0264] The clones that presumably encode proteins belonging to the category of enzymes and/or metabolism-associated proteins are those which showed the terms "metabolism", "oxidoreductase", or "E.C. No. (Enzyme commission number)" in the matching data.

55 [0265] The clones that presumably encode proteins belonging to the category of ATP- and/or GTP-binding proteins

[0266] The clones that presumably encode proteins belonging to the category of nuclear proteins are those which matched the data with the terms "nuclear protein"

[0267] The clones that presumably encode proteins belonging to the category of DNA- and/or RNA-binding proteins are those which matched the data with the terms "DNA-binding" or "RNA-binding".

[0268] The clones that presumably encode proteins belonging to the category of RNA synthesis-associated proteins are those which matched the data with the terms "RNA splicing", "RNA processing", "RNA helicase", or "polyadenylation".

[0269] The clones that presumably encode proteins belonging to the category of protein synthesis- and/or protein transport-associated proteins are those which matched the data with the terms "translation regulation", "protein biosynthesis", "amino-acid biosynthesis", "ribosomal protein", "protein transport", or "signal recognition particle".

[0270] The clones that presumably encode proteins belonging to the category of cytoskeleton-associated proteins are those which matched the data with the terms "structural protein", "cytoskeleton", "actin-binding", or "microtubules".

[0271] The clones that presumably encode proteins belonging to the category of cell division- and/or cell proliferation-associated proteins are those which matched the data with the terms "cell division", "cell cycle", "mitosis", "chromosomal protein", "cell growth", or "apoptosis".

[0272] The clones that presumably encode proteins belonging to the category of embryogenesis- and/or development-associated proteins are those which matched the data with the terms "developmental protein".

[0273] The clones that presumably encode proteins belonging to the category of cellular defense-associated proteins are those which matched the data with the terms "heat shock", "DNA repair", or "DNA damage".

[0274] When a clone belonged to the above-mentioned multiple functional categories, the clone was classified into the multiple categories. However, the functions of the protein encoded by the clone are not limited to the functions of the categories into which the clone was classified, and therefore, additional functions can be found for the protein by further analyses.

[0275] The following 796 clones are categorized into secretory or membrane proteins.

HEMBA1000356,	HEMBA1000518,	HEMBA1000531,	HEMBA1000637,	HEMBA1000719,	HEMBA1000817,
HEMBA1000822,	HEMBA1000852,	HEMBA1000870,	HEMBA1000991,	HEMBA1001052,	HEMBA1001071,
HEMBA1001085,	HEMBA1001286,	HEMBA1001351,	HEMBA1001407,	HEMBA1001446,	HEMBA1001515,
HEMBA1001557,	HEMBA1001569,	HEMBA1001661,	HEMBA1001734,	HEMBA1001746,	HEMBA1001866,
HEMBA1002125,	HEMBA1002150,	HEMBA1002166,	HEMBA1002417,	HEMBA1002462,	HEMBA1002475,
HEMBA1002477,	HEMBA1002486,	HEMBA1002609,	HEMBA1002659,	HEMBA1002661,	HEMBA1002780,
HEMBA1002818,	HEMBA1002876,	HEMBA1002921,	HEMBA1003071,	HEMBA1003077,	HEMBA1003079,
HEMBA1003086,	HEMBA1003096,	HEMBA1003281,	HEMBA1003286,	HEMBA1003538,	HEMBA1003711,
HEMBA1003742,	HEMBA1003803,	HEMBA1004055,	HEMBA1004143,	HEMBA1004146,	HEMBA1004207,
HEMBA1004341,	HEMBA1004461,	HEMBA1004577,	HEMBA1004637,	HEMBA1004752,	HEMBA1004756,
HEMBA1004850,	HEMBA1004889,	HEMBA1004923,	HEMBA1004930,	HEMBA1005029,	HEMBA1005035,
HEMBA1005050,	HEMBA1005552,	HEMBA1005576,	HEMBA1005581,	HEMBA1005588,	HEMBA1005616,
HEMBA1005699,	HEMBA1005991,	HEMBA1006036,	HEMBA1006038,	HEMBA1006067,	HEMBA1006173,
HEMBA1006198,	HEMBA1006293,	HEMBA1006310,	HEMBA1006492,	HEMBA1006502,	HEMBA1006583,
HEMBA1006659,	HEMBA1006758,	HEMBA1006789,	HEMBA1006921,	HEMBA1006926,	HEMBA1006976,
HEMBA1007203,	HEMBA1007301,	HEMBA1000037,	HEMBA1000050,	HEMBA1000054,	HEMBA1000175,
HEMBA1000317,	HEMBA1000556,	HEMBA1000593,	HEMBA1000631,	HEMBA1000763,	HEMBA1000827,
HEMBA1000915,	HEMBA1000975,	HEMBA1001112,	HEMBA1001151,	HEMBA1001177,	HEMBA1001302,
HEMBA1001348,	HEMBA1001564,	HEMBA1001630,	HEMBA1001871,	HEMBA1001872,	HEMBA1001925,
HEMBA1001962,	HEMBA1002042,	HEMBA1002044,	HEMBA1002142,	HEMBA1002190,	HEMBA1002193,
HEMBA1002247,	HEMBA1002383,	HEMBA1002387,	HEMBA1002550,	HEMBA1002600,	HEMBA1002692,
MAMMA1000045,	MAMMA1000129,	MAMMA1000133,	MAMMA1000277,	MAMMA1000278,	MAMMA1000410,
MAMMA1000416,	MAMMA1000472,	MAMMA1000672,	MAMMA1000684,	MAMMA1000714,	MAMMA1000734,
MAMMA1000778,	MAMMA1000798,	MAMMA1000842,	MAMMA1000859,	MAMMA1000897,	MAMMA1000956,
MAMMA1001008,	MAMMA1001030,	MAMMA1001041,	MAMMA1001073,	MAMMA1001080,	MAMMA1001139,
MAMMA1001154,	MAMMA1001322,	MAMMA1001388,	MAMMA1001411,	MAMMA1001487,	MAMMA1001751,
MAMMA1001754,	MAMMA1001771,	MAMMA1002009,	MAMMA1002427,	MAMMA1002428,	MAMMA1002461,
MAMMA1002524,	MAMMA1002573,	MAMMA1002598,	MAMMA1002655,	MAMMA1002684,	MAMMA1002769,
MAMMA1002844,	MAMMA1002881,	MAMMA1002890,	MAMMA1002938,	MAMMA1002947,	MAMMA1003035,
MAMMA1003089,	MAMMA1003146,	MAMMA1003150,	NT2RM1000035,	NT2RM1000037,	NT2RM1000062,
NT2RM1000080,	NT2RM1000092,	NT2RM1000131,	NT2RM1000199,	NT2RM1000257,	NT2RM1000260,
NT2RM1000355,	NT2RM1000430,	NT2RM1000563,	NT2RM1000648,	NT2RM1000742,	NT2RM1000770,
NT2RM1000800,	NT2RM1000811,	NT2RM1000833,	NT2RM1000857,	NT2RM1000867,	NT2RM1000882,
NT2RM1000991,	NT2RM1001131,	NT2RM2000251,	NT2RM2000261,	NT2RM2000281,	NT2RM2000391,
NT2RM2000402,	NT2RM2000407,	NT2RM2000422,	NT2RM2000490,	NT2RM2000522,	NT2RM2000566,

	NT2RM2000581,	NT2RM2000609,	NT2RM2000821,	NT2RM2001370,	NT2RM2001393,	NT2RM2001499,
	NT2RM2001547,	NT2RM2001613,	NT2RM2001648,	NT2RM2001659,	NT2RM2001671,	NT2RM2001688,
	NT2RM2001698,	NT2RM2001718,	NT2RM2001753,	NT2RM2001760,	NT2RM2001785,	NT2RM2001930,
	NT2RM2001950,	NT2RM2001997,	NT2RM2001998,	NT2RM2002049,	NT2RM2002145,	NT2RM4000233,
5	NT2RM4000433,	NT2RM4000457,	NT2RM4000486,	NT2RM4000496,	NT2RM4000520,	NT2RM4000634,
	NT2RM4000674,	NT2RM4000700,	NT2RM4000764,	NT2RM4000778,	NT2RM4000795,	NT2RM4000820,
	NT2RM4000857,	NT2RM4001032,	NT2RM4001054,	NT2RM4001116,	NT2RM4001455,	NT2RM4001666,
	NT2RM4001810,	NT2RM4001813,	NT2RM4001930,	NT2RM4001987,	NT2RM4002054,	NT2RM4002073,
	NT2RM4002145,	NT2RM4002146,	NT2RM4002189,	NT2RM4002194,	NT2RM4002251,	NT2RM4002339,
10	NT2RM4002438,	NT2RM4002446,	NT2RM4002452,	NT2RM4002460,	NT2RM4002493,	NT2RM4002558,
	NT2RM4002565,	NT2RM4002571,	NT2RM4002594,	NT2RP1000130,	NT2RP1000191,	NT2RP1000326,
	NT2RP1000358,	NT2RP1000413,	NT2RP1000418,	NT2RP1000547,	NT2RP1000609,	NT2RP1000677,
	NT2RP1000767,	NT2RP1000782,	NT2RP1000856,	NT2RP1001113,	NT2RP1001247,	NT2RP1001286,
	NT2RP1001310,	NT2RP1001311,	NT2RP1001313,	NT2RP1001385,	NT2RP1001449,	NT2RP1001546,
15	NT2RP1001569,	NT2RP2000032,	NT2RP2000040,	NT2RP2000056,	NT2RP2000070,	NT2RP2000091,
	NT2RP2000114,	NT2RP2000120,	NT2RP2000173,	NT2RP2000175,	NT2RP2000195,	NT2RP2000257,
	NT2RP2000270,	NT2RP2000283,	NT2RP2000288,	NT2RP2000289,	NT2RP2000459,	NT2RP2000516,
	NT2RP2000660,	NT2RP2000842,	NT2RP2000892,	NT2RP2001081,	NT2RP2001268,	NT2RP2001295,
	NT2RP2001366,	NT2RP2001378,	NT2RP2001576,	NT2RP2001581,	NT2RP2001597,	NT2RP2001613,
20	NT2RP2001947,	NT2RP2001991,	NT2RP2002025,	NT2RP2002066,	NT2RP2002078,	NT2RP2002105,
	NT2RP2002312,	NT2RP2002325,	NT2RP2002385,	NT2RP2002479,	NT2RP2002537,	NT2RP2002643,
	NT2RP2002701,	NT2RP2002740,	NT2RP2002857,	NT2RP2003125,	NT2RP2003297,	NT2RP2003433,
	NT2RP2003446,	NT2RP2003466,	NT2RP2003506,	NT2RP2003513,	NT2RP2003629,	NT2RP2003668,
	NT2RP2003760,	NT2RP2003777,	NT2RP2003781,	NT2RP2004041,	NT2RP2004142,	NT2RP2004194,
25	NT2RP2004270,	NT2RP2004300,	NT2RP2004392,	NT2RP2004655,	NT2RP2004681,	NT2RP2004775,
	NT2RP2004799,	NT2RP2004936,	NT2RP2004959,	NT2RP2005012,	NT2RP2005159,	NT2RP2005227,
	NT2RP2005270,	NT2RP2005344,	NT2RP2005465,	NT2RP2005509,	NT2RP2005752,	NT2RP2005781,
	NT2RP2005784,	NT2RP2005812,	NT2RP2006069,	NT2RP2006100,	NT2RP2006141,	NT2RP2006184,
	NT2RP2006261,	NT2RP2006565,	NT2RP2006571,	NT2RP2006573,	NT2RP3000092,	NT2RP3000109,
30	NT2RP3000134,	NT2RP3000207,	NT2RP3000333,	NT2RP3000341,	NT2RP3000393,	NT2RP3000439,
	NT2RP3000441,	NT2RP3000531,	NT2RP3000685,	NT2RP3000825,	NT2RP3000826,	NT2RP3000852,
	NT2RP3000919,	NT2RP3001084,	NT2RP3001096,	NT2RP3001126,	NT2RP3001140,	NT2RP3001176,
	NT2RP3001260,	NT2RP3001282,	NT2RP3001355,	NT2RP3001383,	NT2RP3001426,	NT2RP3001453,
	NT2RP3001497,	NT2RP3001538,	NT2RP3001589,	NT2RP3001642,	NT2RP3001708,	NT2RP3001716,
35	NT2RP3001727,	NT2RP3001739,	NT2RP3001799,	NT2RP3001943,	NT2RP3001944,	NT2RP3002002,
	NT2RP3002007,	NT2RP3002014,	NT2RP3002054,	NT2RP3002108,	NT2RP3002163,	NT2RP3002351,
	NT2RP3002455,	NT2RP3002549,	NT2RP3002602,	NT2RP3002628,	NT2RP3002650,	NT2RP3002687,
	NT2RP3002701,	NT2RP3002810,	NT2RP3002869,	NT2RP3002969,	NT2RP3002985,	NT2RP3003008,
	NT2RP3003059,	NT2RP3003071,	NT2RP3003101,	NT2RP3003145,	NT2RP3003197,	NT2RP3003203,
40	NT2RP3003242,	NT2RP3003302,	NT2RP3003353,	NT2RP3003409,	NT2RP3003576,	NT2RP3003621,
	NT2RP3003665,	NT2RP3003672,	NT2RP3003701,	NT2RP3003716,	NT2RP3003799,	NT2RP3003828,
	NT2RP3003914,	NT2RP3003918,	NT2RP3003992,	NT2RP3004051,	NT2RP3004148,	NT2RP3004155,
	NT2RP3004207,	NT2RP3004282,	NT2RP3004454,	NT2RP3004480,	NT2RP3004503,	NT2RP4000008,
	NT2RP4000051,	NT2RP4000151,	NT2RP4000212,	NT2RP4000243,	NT2RP4000259,	NT2RP4000323,
45	NT2RP4000417,	NT2RP4000500,	NT2RP4000524,	NT2RP4000556,	NT2RP4000560,	NT2RP4000588,
	NT2RP4000713,	NT2RP4000724,	NT2RP4000817,	NT2RP4000833,	NT2RP4000878,	NT2RP4000907,
	NT2RP4000925,	NT2RP4000928,	NT2RP4000973,	NT2RP4000989,	NT2RP4001057,	NT2RP4001064,
	NT2RP4001079,	NT2RP4001117,	NT2RP4001138,	NT2RP4001149,	NT2RP4001150,	NT2RP4001174,
	NT2RP4001219,	NT2RP4001274,	NT2RP4001313,	NT2RP4001345,	NT2RP4001372,	NT2RP4001373,
50	NT2RP4001379,	NT2RP4001498,	NT2RP4001547,	NT2RP4001571,	NT2RP4001574,	NT2RP4001644,
	NT2RP4001656,	NT2RP4001677,	NT2RP4001730,	NT2RP4001739,	NT2RP4001803,	NT2RP4001822,
	NT2RP4001823,	NT2RP4001950,	NT2RP4001975,	NT2RP4002052,	NT2RP4002075,	NT2RP5003500,
	NT2RP5003506,	NT2RP5003522,	NT2RP5003534,	OVARC1000060,	OVARC1000335,	OVARC1000682,
	OVARC1000689,	OVARC1000700,	OVARC1000722,	OVARC1000751,	OVARC1000850,	OVARC1000890,
55	OVARC1000924	OVARC1000936	OVARC1000959	OVARC1000984	OVARC1000999	OVARC1001034
	OVARC1001034	OVARC1001045	OVARC1001047	OVARC1001050	OVARC1001061	OVARC1001070
	OVARC1001073	OVARC1001113	OVARC1001145	OVARC1001167	OVARC1002127	OVARC1002138

	OVARC1002158,	OVARC1002165,	PLACE1000014,	PLACE1000213,	PLACE1000401,	PLACE1000562,
	PLACE1000611,	PLACE1000656,	PLACE1000712,	PLACE1 000793,	PLACE1000909,	PLACE1000948,
	PLACE1000977,	PLACE1001241,	PLACE1001257,	PLACE1001377,	PLACE1001517,	PLACE1001610,
	PLACE1001761,	PLACE1001771,	PLACE1001817,	PLACE1001983,	PLACE1002046,	PLACE1002140,
5	PLACE1002213,	PLACE1002395,	PLACE1002437,	PLACE1002500,	PLACE1002583,	PLACE1002714,
	PLACE1002722,	PLACE1002782,	PLACE1002794,	PLACE1002851,	PLACE1002908,	PLACE1003030,
	PLACE1003044,	PLACE1003045,	PLACE1003238,	PLACE1003296,	PLACE1003369,	PLACE1003420,
	PLACE1003493,	PLACE1003537,	PLACE1003553,	PLACE1003596,	PLACE1003760,	PLACE1003768,
	PLACE1003771,	PLACE1003903,	PLACE1004149,	PLACE1004197,	PLACE1004203,	PLACE1004258,
10	PLACE1004270,	PLACE1004277,	PLACE1004289,	PLACE1004473,	PLACE1004629,	PLACE1004646,
	PLACE1004743,	PLACE1004751,	PLACE1004793,	PLACE1004840,	PLACE1004969,	PLACE1005086,
	PLACE1005162,	PLACE1005206,	PLACE1005313,	PLACE1005467,	PLACE1005530,	PLACE1005595,
	PLACE1005611,	PLACE1005623,	PLACE1005763,	PLACE1005884,	PLACE1005890,	PLACE1005898,
	PLACE1005934,	PLACE1005953,	PLACE1006157,	PLACE1006225,	PLACE1006239,	PLACE1006288,
15	PLACE1006492,	PLACE1006534,	PLACE1006678,	PLACE1006754,	PLACE1006901,	PLACE1006935,
	PLACE1006956,	PLACE1007111,	PLACE1007243,	PLACE1007274,	PLACE1007282,	PLACE1007317,
	PLACE1007375,	PLACE1007386,	PLACE1007409,	PLACE1007416,	PLACE1007484,	PLACE1007583,
	PLACE1007632,	PLACE1007645,	PLACE1007649,	PLACE1007852,	PLACE1007877,	PLACE1007954,
	PLACE1008273,	PLACE1008309,	PLACE1008331,	PLACE1008402,	PLACE1008424,	PLACE1008429,
20	PLACE1008531,	PLACE1008532,	PLACE1008533,	PLACE1008568,	PLACE1008643,	PLACE1008693,
	PLACE1008715,	PLACE1009045,	PLACE1009094,	PLACE1009298,	PLACE1009319,	PLACE1009338,
	PLACE1009368,	PLACE1009493,	PLACE1009639,	PLACE1009659,	PLACE1009708,	PLACE1009731,
	PLACE1009845,	PLACE1009861,	PLACE1009935,	PLACE1009992,	PLACE1010089,	PLACE1010231,
	PLACE1010321,	PLACE1010362,	PLACE1010599,	PLACE1010622,	PLACE1010662,	PLACE1010811,
25	PLACE1010917,	PLACE1010942,	PLACE1010954,	PLACE1011090,	PLACE1011214,	PLACE1011221,
	PLACE1011371,	PLACE1011399,	PLACE1011492,	PLACE1011646,	PLACE1011749,	PLACE1011896,
	PLACE2000034,	PLACE2000062,	PLACE2000111,	PLACE2000132,	PLACE2000176,	PLACE2000187,
	PLACE2000216,	PLACE2000335,	PLACE2000341,	PLACE2000373,	PLACE2000379,	PLACE2000398,
	PLACE2000399,	PLACE2000425,	PLACE2000438,	PLACE2000458,	PLACE2000477,	PLACE3000020,
30	PLACE3000218,	PLACE3000226,	PLACE3000242,	PLACE3000244,	PLACE3000339,	PLACE3000373,
	PLACE3000399,	PLACE3000406,	PLACE3000413,	PLACE3000455,	PLACE4000052,	PLACE4000063,
	PLACE4000129,	PLACE4000247,	PLACE4000250,	PLACE4000259,	PLACE4000300,	PLACE4000387,
	PLACE4000431,	PLACE4000487,	PLACE4000494,	PLACE4000522,	PLACE4000548,	PLACE4000581,
	PLACE4000593,	PLACE4000650,	THYRO1000156,	THYRO1000327,	THYRO1000394,	THYRO1000395,
35	THYRO1000570,	THYRO1000748,	THYRO1000756,	THYRO1000783,	THYRO1001134,	THYRO1001271,
	THYRO1001287,	THYRO1001320,	THYRO1001401,	THYRO1001534,	THYRO1001537,	THYRO1001541,
	THYRO1001828,	Y79AA1000258,	Y79AA1000420,	Y79AA1000469,	Y79AA1000734,	Y79AA1000800,
	Y79AA1000976,	Y79AA1001023,	Y79AA1001177,	Y79AA1001384,	Y79AA1001394,	Y79AA1001603,
	Y79AA1001647,	Y79AA1001846,	Y79AA1001874,	Y79AA1002139,	Y79AA1002246,	Y79AA1002351,
40	Y79AA1002399,	Y79AA1002416,				

[0276] The following 141 clones are categorized into glycoproteins-associated proteins.

	HEMBA1000156,	HEMBA1000518,	HEMBA1000852,	HEMBA1001071,	HEMBA1001286,	HEMBA1001661,
	HEMBA1001734,	HEMBA1001866,	HEMBA1003071,	HEMBA1003077,	HEMBA1003281,	HEMBA1003538,
	HEMBA1003679,	HEMBA1003866,	HEMBA1005576,	HEMBA1005581,	HEMBA1005699,	HEMBA1006038,
45	HEMBA1006976,	HEMBA1007301,	HEMBB1000317,	HEMBB1000915,	HEMBB1001871,	HEMBB1001872,
	HEMBB1002193,	MAMMA1000672,	MAMMA1000897,	MAMMA1001030,	MAMMA1001388,	MAMMA1002329,
	MAMMA1002428,	MAMMA1002573,	MAMMA1003150,	NT2RM1000648,	NT2RM1001115,	NT2RM2000260,
	NT2RM2000407,	NT2RM2000422,	NT2RM2000490,	NT2RM2001499,	NT2RM2001659,	NT2RM2001930,
	NT2RM4000820,	NT2RM4000857,	NT2RM4001810,	NT2RM4001813,	NT2RM4001987,	NT2RM4002145,
50	NT2RM4002189,	NT2RM4002251,	NT2RM4002460,	NT2RM4002558,	NT2RP1000677,	NT2RP1000782,
	NT2RP1000856,	NT2RP1001546,	NT2RP2000056,	NT2RP2000070,	NT2RP2001295,	NT2RP2001378,
	NT2RP2001597,	NT2RP2001991,	NT2RP2002025,	NT2RP2002078,	NT2RP2002385,	NT2RP2004587,
	NT2RP2004732,	NT2RP2005531,	NT2RP3000207,	NT2RP3000531,	NT2RP3000825,	NT2RP3001140,
	NT2RP3002810,	NT2RP3003672,	NT2RP3003701,	NT2RP3003716,	NT2RP3003914,	NT2RP3004148,
55	NT2RP4000212,	NT2RP4000417,	NT2RP4000724,	NT2RP4000817,	NT2RP4000925,	NT2RP4001150,
	OVARC1000288,	OVARC100068,	OVARC100105,	OVARC100150,	OVARC100171,	OVARC100210
	PLACE1000213,	PLACE1000401,	PLACE1002437,	PLACE1002583,		

PLACE1002722, PLACE1003045, PLACE1003238, PLACE1003258, PLACE1003493, PLACE1004197,
 PLACE1004793, PLACE1005953, PLACE1005955, PLACE1006157, PLACE1006239, PLACE1006368,
 PLACE1006534, PLACE1006754, PLACE1006956, PLACE1007416, PLACE1007632, PLACE1007649,
 PLACE1008643, PLACE1009094, PLACE1009992, PLACE1010231, PLACE1010662, PLACE1011371,
 5 PLACE2000034, PLACE2000373, PLACE2000398, PLACE2000399, PLACE2000438, PLACE2000458,
 PLACE3000339, PLACE4000063, PLACE4000230, PLACE4000522, PLACE4000548, PLACE4000581,
 THYRO1000327, THYRO1000756, THYRO1001287, Y79AA1001603, Y79AA1001874

[0277] The following 129 clones are categorized into signal transduction-associated proteins.

10 HEMBA1000303, HEMBA1000369, HEMBA1000608, HEMBA1000657, HEMBA1000919, HEMBA1001019,
 HEMBA1001174, HEMBA1001822, HEMBA1001921, HEMBA1002139, HEMBA1002212, HEMBA1002341,
 HEMBA1002417, HEMBA1002768, HEMBA1003250, HEMBA1003291, HEMBA1003645, HEMBA1004286,
 HEMBA1005737, HEMBA1006130, HEMBA1006708, HEMBB1000083, HEMBB1000266, HEMBB1000632,
 HEMBB1000781, HEMBB1000831, HEMBB1002193, MAMMA1000173, MAMMA1001038, MAMMA1001198,
 MAMMA1002842, MAMMA1003057, NT2RM1000702, NT2RM1000772, NT2RM1001072, NT2RM2000030,
 15 NT2RM2000469, NT2RM2000612, NT2RM2001221, NT2RM2001345, NT2RM2002128, NT2RM4000229,
 NT2RM4000354, NT2RM4000611, NT2RM4000798, NT2RM4001411, NT2RM4001412, NT2RM4001629,
 NT2RM4001758, NT2RM4002013, NT2RM4002527, NT2RP1000018, NT2RP1000701, NT2RP1001294,
 NT2RP1001302, NT2RP2000668, NT2RP2001440, NT2RP2001560, NT2RP2002058, NT2RP2002193,
 NT2RP2002408, NT2RP2002710, NT2RP2002929, NT2RP2003164, NT2RP2003912, NT2RP2004232,
 20 NT2RP2004768, NT2RP2006071, NT2RP2006534, NT2RP3000759, NT2RP3000845, NT2RP3001646,
 NT2RP3001857, NT2RP3001938, NT2RP3002004, NT2RP3002785, NT2RP3002909, NT2RP3002988,
 NT2RP3003800, NT2RP3004189, NT2RP3004544, NT2RP4000147, NT2RP4000839, NT2RP4001122,
 NT2RP4001148, NT2RP4001336, NT2RP4001375, NT2RP4001644, NT2RP4001725, NT2RP4001849,
 NT2RP4001896, NT2RP4001927, NT2RP4002408, NT2RP5003477, OVARC1000013, OVARC1000437,
 25 OVARC1000556, OVARC1000649, OVARC 1000945, OVARC1001200, OVARC1002182, PLACE1000977,
 PLACE1001387, PLACE1002493, PLACE1002591, PLACE1003190, PLACE1003353, PLACE1004128,
 PLACE1004302, PLACE1004937, PLACE1005243, PLACE1008000, PLACE1008244, PLACE1008650,
 PLACE1009468, PLACE1009596, PLACE1009708, PLACE1009845, PLACE1010926, PLACE1011041,
 PLACE2000164, PLACE2000371, PLACE3000145, PLACE3000350, THYRO1000072, THYRO1000748,
 30 THYRO1001120, Y79AA1000328, Y79AA1002431

[0278] The following 309 clones are categorized into transcription-associated proteins.

HEMBA1000158, HEMBA1000201, HEMBA1000216, HEMBA1000555, HEMBA1000561, HEMBA1000851,
 HEMBA1001077, HEMBA1001137, HEMBA1001405, HEMBA1001510, HEMBA1001635, HEMBA1001804,
 HEMBA1001809, HEMBA1001819, HEMBA1001847, HEMBA1001869, HEMBA1002035, HEMBA1002092,
 35 HEMBA1002177, HEMBA1002770, HEMBA1002935, HEMBA1003408, HEMBA1003545, HEMBA1003568,
 HEMBA1003662, HEMBA1003684, HEMBA1003760, HEMBA1003953, HEMBA1004097, HEMBA1004321,
 HEMBA1004353, HEMBA1004389, HEMBA1004479, HEMBA1004758, HEMBA1004973, HEMBA1005219,
 HEMBA1005359, HEMBA1005513, HEMBA1005528, HEMBA1005548, HEMBA1005558, HEMBA1005931,
 HEMBA1006158, HEMBA1006248, HEMBA1006278, HEMBA1006283, HEMBA1006347, HEMBA1006359,
 40 HEMBA1006559, HEMBA1006941, HEMBB1000789, HEMBB1001011, HEMBB1001314, HEMBB1001482,
 HEMBB1001673, HEMBB1001749, HEMBB1001839, HEMBB1001908, HEMBB1002134, HEMBB1002217,
 HEMBB1002342, HEMBB1002607, MAMMA1000183, MAMMA1000388, MAMMA1001105, MAMMA1001222,
 MAMMA1001260, MAMMA1001627, MAMMA1001633, MAMMA1001743, MAMMA1001820, MAMMA1001837,
 MAMMA1002617, MAMMA1002650, MAMMA1002937, NT2RM1000055, NT2RM1000086, NT2RM1000746,
 45 NT2RM1000885, NT2RM1000894, NT2RM1001092, NT2RM2000013, NT2RM2000452, NT2RM2000735,
 NT2RM2000740, NT2RM2001035, NT2RM2001105, NT2RM2001575, NT2RM2001670, NT2RM2001716,
 NT2RM2001771, NT2RM2002091, NT2RM4000024, NT2RM4000046, NT2RM4000104, NT2RM4000202,
 NT2RM4000531, NT2RM4000595, NT2RM4000733, NT2RM4000734,
 NT2RM4000741, NT2RM4000751, NT2RM4000996, NT2RM4001092, NT2RM4001140, NT2RM4001200,
 50 NT2RM4001483, NT2RM4001592, NT2RM4001783, NT2RM4001823, NT2RM4001828, NT2RM4001858,
 NT2RM4001979, NT2RM4002066, NT2RP1000086, NT2RP1000111, NT2RP1000574, NT2RP1000902,
 NT2RP1001013, NT2RP2000008, NT2RP2000126, NT2RP2000297, NT2RP2000420, NT2RP2001174,
 NT2RP2001233, NT2RP2001756, NT2RP2001869, NT2RP2002046, NT2RP2002252, NT2RP2002270,
 NT2RP2002464, NT2RP2002503, NT2RP2002520, NT2RP2002591, NT2RP2002880, NT2RP2002939,
 55 NT2RP2002993, NT2RP2003243, NT2RP2003329, NT2RP2003347, NT2RP2003480, NT2RP2003522,
 NT2RP2003581, NT2RP2003671, NT2RP2004045, NT2RP2004061, NT2RP2004118, NT2RP2004491,
 NT2RP200496, NT2RP2005000, NT2RP2005130, NT2RP2005325, NT2RP2005496, NT2RP2005701,
 NT2RP2005722, NT2RP2005776, NT2RP2005942, NT2RP2006238, NT2RP2006436, NT2RP3000050.

	NT2RP3000320,	NT2RP3000512,	NT2RP3000527,	NT2RP3000590,	NT2RP3000603,	NT2RP3000605,
	NT2RP3000632,	NT2RP3001057,	NT2RP3001107,	NT2RP3001111,	NT2RP3001120,	NT2RP3001150,
	NT2RP3001268,	NT2RP3001338,	NT2RP3001398,	NT2RP3001527,	NT2RP3001688,	NT2RP3001855,
	NT2RP3002165,	NT2RP3002399,	NT2RP3002876,	NT2RP3003133,	NT2RP3003193,	NT2RP3003251,
5	NT2RP3003313,	NT2RP3003327,	NT2RP3003555,	NT2RP3004016,	NT2RP3004125,	NT2RP3004242,
	NT2RP3004428,	NT2RP3004498,	NT2RP3004566,	NT2RP3004617,	NT2RP4000210,	NT2RP4000398,
	NT2RP4000455,	NT2RP4000648,	NT2RP4000837,	NT2RP4000865,	NT2RP4000997,	NT2RP4001029,
	NT2RP4001080,	NT2RP4001213,	NT2RP4001433,	NT2RP4001529,	NT2RP4001551,	NT2RP4001568,
	NT2RP4001638,	NT2RP4001753,	NT2RP4001760,	NT2RP4001790,	NT2RP4001838,	NT2RP4001938,
10	NT2RP4002078,	NT2RP4002081,	NT2RP5003461,	OVARC1000151,	OVARC1000241,	OVARC1000479,
	OVARC1001271,	OVARC1001417,	OVARC1001436,	PLACE1000133,	PLACE1000583,	PLACE1000706,
	PLACE1000786,	PLACE1000979,	PLACE1001118,	PLACE1001238,	PLACE1001294,	PLACE1001304,
	PLACE1001383,	PLACE1001602,	PLACE1001632,	PLACE1002171,	PLACE1002438,	PLACE1002450,
	PLACE1002532,	PLACE1002775,	PLACE1002834,	PLACE1003302,	PLACE1003605,	PLACE1003738,
15	PLACE1003885,	PLACE1004471,	PLACE1005584,	PLACE1005803,	PLACE1005966,	PLACE1006167,
	PLACE1006318,	PLACE1006438,	PLACE1006482,	PLACE1007239,	PLACE1007346,	PLACE1007488,
	PLACE1007547,	PLACE1007598,	PLACE1007955,	PLACE1008132,	PLACE1008201,	PLACE1009099,
	PLACE1009246,	PLACE1009308,	PLACE1009398,	PLACE1009798,	PLACE1010134,	PLACE1010702,
	PLACE1010771,	PLACE1010870,	PLACE1011160,	PLACE1011433,	PLACE1011576,	PLACE3000009,
20	PLACE3000169,	PLACE3000254,	PLACE4000128,	PLACE4000156,	PLACE4000192,	PLACE4000211,
	PLACE4000261,	PLACE4000450,	PLACE4000489,	THYRO1000085,	THYRO1000121,	THYRO1000242,
	THYRO1000488,	THYRO1000501,	THYRO1000569,	THYRO 1001100,	THYRO1001189,	THYRO1001809,
	Y79AA1000013,	Y79AA1000033,	Y79AA1000037,	Y79AA1000342,	Y79AA1000627,	Y79AA1000705,
	Y79AA1001299,	Y79AA1001312,	Y79AA1001391,	Y79AA1001533,	Y79AA1001613,	Y79AA1001866,
25	Y79AA1002103,	Y79AA1002229,	Y79AA1002433,	Y79AA1002472,	Y79AA1002482,	
	[0279] The following 392 clones are categorized into disease-associated proteins.					
	HEMBA1000020,	HEMBA1000216,	HEMBA1000304,	HEMBA1000561,	HEMBA1000569,	HEMBA1000910,
	HEMBA1001043,	HEMBA1001059,	HEMBA1001071,	HEMBA1001088,	HEMBA1001569,	HEMBA1001661,
	HEMBA1001672,	HEMBA1001819,	HEMBA1001921,	HEMBA1002267,	HEMBA1002419,	HEMBA1002469,
30	HEMBA1002547,	HEMBA1002555,	HEMBA1002810,	HEMBA1002939,	HEMBA1002997,	HEMBA1003148,
	HEMBA1003369,	HEMBA1003417,	HEMBA1003418,	HEMBA1003433,	HEMBA1003538,	HEMBA1003555,
	HEMBA1003568,	HEMBA1003569,	HEMBA1003581,	HEMBA1004168,	HEMBA1004202,	HEMBA1004248,
	HEMBA1004275,	HEMBA1004321,	HEMBA1004353,	HEMBA1004356,	HEMBA1004479,	HEMBA1004509,
	HEMBA1004669,	HEMBA1005009,	HEMBA1005338,	HEMBA1005367,	HEMBA1005423,	HEMBA1005528,
35	HEMBA1005581,	HEMBA1005621,	HEMBA1005699,	HEMBA1006507,	HEMBA1006650,	HEMBA1006652,
	HEMBA1006737,	HEMBA1006807,	HEMBA1006877,	HEMBA1007121,	HEMBA1007243,	HEMBA1007248,
	HEMBA100693,	HEMBA1006927,	HEMBA1006985,	HEMBA1007068,	HEMBA1007128,	HEMBA1007139,
	HEMBA1001482,	HEMBA1001564,	HEMBA1001802,	HEMBA1001905,	HEMBA1001908,	HEMBA1002217,
	HEMBA1002477,	MAMMA1000388,	MAMMA1000731,	MAMMA1001305,	MAMMA1001633,	MAMMA1001868,
40	MAMMA1002170,	MAMMA1002198,	MAMMA1002268,	MAMMA1002485,	MAMMA1002530,	MAMMA1002858,
	MAMMA1002869,	MAMMA1002881,	MAMMA1003047,	MAMMA1003146,	MAMMA1003166,	NT2RM1000001,
	NT2RM1000153,	NT2RM1000252,	NT2RM1000555,	NT2RM1000770,	NT2RM1000826,	NT2RM1000850,
	NT2RM1001003,	NT2RM1001092,	NT2RM1001102,	NT2RM2000191,		
	NT2RM2000363,	NT2RM2000594,	NT2RM2000624,	NT2RM2000714,	NT2RM2000821,	NT2RM2001035,
45	NT2RM2001575,	NT2RM2001652,	NT2RM2001664,	NT2RM2001668,	NT2RM2001698,	NT2RM2001803,
	NT2RM2001839,	NT2RM4000155,	NT2RM4000471,	NT2RM4000486,	NT2RM4000657,	NT2RM4000751,
	NT2RM4000996,	NT2RM4001629,	NT2RM4001810,	NT2RM4001819,	NT2RM4001865,	NT2RM4001876,
	NT2RM4001940,	NT2RM4002066,	NT2RM4002093,	NT2RM4002146,	NT2RM4002161,	NT2RM4002323,
	NT2RM4002558,	NT2RM4002571,	NT2RP1000086,	NT2RP1000574,	NT2RP1000738,	NT2RP1000825,
50	NT2RP1000833,	NT2RP1000959,	NT2RP1000966,	NT2RP1001013,	NT2RP1001185,	NT2RP1001482,
	NT2RP1001665,	NT2RP2000070,	NT2RP2000147,	NT2RP2000224,	NT2RP2000248,	NT2RP2000297,
	NT2RP2000310,	NT2RP2000414,	NT2RP2000420,	NT2RP2000523,	NT2RP2000809,	NT2RP2000812,
	NT2RP2001233,	NT2RP2001327,	NT2RP2001378,	NT2RP2001394,	NT2RP2001397,	NT2RP2001460,
	NT2RP2001520,	NT2RP2001536,	NT2RP2001876,	NT2RP2001898,	NT2RP2002025,	NT2RP2002058,
55	NT2RP2002124,	NT2RP2002325,	NT2RP2002503,	NT2RP2002959,	NT2RP2003000,	NT2RP2003157,
	NT2RP2003322,	NT2RP2003322,	NT2RP2003322,	NT2RP2003322,	NT2RP2003322,	NT2RP2003322,
	NT2RP2003373,	NT2RP2003373,	NT2RP2003373,	NT2RP2003373,	NT2RP2003373,	NT2RP2003373,
	NT2RP2004732,	NT2RP2004933,	NT2RP2005003,	NT2RP2005144,	NT2RP2005239,	NT2RP2005276,

	NT2RP2005288,	NT2RP2005315,	NT2RP2005325,	NT2RP2005336,	NT2RP2005358,	NT2RP2005407,
	NT2RP2005436,	NT2RP2005476,	NT2RP2005525,	NT2RP2005694,	NT2RP2005719,	NT2RP2006043,
	NT2RP2006071,	NT2RP2006219,	NT2RP2006312,	NT2RP2006456,	NT2RP3000050,	NT2RP3000068,
	NT2RP3000085,	NT2RP3000299,	NT2RP3000403,	NT2RP3000596,	NT2RP3000739,	NT2RP3000753,
5	NT2RP3000875,	NT2RP3001057,	NT2RP3001081,	NT2RP3001216,	NT2RP3001307,	NT2RP3001338,
	NT2RP3001427,	NT2RP3001428,	NT2RP3001679,	NT2RP3001723,	NT2RP3001855,	NT2RP3001898,
	NT2RP3001969,	NT2RP3002056,	NT2RP3002062,	NT2RP3002151,	NT2RP3002351,	NT2RP3002399,
	NT2RP3002953,	NT2RP3002988,	NT2RP3003078,	NT2RP3003251,	NT2RP3003282,	NT2RP3003313,
	NT2RP3003327,	NT2RP3003409,	NT2RP3003672,	NT2RP3003831,	NT2RP3004016,	NT2RP3004078,
10	NT2RP3004209,	NT2RP3004258,	NT2RP3004490,	NT2RP3004534,	NT2RP3004569,	NT2RP3004572,
	NT2RP4000109,	NT2RP4000367,	NT2RP4000376,	NT2RP4000449,	NT2RP4000855,	NT2RP4000879,
	NT2RP4000925,	NT2RP4001086,	NT2RP4001126,	NT2RP4001150,	NT2RP4001213,	NT2RP4001276,
	NT2RP4001407,	NT2RP4001433,	NT2RP4001483,	NT2RP4001575,	NT2RP4001760,	NT2RP4001861,
	NT2RP4002078,	NT2RP4002791,	OVARC1000014,	OVARC1000139,	OVARC1000520,	OVARC1000722,
15	OVARC1000771,	OVARC1000834,	OVARC1001051,	OVARC1001113,	OVARC1001244,	OVARC1001372,
	OVARC1001417,	OVARC1001496,	OVARC1001506,	OVARC1001577,	OVARC1001726,	OVARC1001766,
	OVARC1001809,	OVARC1002165,	PLACE1000133,	PLACE1000383,	PLACE1000420,	PLACE1000583,
	PLACE1000588,	PLACE1001171,	PLACE1001387,	PLACE1001602,	PLACE1002046,	PLACE1002140,
	PLACE1002437,	PLACE1002474,	PLACE1002685,	PLACE1002782,	PLACE1002834,	PLACE1002908,
20	PLACE1003045,	PLACE1003302,	PLACE1003353,	PLACE1003366,	PLACE1003493,	PLACE1003669,
	PLACE1003704,	PLACE1003903,	PLACE1003968,	PLACE1004183,	PLACE1004197,	PLACE1004277,
	PLACE1004316,	PLACE1004358,	PLACE1004471,	PLACE1004506,	PLACE1004510,	PLACE1004674,
	PLACE1004777,	PLACE1004814,	PLACE1005494,	PLACE1006040,	PLACE1006170,	PLACE1006438,
	PLACE1006615,	PLACE1007140,	PLACE1007239,	PLACE1007257,	PLACE1007511,	PLACE1007598,
25	PLACE1008177,	PLACE1008356,	PLACE1008402,	PLACE1008696,	PLACE1009027,	PLACE1009113,
	PLACE1009158,	PLACE1009444,	PLACE1009524,	PLACE1010529,	PLACE1010870,	PLACE1010896,
	PLACE1011635,	PLACE1011858,	PLACE1011922,	PLACE2000015,	PLACE2000072,	PLACE2000216,
	PLACE2000399,	PLACE2000438,	PLACE2000458,	PLACE3000242,	PLACE4000009,	PLACE4000014,
	PLACE4000156,	PLACE4000369,	SKNMC1000046,	SKNMC1000050,	THYRO1000034,	THYRO1000327,
30	THYRO1000343,	THYRO1000358,	THYRO1000501,	THYRO1000662,	THYRO1000684,	THYRO1000748,
	THYRO1000934,	THYRO1001120,	THYRO1001189,	THYRO1001204,	THYRO1001458,	THYRO1001617,
	THYRO1001671,	Y79AA1000346,	Y79AA1000469,	Y79AA1000560,	Y79AA1000734,	Y79AA1000782,
	Y79AA1001391,	Y79AA1001548,	Y79AA1001594,	Y79AA1001711,	Y79AA1001874,	Y79AA1002204,
	Y79AA1002210,	Y79AA1002258,	Y79AA1002472,	Y79AA1002482,		
35	[0280] Among them, Swiss-Prot database search and GenBank or UniGene database search revealed that the following 380 clones matched the data of genes or proteins which had been registered in the database of Online Mendelian Inheritance in Man (OMIM) (http://www.ncbi.nlm.nih.gov/Omim/), which is a database of human genes and diseases. (The corresponding OMIM numbers are parenthetically indicated following the clone names.)					
	HEMBB1000985(147485),	HEMBB1001068(603142),	HEMBB1001282(182900),	HEMBB1001339(300080),		
40	HEMBB1001482(603971),	HEMBB1001564(603931),	HEMBB1001802(125660),	HEMBB1001905(190370),		
	HEMBB1001908(601408),	HEMBB1002217(603971),	HEMBB1002477(604439),	MAMMA1000388(604865),		
	MAMMA1000731(602118),	MAMMA1001305(602732),	MAMMA1001633(600834),	MAMMA1001868(190370),		
	MAMMA1002170(603624),	MAMMA1002198(600538),	MAMMA1002268(603730),	MAMMA1002485(603665),		
	MAMMA1002530(603602),	MAMMA1002858(601064),	MAMMA1002869(602567),	MAMMA1002881(602692),		
45	MAMMA1003047(603566),	MAMMA1003146(603094),	MAMMA1003166(604061),	NT2RM1000001(601169),		
	NT2RM1000153(600417),	NT2RM1000252(604108),	NT2RM1000555(191510),	NT2RM1000770(300061),		
	NT2RM1000826(191510),	NT2RM1000850(182900),	NT2RM1001003(604785),	NT2RM1001092(603971),		
	NT2RM1001102(604533),	NT2RM2000191(602973),	NT2RM2000363(151410),	NT2RM2000594(602900),		
	NT2RM2000624(601940),	NT2RM2000714(179555),	NT2RM2000821(600959),	NT2RM2001035(604913),		
50	NT2RM2001575(109092),	NT2RM2001652(604141),	NT2RM2001664(603722),	NT2RM2001668(602952),		
	NT2RM2001698(604327),	NT2RM2001803(603722),	NT2RM2001839(603420),	NT2RM4000155(187790),		
	NT2RM4000471(603485),	NT2RM4000486(168730),	NT2RM4000657(602142),	NT2RM4000751(602277),		
	NT2RM4000996(603971),	NT2RM4001629(601114),	NT2RM4001810(155760),	NT2RM4001819(176873),		
	NT2RM4001876(179555),	NT2RM4001940(603887),	NT2RM4002066(300188),	NT2RM4002093(600693),		
55	NT2RM4002146(602603),	NT2RM4002161(254780),	NT2RM4002558(604194),	NT2RM4002571(602274),		
	NT2RP1000959(180511),	NT2RP1000966(164035),	NT2RP1001013(194558),	NT2RP1001185(243500),		
	NT2RP1001482(600586),	NT2RP1001665(114180),	NT2RP2000070(600976),	NT2RP2000147(603535),		

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	NT2RP2000248(603367),	NT2RP2000297(602277),	NT2RP2000310(239500),	NT2RP2000414(601037),
	NT2RP2000420(600834),	NT2RP2000523(600130),	NT2RP2000809(603885),	NT2RP2000812(160777),
	NT2RP2001233(603971),	NT2RP2001327(191161),	NT2RP2001378(158370),	NT2RP2001394(300208),
	NT2RP2001397(602755),	NT2RP2001460(190370),	NT2RP2001520(603667),	NT2RP2001536(600675),
5	NT2RP2001876(601833),	NT2RP2001898(147264),	NT2RP2002025(601581),	NT2RP2002058(604737),
	NT2RP2002124(603486),	NT2RP2002325(603866),	NT2RP2002503(601781),	NT2RP2002959(602962),
	NT2RP2003000(191161),	NT2RP2003157(601940),	NT2RP2003164(604746),	NT2RP2003228(602638),
	NT2RP2003295(603494),	NT2RP2003517(190040),	NT2RP2003564(109092),	NT2RP2003604(604785),
	NT2RP2003714(603971),	NT2RP2003737(602962),	NT2RP2003952(602675),	NT2RP2004013(602542),
10	NT2RP2004170(300196),	NT2RP2004587(162250),	NT2RP2004732(162250),	NT2RP2004933(603289),
	NT2RP2005003(109092),	NT2RP2005144(604730),	NT2RP2005239(603485),	NT2RP2005276(602371),
	NT2RP2005288(603524),	NT2RP2005315(604039),	NT2RP2005325(603759),	NT2RP2005336(190370),
	NT2RP2005358(603573),	NT2RP2005407(167040),	NT2RP2005436(601940),	NT2RP2005476(602680),
	NT2RP2005525(602655),	NT2RP2005719(601178),	NT2RP2006043(601940),	NT2RP2006071(604299),
15	NT2RP2006219(601279),	NT2RP2006312(603111),	NT2RP2006456(604619),	NT2RP3000050(603971),
	NT2RP3000068(182530),	NT2RP3000085(300032),	NT2RP3000299(602941),	NT2RP3000403(604981),
	NT2RP3000596(190370),	NT2RP3000739(125370),	NT2RP3000753(162230),	NT2RP3001057(603971),
	NT2RP3001081(603524),	NT2RP3001216(603121),	NT2RP3001307(180069),	NT2RP3001338(314998),
	NT2RP3001428(189940),	NT2RP3001723(604569),	NT2RP3001855(602100),	NT2RP3001898(604561),
20	NT2RP3001969(190370),	NT2RP3002056(180201),	NT2RP3002062(603885),	NT2RP3002151(139259),
	NT2RP3002351(604887),	NT2RP3002399(602638),	NT2RP3002953(604967),	NT2RP3002988(603258),
	NT2RP3003251(109092),	NT2RP3003282(602378),	NT2RP3003313(603810),	NT2RP3003409(604533),
	NT2RP3003672(313470),	NT2RP3003831(604051),	NT2RP3004016(601742),	NT2RP3004078(142765),
	NT2RP3004209(125255),	NT2RP3004258(604347),	NT2RP3004490(603328),	NT2RP3004534(600586),
25	NT2RP3004569(106410),	NT2RP3004572(604912),	NT2RP4000109(603745),	NT2RP4000367(603722),
	NT2RP4000376(603873),	NT2RP4000449(604479),	NT2RP4000855(602675),	NT2RP4000879(314370),
	NT2RP4000925(600245),	NT2RP4001086(162230),	NT2RP4001126(190370),	NT2RP4001150(601581),
	NT2RP4001213(602277),	NT2RP4001276(190370),	NT2RP4001407(190370),	NT2RP4001433(602277),
	NT2RP4001483(203740),	NT2RP4001575(603443),	NT2RP4001760(305400),	NT2RP4001861(190370),
30	NT2RP4002078(603971),	NT2RP4002791(189940),	OVARC1000014(603371),	OVARC1000139(603486),
	OVARC1000520(604126),	OVARC1000722(604014),	OVARC1000771(179509),	OVARC1001051(600051),
	OVARC1001113(602121),	OVARC1001244(601540),	OVARC1001372(603145),	OVARC1001417(300182),
	OVARC1001496(602619),	OVARC1001506(601313),	OVARC1001577(603269),	OVARC1001726(300103),
	OVARC1001766(603910),	OVARC1001809(603730),	PLACE1000133(602542),	PLACE1000383(300171),
35	PLACE1000420(600312),	PLACE1000583(194558),	PLACE1000588(600411),	PLACE1001171(310400),
	PLACE1001387(600206),	PLACE1001602(604913),	PLACE1002046(151625),	PLACE1002140(603748),
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	PLACE1002834(194558),	PLACE1002908(604327),	PLACE1003045(173910),	PLACE1003302(194558),
	PLACE1003353(604704),	PLACE1003366(603681),	PLACE1003493(601456),	PLACE1003669(190370),
40	PLACE1003704(601940),	PLACE1003903(123860),	PLACE1003968(602742),	PLACE1004183(604701),
	PLACE1004197(601610),	PLACE1004277(603493),	PLACE1004316(604261),	PLACE1004358(603272),
	PLACE1004471(194558),	PLACE1004506(603450),	PLACE1004510(604912),	PLACE1004674(601057),
	PLACE1004777(118423),	PLACE1004814(601940),	PLACE1005494(603652),	PLACE1006040(603061),
	PLACE1006170(601026),	PLACE1006438(600834),	PLACE1006615(603910),	PLACE1007140(190370),
45	PLACE1007239(604784),	PLACE1007257(300108),	PLACE1007511(148020),	PLACE1007598(602277),
	PLACE1008177(190370),	PLACE1008356(604039),	PLACE1008402(603344),	PLACE1008696(602141),
	PLACE1009027(300121),	PLACE1009113(600675),	PLACE1009158(604140),	PLACE1009444(600286),
	PLACE1009524(602488),	PLACE1010529(604834),	PLACE1010870(603971),	PLACE1010896(160776),
	PLACE1011635(604058),	PLACE1011858(603882),	PLACE1011922(160776),	PLACE2000015(600051),
50	PLACE2000072(603430),	PLACE2000216(182790),	PLACE2000399(313470),	PLACE2000438(602273),
	PLACE2000458(600976),	PLACE3000242(300132),	PLACE4000009(160776),	PLACE4000014(300032),
	PLACE4000156(603971),	PLACE4000369(603808),	SKNMC1000046(603144),	SKNMC1000050(114230),
	THYRO1000034(190370),	THYRO1000327(603243),	THYRO1000343(125370),	THYRO1000358(604188),
	THYRO1000501(109092),	THYRO1000662(278750),	THYRO1000684(603885),	THYRO1000748(300023),
55	THYRO1000934(179035),	THYRO1001120(602582),	THYRO1001189(603971),	THYRO1001204(603169),
	79AA1000469(602434),	79AA1000560(601026),	79AA1000734(603867),	79AA1000782(600417),
	79AA1001391(142959),	79AA1001548(600286),	79AA1001594(600936),	79AA1001711(600063),

Y79AA1001874(600315), Y79AA1002204(605033), Y79AA1002210(191161), Y79AA1002472(603971),
Y79AA1002482(603971).

[0281] The following 425 clones presumably belong to enzymes and/or metabolism-associated proteins.

	HEMBA100012,	HEMBA1000129,	HEMBA1000141,	HEMBA1000150,	HEMBA1000542,	HEMBA1000852,
5	HEMBA1001019,	HEMBA1001257,	HEMBA1001526,	HEMBA1001620,	HEMBA1001866,	HEMBA1001896,
	HEMBA1002212,	HEMBA1002513,	HEMBA1002746,	HEMBA1002973,	HEMBA1003046,	HEMBA1003136,
	HEMBA1003179,	HEMBA1003250,	HEMBA1003291,	HEMBA1003408,	HEMBA1003538,	HEMBA1003679,
	HEMBA1003680,	HEMBA1004199,	HEMBA1004227,	HEMBA1004408,	HEMBA1004509,	HEMBA1004734,
	HEMBA1004768,	HEMBA1005394,	HEMBA1005513,	HEMBA1005737,	HEMBA1005815,	HEMBA1006031,
10	HEMBA1006272,	HEMBA1006278,	HEMBA1006291,	HEMBA1006309,	HEMBA1006347,	HEMBA1006485,
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[0282] The following 217 clones presumably belong to a group of cDNAs encoding ATP- and/or GTP-binding proteins.

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[0283] The following 320 clones presumably belong to nuclear proteins

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	THYRO1000585,	THYRO1001100,	THYRO1001189,	THYRO1001809,	Y79AA1000037,	Y79AA1000214,
50	Y79AA1000231,	Y79AA1000589,	Y79AA1000752,	Y79AA1001391,	Y79AA1001613,	Y79AA1001705,
	Y79AA1001963,	Y79AA1002431,	Y79AA1002472,	Y79AA1002482		

[0284] The following 292 clones presumably belong to DNA- and/or RNA-binding proteins.

	HEMBA1000158,	HEMBA1000216,	HEMBA1000561,	HEMBA1000591,	HEMBA1000851,	HEMBA1001088,
	HEMBA1001137,	HEMBA1001405,	HEMBA1001510,	HEMBA1001804,	HEMBA1001809,	HEMBA1001819,
55	HEMBA1001847	HEMBA1001869	HEMBA1002177	HEMBA1002935	HEMBA1003408	HEMBA1003545
	HEMBA1003561	HEMBA1003569	HEMBA1003666	HEMBA1003684	HEMBA1003760	HEMBA1004203
	HEMBA1003805	HEMBA1003953	HEMBA1004321	HEMBA1004354	HEMBA1004389	HEMBA1004479
	HEMBA1004669	HEMBA1004847	HEMBA1004973	HEMBA1005202	HEMBA1005359	HEMBA1005931

	HEMBA1006248,	HEMBA1006278,	HEMBA1006283,	HEMBA1006359,	HEMBA1006652,	HEMBA1007087,
	HEMBA1007194,	HEMBA1000264,	HEMBA1000789,	HEMBA1001011,	HEMBA1001482,	HEMBA1001736,
	HEMBA1001749,	HEMBA1001839,	HEMBA1002217,	MAMMA1000183,	MAMMA1000284,	MAMMA1000731,
	MAMMA1001105,	MAMMA1001222,	MAMMA1001260,	MAMMA1001743,	MAMMA1001837,	MAMMA1002385,
5	MAMMA1002617,	MAMMA1002869,	MAMMA1002937,	MAMMA1003011,	NT2RM1000086,	NT2RM1000539,
	NT2RM1000555,	NT2RM1000666,	NT2RM1000691,	NT2RM1000826,	NT2RM1000885,	NT2RM1001059,
	NT2RM1001092,	NT2RM2000371,	NT2RM2000624,	NT2RM2000735,	NT2RM2001105,	NT2RM2001424,
	NT2RM2001575,	NT2RM2001605,	NT2RM2001670,	NT2RM2001771,	NT2RM2001823,	NT2RM2001989,
	NT2RM2002004,	NT2RM2002014,	NT2RM2002088,	NT2RM2002091,	NT2RM4000046,	NT2RM4000104,
10	NT2RM4000167,	NT2RM4000191,	NT2RM4000202,	NT2RM4000531,	NT2RM4000595,	NT2RM4000733,
	NT2RM4000751,	NT2RM4000996,	NT2RM4001092,	NT2RM4001140,		
	NT2RM4001178,	NT2RM4001200,	NT2RM4001483,	NT2RM4001592,	NT2RM4001783,	NT2RM4001823,
	NT2RM4001828,	NT2RM4001858,	NT2RM4001880,	NT2RM4001979,	NT2RM4002093,	NT2RM4002109,
	NT2RP1000470,	NT2RP1000493,	NT2RP1000574,	NT2RP1000902,	NT2RP1000966,	NT2RP1001013,
15	NT2RP1001073,	NT2RP1001080,	NT2RP2000008,	NT2RP2000153,	NT2RP2000258,	NT2RP2000297,
	NT2RP2001127,	NT2RP2001174,	NT2RP2001233,	NT2RP2001511,	NT2RP2001756,	NT2RP2001869,
	NT2RP2002079,	NT2RP2002099,	NT2RP2002503,	NT2RP2002591,	NT2RP2002939,	NT2RP2003157,
	NT2RP2003329,	NT2RP2003347,	NT2RP2003480,	NT2RP2003522,	NT2RP2003564,	NT2RP2003714,
	NT2RP2004187,	NT2RP2004568,	NT2RP2004920,	NT2RP2005003,	NT2RP2005139,	NT2RP2005168,
20	NT2RP2005436,	NT2RP2005496,	NT2RP2005701,	NT2RP2005763,	NT2RP2005776,	NT2RP2005942,
	NT2RP2006043,	NT2RP2006436,	NT2RP2006464,	NT2RP3000050,	NT2RP3000512,	NT2RP3000527,
	NT2RP3000562,	NT2RP3000590,	NT2RP3000603,	NT2RP3000624,	NT2RP3000632,	NT2RP3000994,
	NT2RP3001057,	NT2RP3001107,	NT2RP3001120,	NT2RP3001150,	NT2RP3001155,	NT2RP3001338,
	NT2RP3001398,	NT2RP3001472,	NT2RP3001672,	NT2RP3001688,	NT2RP3001724,	NT2RP3001792,
25	NT2RP3001855,	NT2RP3002165,	NT2RP3002399,	NT2RP3002876,	NT2RP3003138,	NT2RP3003193,
	NT2RP3003251,	NT2RP3003327,	NT2RP3003555,	NT2RP3004013,	NT2RP3004078,	NT2RP3004428,
	NT2RP3004490,	NT2RP3004566,	NT2RP3004594,	NT2RP3004617,	NT2RP3004618,	NT2RP4000111,
	NT2RP4000398,	NT2RP4000455,	NT2RP4000518,	NT2RP4000648,	NT2RP4000865,	NT2RP4000929,
	NT2RP4001080,	NT2RP4001095,	NT2RP4001213,	NT2RP4001433,	NT2RP4001568,	NT2RP4001696,
30	NT2RP4001753,	NT2RP4001838,	NT2RP4001938,	NT2RP4002078,	OVARC1000006,	OVARC1000087,
	OVARC1000241,	OVARC1000746,	OVARC1000846,	OVARC1001232,	OVARC1001271,	OVARC1001306,
	OVARC1001987,	OVARC1002112,	PLACE1000406,	PLACE1000583,	PLACE1000979,	PLACE1001118,
	PLACE1001632,	PLACE1001739,	PLACE1002438,	PLACE1002532,	PLACE1002775,	PLACE1002834,
	PLACE1003302,	PLACE1003519,	PLACE1003605,	PLACE1003704,	PLACE1003738,	PLACE1003885,
35	PLACE1004471,	PLACE1004564,	PLACE1004814,	PLACE1005584,	PLACE1005876,	PLACE1005951,
	PLACE1006196,	PLACE1006482,	PLACE1006488,	PLACE1006531,	PLACE1006917,	PLACE1007346,
	PLACE1007547,	PLACE1007598,	PLACE1007688,	PLACE1007969,	PLACE1008132,	PLACE1009099,
	PLACE1009246,	PLACE1009398,	PLACE1009476,	PLACE1009622,	PLACE1010053,	PLACE1010194,
	PLACE1010702,	PLACE1010870,	PLACE1011056,	PLACE1011114,	PLACE1011433,	PLACE2000427,
40	PLACE3000009,	PLACE3000169,	PLACE4000014,	PLACE4000156,	PLACE4000192,	PLACE4000261,
	PLACE4000489,	SKNMC1000091,	THYRO1000085,	THYRO1000242,	THYRO1000501,	THYRO1001100,
	THYRO1001189,	THYRO1001809,	Y79AA1000037,	Y79AA1000349,	Y79AA1000752,	Y79AA1001211,
	Y79AA1001312,	Y79AA1001391,	Y79AA1001613,	Y79AA1002103,	Y79AA1002472,	Y79AA1002482,
	[0285] The following 66 clones presumably belong to the category of RNA synthesis-associated proteins.					
45	HEMBA1000591,	HEMBA1001579,	HEMBA1003179,	HEMBA1003591,	HEMBA1006278,	HEMBA1000226,
	NT2RM1000187,	NT2RM1000852,	NT2RM2000624,	NT2RM2001989,	NT2RM2002100,	NT2RM4000191,
	NT2RM4001178,	NT2RM4002093,	NT2RP1000035,	NT2RP1000272,	NT2RP1000470,	NT2RP1001080,
	NT2RP2000153,	NT2RP2002928,	NT2RP2003157,	NT2RP2004568,	NT2RP2005126,	NT2RP2005436,
	NT2RP2005539,	NT2RP2005605,	NT2RP2005776,	NT2RP2005942,	NT2RP2006043,	NT2RP2006238,
50	NT2RP3000361,	NT2RP3000397,	NT2RP3001671,	NT2RP3004504,	NT2RP4000078,	NT2RP4000111,
	NT2RP4000481,	NT2RP4000518,	NT2RP4000614,	NT2RP4000929,	NT2RP4001696,	NT2RP4002058,
	OVARC1001232,	OVARC1001577,	PLACE1000406,	PLACE1000596,	PLACE1000755,	PLACE1001739,
	PLACE1003704,	PLACE1003885,	PLACE1004564,	PLACE1004814,	PLACE1004902,	PLACE1005373,
	PLACE1005646,	PLACE1005876,	PLACE1006196,	PLACE1006626,	PLACE1006878,	PLACE1006917,
55	PLACE1009476,	PLACE1009925,	PLACE1010194,	PLACE1011114,	THYRO1000121,	Y79AA1001963
	[0286]					
	ated proteins.					
	HEMBA1000012,	HEMBA1000141,	HEMBA1000592,	HEMBA1003617,	HEMBA1003773,	HEMBA1004202,

	HEMBA1004276,	HEMBA1004734,	HEMBA1004847,	HEMBA1004929,	HEMBA1004930,	HEMBA1005047,
	HEMBA1005202,	HEMBA1006031,	HEMBA1006272,	HEMBA1006474,	HEMBA1006652,	HEMBA1006914,
	HEMBA1006973,	HEMBA1007224,	HEMBA1000915,	HEMBA1001112,	HEMBA1001137,	HEMBA1001736,
	HEMBA1001831,	HEMBA1001915,	MAMMA1000085,	MAMMA1000734,	MAMMA1001008,	MAMMA1002170,
5	MAMMA1002219,	MAMMA1002236,	MAMMA1002619,	NT2RM1000661,	NT2RM1000833,	NT2RM2000092,
	NT2RM2000504,	NT2RM2000577,	NT2RM2000821,	NT2RM2001201,	NT2RM2001592,	NT2RM2001613,
	NT2RM2001648,	NT2RM2001730,	NT2RM2001760,	NT2RM2002055,	NT2RM4000155,	NT2RM4000169,
	NT2RM4000344,	NT2RM4000356,	NT2RM4000421,	NT2RM4000712,	NT2RM4001054,	NT2RM4001203,
	NT2RM4001382,	NT2RM4001444,	NT2RM4002062,	NT2RM4002205,	NT2RM4002623,	NT2RP1000326,
10	NT2RP1000522,	NT2RP1000547,	NT2RP1000746,	NT2RP1000947,	NT2RP1001569,	NT2RP2000147,
	NT2RP2000710,	NT2RP2000880,	NT2RP2000943,	NT2RP2001290,	NT2RP2001392,	NT2RP2001601,
	NT2RP2001613,	NT2RP2001660,	NT2RP2001740,	NT2RP2002124,	NT2RP2002606,	NT2RP2002862,
	NT2RP2002959,	NT2RP2002980,	NT2RP2003137,	NT2RP2003158,	NT2RP2003391,	NT2RP2003394,
	NT2RP2003401,	NT2RP2003433,	NT2RP2003704,	NT2RP2003713,	NT2RP2003737,	NT2RP2003760,
15	NT2RP2003981,	NT2RP2004366,	NT2RP2004389,	NT2RP2004791,	NT2RP2005012,	NT2RP2005116,
	NT2RP2005360,	NT2RP2005763,	NT2RP2005784,	NT2RP3000366,		
	NT2RP3000759,	NT2RP3000968,	NT2RP3001113,	NT2RP3001690,	NT2RP3002045,	NT2RP3002151,
	NT2RP3002529,	NT2RP3002671,	NT2RP3003301,	NT2RP3003846,	NT2RP3003876,	NT2RP3004209,
	NT2RP4000370,	NT2RP4000457,	NT2RP4000879,	NT2RP4000927,	NT2RP4001041,	NT2RP4001117,
20	NT2RP4001313,	NT2RP4001315,	NT2RP4001574,	NT2RP4001592,	OVARC1000013,	OVARC1000071,
	OVARC1000085,	OVARC1000465,	OVARC1000564,	OVARC1000771,	OVARC1000862,	OVARC1001171,
	OVARC1001180,	OVARC1001342,	PLACE1000007,	PLACE1000061,	PLACE1000081,	PLACE1000492,
	PLACE1000863,	PLACE1001092,	PLACE1001748,	PLACE1002090,	PLACE1003174,	PI ACF1003915,
	PLACE1004104,	PLACE1004270,	PLACE1004743,	PLACE1005557,	PLACE1005813,	PLACE1006170,
25	PLACE1006488,	PLACE1006829,	PLACE1007706,	PLACE1007729,	PLACE1008273,	PLACE1008402,
	PLACE1008790,	PLACE1008813,	PLACE1009094,	PLACE1009130,	PLACE1009477,	PLACE1009721,
	PLACE1009845,	PLACE1010074,	PLACE1010547,	PLACE1011109,	PLACE1011229,	PLACE1011477,
	PLACE1012031,	PLACE2000404,	PLACE3000059,	PLACE3000121,	PLACE4000269,	PLACE4000654,
	SKNMC1000011,	THYRO1000983,	THYRO1001003,	THYRO1001313,	Y79AA1000560,	Y79AA1000784,
30	Y79AA1000968,	Y79AA1001493,	Y79AA1001875,	Y79AA1002027,	Y79AA1002209,	
	[0287] The following 130 clones presumably belong to cytoskeletal-associated proteins.					
	HEMBA1000156,	HEMBA1000168,	HEMBA1000411,	HEMBA1000588,	HEMBA1001043,	HEMBA1001651,
	HEMBA1001661,	HEMBA1002102,	HEMBA1002161,	HEMBA1002939,	HEMBA1003235,	HEMBA1003581,
	HEMBA1004499,	HEMBA1004534,	HEMBA1004697,	HEMBA1004929,	HEMBA1004972,	HEMBA1005582,
35	HEMBA1005595,	HEMBA1006344,	HEMBA1006737,	HEMBA1001175,	HEMBA1001282,	HEMBA1001562,
	HEMBA1001802,	MAMMA1000824,	MAMMA1001041,	MAMMA1001576,	MAMMA1001679,	MAMMA1001735,
	MAMMA1002297,	MAMMA1002351,	MAMMA1002622,	MAMMA1002637,	MAMMA1003127,	NT2RM1000850,
	NT2RM1000898,	NT2RM2000030,	NT2RM2000260,	NT2RM2000691,	NT2RM2001324,	NT2RM4000169,
	NT2RM4000229,	NT2RM4000515,	NT2RM4001217,	NT2RP1000202,	NT2RP1000348,	NT2RP1000460,
40	NT2RP1000478,	NT2RP1001033,	NT2RP1001294,	NT2RP1001302,	NT2RP2000070,	NT2RP2000812,
	NT2RP2000814,	NT2RP2001168,	NT2RP2001245,	NT2RP2001634,	NT2RP2001900,	NT2RP2003307,
	NT2RP2003394,	NT2RP2004041,	NT2RP2004242,	NT2RP2004538,	NT2RP2004587,	NT2RP2004681,
	NT2RP2004732,	NT2RP2004978,	NT2RP2005491,	NT2RP2005531,	NT2RP2005712,	NT2RP2006275,
	NT2RP3000753,	NT2RP3001113,	NT2RP3001216,	NT2RP3001239,	NT2RP3001272,	NT2RP3001554,
45	NT2RP3001690,	NT2RP3001799,	NT2RP3002688,	NT2RP3003061,	NT2RP3003185,	NT2RP3003230,
	NT2RP3004569,	NT2RP3004578,	NT2RP4001004,	NT2RP4001086,	NT2RP4001256,	NT2RP4001567,
	NT2RP4001927,	OVARC1000001,	OVARC1000106,	OVARC1000437,	OVARC1000520,	OVARC1000679,
	OVARC1001731,	OVARC1002050,	PLACE1001104,	PLACE1002571,		
	PLACE1002591,	PLACE1002655,	PLACE1002714,	PLACE1003625,	PLACE1005287,	PLACE1006552,
50	PLACE1007946,	PLACE1008426,	PLACE1010148,	PLACE1010547,	PLACE1010743,	PLACE1010896,
	PLACE1010960,	PLACE1011310,	PLACE1011922,	PLACE2000216,	PLACE2000274,	PLACE2000371,
	PLACE2000458,	PLACE3000145,	PLACE3000416,	PLACE4000009,	THYRO1000132,	THYRO1001405,
	THYRO1001458,	Y79AA1000368,	Y79AA1000794,	Y79AA1000833,	Y79AA1000962,	Y79AA1002208,
	[0288] The following 54 clones presumably belong to cell division-associated and/or cell proliferation-associated proteins					
55	HEMBA1000156,	HEMBA1000168,	HEMBA1000411,	HEMBA1000588,	HEMBA1001043,	HEMBA1001651,
	HEMBA1001661,	HEMBA1002102,	HEMBA1002161,	HEMBA1002939,	HEMBA1003235,	HEMBA1003581,
	HEMBA1004499,	HEMBA1004534,	HEMBA1004697,	HEMBA1004929,	HEMBA1004972,	HEMBA1005582,
35	HEMBA1005595,	HEMBA1006344,	HEMBA1006737,	HEMBA1001175,	HEMBA1001282,	HEMBA1001562,
	HEMBA1001802,	MAMMA1000824,	MAMMA1001041,	MAMMA1001576,	MAMMA1001679,	MAMMA1001735,
	MAMMA1002297,	MAMMA1002351,	MAMMA1002622,	MAMMA1002637,	MAMMA1003127,	NT2RM1000850,
	NT2RM1000898,	NT2RM2000030,	NT2RM2000260,	NT2RM2000691,	NT2RM2001324,	NT2RM4000169,
	NT2RM4000229,	NT2RM4000515,	NT2RM4001217,	NT2RP1000202,	NT2RP1000348,	NT2RP1000460,
40	NT2RP1000478,	NT2RP1001033,	NT2RP1001294,	NT2RP1001302,	NT2RP2000070,	NT2RP2000812,
	NT2RP2000814,	NT2RP2001168,	NT2RP2001245,	NT2RP2001634,	NT2RP2001900,	NT2RP2003307,
	NT2RP2003394,	NT2RP2004041,	NT2RP2004242,	NT2RP2004538,	NT2RP2004587,	NT2RP2004681,
	NT2RP2004732,	NT2RP2004978,	NT2RP2005491,	NT2RP2005531,	NT2RP2005712,	NT2RP2006275,
	NT2RP3000753,	NT2RP3001113,	NT2RP3001216,	NT2RP3001239,	NT2RP3001272,	NT2RP3001554,
45	NT2RP3001690,	NT2RP3001799,	NT2RP3002688,	NT2RP3003061,	NT2RP3003185,	NT2RP3003230,
	NT2RP3004569,	NT2RP3004578,	NT2RP4001004,	NT2RP4001086,	NT2RP4001256,	NT2RP4001567,
	NT2RP4001927,	OVARC1000001,	OVARC1000106,	OVARC1000437,	OVARC1000520,	OVARC1000679,
	OVARC1001731,	OVARC1002050,	PLACE1001104,	PLACE1002571,		
	PLACE1002591,	PLACE1002655,	PLACE1002714,	PLACE1003625,	PLACE1005287,	PLACE1006552,
50	PLACE1007946,	PLACE1008426,	PLACE1010148,	PLACE1010547,	PLACE1010743,	PLACE1010896,
	PLACE1010960,	PLACE1011310,	PLACE1011922,	PLACE2000216,	PLACE2000274,	PLACE2000371,
	PLACE2000458,	PLACE3000145,	PLACE3000416,	PLACE4000009,	THYRO1000132,	THYRO1001405,
	THYRO1001458,	Y79AA1000368,	Y79AA1000794,	Y79AA1000833,	Y79AA1000962,	Y79AA1002208,
	[0288] The following 54 clones presumably belong to cell division-associated and/or cell proliferation-associated proteins					
55	HEMBA1000156,	HEMBA1000168,	HEMBA1000411,	HEMBA1000588,	HEMBA1001043,	HEMBA1001651,
	HEMBA1001661,	HEMBA1002102,	HEMBA1002161,	HEMBA1002939,	HEMBA1003235,	HEMBA1003581,
	HEMBA1004499,	HEMBA1004534,	HEMBA1004697,	HEMBA1004929,	HEMBA1004972,	HEMBA1005582,
35	HEMBA1005595,	HEMBA1006344,	HEMBA1006737,	HEMBA1001175,	HEMBA1001282,	HEMBA1001562,
	HEMBA1001802,	MAMMA1000824,	MAMMA1001041,	MAMMA1001576,	MAMMA1001679,	MAMMA1001735,
	MAMMA1002297,	MAMMA1002351,	MAMMA1002622,	MAMMA1002637,	MAMMA1003127,	NT2RM1000850,
	NT2RM1000898,	NT2RM2000030,	NT2RM2000260,	NT2RM2000691,	NT2RM2001324,	NT2RM4000169,
	NT2RM4000229,	NT2RM4000515,	NT2RM4001217,	NT2RP1000202,	NT2RP1000348,	NT2RP1000460,
40	NT2RP1000478,	NT2RP1001033,	NT2RP1001294,	NT2RP1001302,	NT2RP2000070,	NT2RP2000812,
	NT2RP2000814,	NT2RP2001168,	NT2RP2001245,	NT2RP2001634,	NT2RP2001900,	NT2RP2003307,
	NT2RP2003394,	NT2RP2004041,	NT2RP2004242,	NT2RP2004538,	NT2RP2004587,	NT2RP2004681,
	NT2RP2004732,	NT2RP2004978,	NT2RP2005491,	NT2RP2005531,	NT2RP2005712,	NT2RP2006275,
	NT2RP3000753,	NT2RP3001113,	NT2RP3001216,	NT2RP3001239,	NT2RP3001272,	NT2RP3001554,
45	NT2RP3001690,	NT2RP3001799,	NT2RP3002688,	NT2RP3003061,	NT2RP3003185,	NT2RP3003230,
	NT2RP3004569,	NT2RP3004578,	NT2RP4001004,	NT2RP4001086,	NT2RP4001256,	NT2RP4001567,
	NT2RP4001927,	OVARC1000001,	OVARC1000106,	OVARC1000437,	OVARC1000520,	OVARC1000679,
	OVARC1001731,	OVARC1002050,	PLACE1001104,	PLACE1002571,		
	PLACE1002591,	PLACE1002655,	PLACE1002714,	PLACE1003625,	PLACE1005287,	PLACE1006552,
50	PLACE1007946,	PLACE1008426,	PLACE1010148,	PLACE1010547,	PLACE1010743,	PLACE1010896,
	PLACE1010960,	PLACE1011310,	PLACE1011922,	PLACE2000216,	PLACE2000274,	PLACE2000371,
	PLACE2000458,	PLACE3000145,	PLACE3000416,	PLACE4000009,	THYRO1000132,	THYRO1001405,
	THYRO1001458,	Y79AA1000368,	Y79AA1000794,	Y79AA1000833,	Y79AA1000962,	Y79AA1002208,
	[0288] The following 54 clones presumably belong to cell division-associated and/or cell proliferation-associated proteins					
55	HEMBA1000156,	HEMBA1000168,	HEMBA1000411,	HEMBA1000588,	HEMBA1001043,	HEMBA1001651,
	HEMBA1001661,	HEMBA1002102,	HEMBA1002161,	HEMBA1002939,	HEMBA1003235,	HEMBA1003581,
	HEMBA1004499,	HEMBA1004534,	HEMBA1004697,	HEMBA1004929,	HEMBA1004972,	HEMBA1005582,
35	HEMBA1005595,	HEMBA1006344,	HEMBA1006737,	HEMBA1001175,	HEMBA1001282,	HEMBA1001562,
	HEMBA1001802,	MAMMA1000824,	MAMMA1001041,	MAMMA1001576,	MAMMA1001679,	MAMMA1001735,
	MAMMA1002297,	MAMMA1002351,	MAMMA1002622,	MAMMA1002637,	MAMMA1003127,	NT2RM1000850,
	NT2RM1000898,	NT2RM2000030,	NT2RM2000260,	NT2RM2000691,	NT2RM2001324,	NT2RM4000169,
	NT2RM4000229,	NT2RM4000515,	NT2RM4001217,	NT2RP1000202,	NT2RP1000348,	NT2RP1000460,
40	NT2RP1000478,	NT2RP1001033,	NT2RP1001294,	NT2RP1001302,	NT2RP2000070,	NT2RP2000812,
	NT2RP2000814,	NT2RP2001168,	NT2RP2001245,	NT2RP2001634,	NT2RP2001900,	NT2RP2003307,
	NT2RP2003394,	NT2RP2004041,	NT2RP2004242,	NT2RP2004538,	NT2RP2004587,	NT2RP2004681,
	NT2RP2004732,	NT2RP2004978,	NT2RP2005491,	NT2RP2005531,	NT2RP2005712,	NT2RP2006275,
	NT2RP3000753,	NT2RP3001113,	NT2RP3001216,	NT2RP3001239,	NT2RP3001272,	NT2RP3001554,
45	NT2RP3001690,	NT2RP3001799,	NT2RP3002688,	NT2RP3003061,	NT2RP3003185,	NT2RP3003230,
	NT2RP3004569,	NT2RP3004578,	NT2RP4001004,	NT2RP4001086,	NT2RP4001256,	NT2RP4001567,
	NT2RP4001927,	OVARC1000001,	OVARC1000106,	OVARC1000437,	OVARC1000520,	OVARC1000679,
	OVARC1001731,	OVARC1002050,	PLACE1001104,	PLACE1002571,		
	PLACE1002591,	PLACE1002655,	PLACE1002714,	PLACE1003625,	PLACE1005287,	PLACE1006552,
50	PLACE1007946,	PLACE1008426,	PLACE1010148,	PLACE1010547,	PLACE1010743,	PLACE1010896,
	PLACE1010960,	PLACE1011310,	PLACE1011922,	PLACE2000216,	PLACE2000274,	PLACE2000371,
	PLACE2000458,	PLACE3000145,	PLACE3000416,	PLACE4000009,	THYRO1000132,	THYRO1001405,
	THYRO1001458,	Y79AA1000368,	Y79AA1000794,	Y79AA1000833,	Y79AA1000962,	Y79AA1002208,
	[0288] The following 54 clones presumably belong to cell division-associated and/or cell proliferation-associated proteins					
55	HEMBA1000156,	HEMBA1000168,	HEMBA1000411,	HEMBA1000588,	HEMBA1001043,	HEMBA1001651,
	HEMBA1001661,	HEMBA1002102,	HEMBA1002161,	HEMBA1002939,	HEMBA1003235,	HEMBA1003581,
	HEMBA1004499,	HEMBA1004534,	HEMBA1004697,	HEMBA1004929,	HEMBA1004972,	HEMBA1005582,
35	HEMBA1005595,	HEMBA1006344,	HEMBA1006737,	HEMBA1001175,	HEMBA1001282,	HEMBA1001562,
	HEMBA1001802,	MAMMA1000824,	MAMMA			

NT2RM2001896, NT2RM2002145, NT2RM4000215, NT2RM4001714, NT2RP1000163, NT2RP1000333,
 NT2RP1000439, NT2RP2000346, NT2RP2001397, NT2RP2002595, NT2RP2003177, NT2RP2003596,
 NT2RP2003912, NT2RP2004396, NT2RP2005037, NT2RP2005520, NT2RP2005669, NT2RP2005835,
 NT2RP3001730, NT2RP3002081, NT2RP4000210, NT2RP4000415, NT2RP4001414, NT2RP4001634,
 5 OVARC1000013, OVARC1000937, PLACE1001383, PLACE1002433, PLACE1004316, PLACE1005287,
 PLACE1008808, PLACE1010720, PLACE1010833, Y79AA1000748, Y79AA1001236, Y79AA1001394,

[0289] The following 36 clones presumably belong to the category of embryogenesis- and/or development-associated proteins.

HEMBA1000518, HEMBA1001847, HEMBA1001869, HEMBA1003545, HEMBA1004973, HEMBB1002442,
 10 MAMMA1001837, NT2RM2001670, NT2RM4000046, NT2RM4000531, NT2RM4001140, NT2RM4001858,
 NT2RP2002078, NT2RP2004187, NT2RP2006436, NT2RP3000603, NT2RP3000994, NT2RP3001580,
 NT2RP3001708, NT2RP3003071, NT2RP3004472, NT2RP3004617, NT2RP4000246, NT2RP4001567,
 OVARC1000304, OVARC1000746, PLACE1000793, PLACE1002532, PLACE1003258, PLACE1003625,
 PLACE1004460, PLACE1009622, PLACE4000558, THYRO1000085, Y79AA1001391, Y79AA1001692,

15 [0290] The following 30 clones presumably belong to cellular defense-associated proteins.

HEMBA1000005, HEMBA1000531, HEMBA1003417, HEMBA1006253, NT2RM4000354, NT2RM4001880,
 NT2RP1000333, NT2RP1000493, NT2RP2000006, NT2RP2000045, NT2RP2000809, NT2RP2001536,
 NT2RP2002464, NT2RP2004920, NT2RP2005037, NT2RP3000590, NT2RP3001426, NT2RP3002062,
 NT2RP3002785, NT2RP3004262, NT2RP4001555, NT2RP4001638, PLACE1006958, PLACE1008275,
 20 PLACE1009113, PLACE1011858, PLACE4000014, THYRO1000684, Y79AA1002139, Y79AA1002229,

[0291] Although it is unclear whether or not 261 clones out of clones other than the above-mentioned clones belong to any of the above-described categories, these clones are predicted to have some functions, based on the homology search using the full length sequences thereof. The clone names and the gene definitions found in the result of homology search are shown below, separated with a double-slash mark, //.

25 HEMBA1000030//Homo sapiens ARF GTPase-activating protein GIT1 mRNA, complete cds.

HEMBA1000307//CARNITINE DEFICIENCY-ASSOCIATED PROTEIN EXPRESSED IN VENTRICLE 1

30 HEMBA1000333//Homo sapiens F-box protein Fbx21 (FBX21) mRNA, complete cds.

HEMBA1000488//RING CANAL PROTEIN (KELCH PROTEIN).

HEMBA1000523//TESTIS-SPECIFIC PROTEIN PBS13.

HEMBA1001197//Homo sapiens rap2 interacting protein x mRNA, complete cds.

HEMBA1001302//Homo sapiens calcium binding protein precursor, mRNA, complete cds.

35 HEMBA1001455//Mus musculus transposon-derived Buster2 transposase-like protein gene, partial cds.

HEMBA1001675//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS9.

HEMBA1001714//Homo sapiens mRNA for ATPase inhibitor precursor, complete cds.

HEMBA1001744//SCY1 PROTEIN.

HEMBA1001967//Homo sapiens NY-REN-57 antigen mRNA, partial cds.

40 HEMBA1002151//Rattus norvegicus p34 mRNA, complete cds.

HEMBA1002215//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].

HEMBA1002458//OVARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74.

HEMBA1002777//Fugu rubripes BAW (BAW) mRNA, complete cds.

HEMBA1003098//Homo sapiens NY-REN-6 antigen mRNA, partial cds.

45 HEMBA1003199//Homo sapiens chromosome 5 F-box protein Fbx4 (FBX4) mRNA, complete cds.

HEMBA1003615//Homo sapiens ART-4 mRNA, complete cds.

HEMBA1003836//MOB1 PROTEIN (MPS1 BINDER 1).

HEMBA1004295//Homo sapiens NY-REN-25 antigen mRNA, partial cds.

HEMBA1004573//Homo sapiens mRNA for HELG protein.

50 HEMBA1004604//Homo sapiens COP9 complex subunit 7a mRNA, complete cds.

HEMBA1004795//CDC4-LIKE PROTEIN (FRAGMENT).

HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds.

HEMBA1005201//Homo sapiens CGI-07 protein mRNA, complete cds.

HEMBA1005206//Drosophila simulans anon73B1 gene and Su(P) gene.

55 HEMBA1005530//Homo sapiens anaphase-promoting complex subunit 7 (APC7) mRNA, complete cds.

HEMBA1005530//Homo sapiens anaphase-promoting complex subunit 7 (APC7) mRNA, complete cds.

HEMBA1005990//Homo sapiens receptor candidate protein mRNA, complete cds.

HEMBA1006268//Homo sapiens HQOO24c mRNA, complete cds.

HEMBA1006398//Human L1 element L1.6 putative p150 gene, complete cds.
 HEMBA1006445//Homo sapiens putative tumor supressor NOEY2 mRNA, complete cds.
 HEMBA1007174//Homo sapiens epsin 2b mRNA, complete cds.
 HEMBA1007251//Homo sapiens F-box protein FBX29 (FBX29) mRNA, partial cds. HEMBB1000036//Homo sapi-
 5 ens CGI-51 protein mRNA, complete cds.
 HEMBB1000144//GUANYLATE CYCLASE ACTIVATING PROTEIN 2 (GCAP 2) (RETINAL
 GUANYLYL CYCLASE ACTIVATOR PROTEIN P24).
 HEMBB1000973//Mus musculus schlafen3 (Slfn3) mRNA, complete cds.
 HEMBB1001058//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds
 10 HEMBB1001234//65 KD YES-ASSOCIATED PROTEIN (YAP65).
 HEMBB1001288//COPPER HOMEOSTASIS PROTEIN CUTC.
 HEMBB1001331//Mus musculus mRNA for hepatoma-derived growth factor, complete cds, strain:BALB/c.
 HEMBB1001384//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.
 HEMBB1002266//NEURONAL PROTEIN.
 15 HEMBB1002510//GYP7 PROTEIN.
 HEMBB1002705//Homo sapiens CGI-27 protein mRNA, complete cds.
 MAMMA1000055//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TEST)].
 MAMMA1000625//GYP7 PROTEIN.
 MAMMA1001075//Homo sapiens CGI-72 protein mRNA, complete cds.
 20 MAMMA1001181//ABC1 PROTEIN HOMOLOG PRECURSOR.
 MAMMA1001259//Mus musculus F-box protein FBX18 mRNA, partial cds.
 MAMMA1001730//Homo sapiens brain and nasopharyngeal carcinoma susceptibility protein NSG-x mRNA, partial
 cds.
 MAMMA1002143//Homo sapiens Cdc42 effector protein 4 mRNA, complete cds.
 25 MAMMA1002699//Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds.
 MAMMA1002972//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS27.
 MAMMA1003113//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds.
 NT2RM1000118//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CAL-
 CINEURIN REGULATORY SUBUNIT).
 30 NT2RM1000186//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CAL-
 CINEURIN REGULATORY SUBUNIT).
 NT2RM1000244//Homo sapiens TRAF4 associated factor 1 mRNA, partial cds.
 NT2RM1000421//RIBONUCLEASE INHIBITOR.
 NT2RM1000499//Caenorhabditis elegans mRNA for centaurin gamma 1A.
 35 NT2RM1000623//RIBONUCLEASE INHIBITOR.
 NT2RM1000883//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.
 NT2RM2000502//Rattus norvegicus W3O7 mRNA, complete cds.
 NT2RM2000599//Homo sapiens F-box protein Lilina (LILINA) mRNA, complete cds.
 NT2RM2000718//Homo sapiens endocrine regulator mRNA, complete cds.
 40 NT2RM2001065//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.
 NT2RM2001196//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).
 NT2RM2001983//Homo sapiens RGS-GAIP interacting protein GIPC mRNA, complete cds.
 NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds.
 NT2RM2002142//GASTRULATION SPECIFIC PROTEIN G12.
 45 NT2RM4000030//LAS1 PROTEIN.
 NT2RM4000139//R.norvegicus trg mRNA.
 NT2RM4000156//H. sapiens HPBR11-7 gene.
 NT2RM4000386//Mus musculus ODZ3 (Odz3) mRNA, partial cds.
 NT2RM4000590//RING CANAL PROTEIN (KELCH PROTEIN).
 50 NT2RM4001047//MO25 PROTEIN.
 NT2RM4001155//ADRENAL MEDULLA 50 KD PROTEIN.
 NT2RM4001256//Xenopus laevis putative Zic3 binding protein mRNA, complete cds.
 NT2RM4001320//Homo sapiens mRNA for Neuroblastoma, complete cds.
 NT2RM4001340//UTR4 PROTEIN (UNKNOWN TRANSCRIPT 4 PROTEIN).
 55 NT2RM4001347//Homo sapiens NY-RFN-25 antigen mRNA, partial cds.
 NT2RM4001582//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds.
 NT2RM4001611//SIS2 PROTEIN (HALOTOLERANCE PROTEIN HAL3)

NT2RM4001731//Homo sapiens F-box protein Lilina (LILINA) mRNA, complete cds.
 NT2RM4001969//R.norvegicus mRNA for IP63 protein.
 NT2RM4002034//Homo sapiens hiwi mRNA, partial cds.
 NT2RM4002075//RING CANAL PROTEIN (KELCH PROTEIN).
 5 NT2RM4002226//GTPASE ACTIVATING PROTEIN ROTUND.
 NT2RP1000040//Mus musculus donson protein (Donson) mRNA, partial cds.
 NT2RP1000363//R.norvegicus LL5 mRNA.
 NT2RP1000481//Homo sapiens antigen NY-CO-3 (NY-CO-3) mRNA, partial cds.
 NT2RP1000513//Human NifU-like protein (hNifU) mRNA, partial cds.
 10 NT2RP1000733//Human mRNA for GSPT1-TK protein, complete cds.
 NT2RP1000860//Homo sapiens KLO4P mRNA, complete cds.
 NT2RP1000954//RING CANAL PROTEIN (KELCH PROTEIN).
 NT2RP1001011//Drosophila melanogaster putative 43 kDa protein (TH1) mRNA, complete cds.
 NT2RP1001395//Homo sapiens COP9 complex subunit 7a mRNA, complete cds.
 15 NT2RP1001457//Homo sapiens partial mRNA for beta-transducin family protein (putative).
 NT2RP1001494//MALE STERILITY PROTEIN 2.
 NT2RP2000054//Homo sapiens putative ring zinc finger protein NY-REN-43 antigen mRNA, complete cds.
 NT2RP2000067//Mus musculus ODZ3 (Odz3) mRNA, partial cds.
 NT2RP2000133//Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds.
 20 NT2RP2000157//MLO2 PROTEIN.
 NT2RP2000764//NIFS PROTEIN.
 NT2RP2000965//Homo sapiens mRNA for fls353, complete cds.
 NT2RP2001839//SCY1 PROTEIN.
 NT2RP2001883//Homo sapiens CGI-01 protein mRNA, complete cds.
 25 NT2RP2001976//Mus musculus calmodulin-binding protein SHA1 (Sha1) mRNA, complete cds.
 NT2RP2001985//Homo sapiens high-risk human papilloma viruses E6 oncoproteins targeted protein E6TP1 alpha
 mRNA, complete cds.
 NT2RP2002185//Homo sapiens ubiquilin mRNA, complete cds.
 NT2RP2002442//HESA PROTEIN.
 30 NT2RP2002727//Rattus norvegicus tulip 2 mRNA, complete cds.
 NT2RP2002741//Homo sapiens mRNA for Neuroblastoma, complete cds.
 NT2RP2002986//Homo sapiens mRNA for Kelch motif containing protein, complete cds.
 NT2RP2003121//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.
 NT2RP2003265//Homo sapiens CGI-53 protein mRNA, complete cds.
 35 NT2RP2003272//Homo sapiens ubiquilin mRNA, complete cds.
 NT2RP2003857//MYOTROPHIN (V-1 PROTEIN) (GRANULE CELL DIFFERENTIATION PROTEIN).
 NT2RP2003871//Homo sapiens transposon-derived Buster1 transposase-like protein gene, complete cds.
 NT2RP2004425//Mus musculus axotrophin mRNA, complete cds.
 NT2RP2004476//Homo sapiens cyclin L ania-6a mRNA, complete cds.
 40 NT2RP2004710//Mus musculus formin binding protein 30 mRNA, complete cds.
 NT2RP2004816//H58 PROTEIN.
 NT2RP2005441//Homo sapiens hypothalamus protein HT002 mRNA, complete cds.
 NT2RP2005490//Mus musculus D3Mm3e (D3Mm3e) mRNA, complete cds.
 NT2RP2005620//Homo sapiens epsin 2a mRNA, complete cds.
 45 NT2RP2005654//CYSTEINE STRING PROTEIN (CCCS1).
 NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.
 NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.
 NT2RP2005841//Homo sapiens mRNA for ALEX3, complete cds.
 NT2RP2006598//Homo sapiens retinoid x receptor interacting protein mRNA, complete cds.
 50 NT2RP3000047//NPL4 PROTEIN.
 NT2RP3000233//RING CANAL PROTEIN (KELCH PROTEIN).
 NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete
 cds.
 NT2RP3000869//Drosophila melanogaster AAA family protein Bor (bor) mRNA, complete cds.
 55 NT2RP3001399//SSU72 PROTEIN
 NT2RP3001457//Drosophila melanogaster Melted (melt) mRNA, partial cds.
 NT2RP3001587//Human anthracycline-associated resistance ARX mRNA, complete cds

- NT2RP3001712//Homo sapiens HP1-BP74 protein mRNA, complete cds.
 NT2RP3001819//RING CANAL PROTEIN (KELCH PROTEIN).
 NT2RP3001854//Homo sapiens novel retinal pigment epithelial cell protein (NORPEG) mRNA, complete cds.
 NT2RP3001931//Rattus norvegicus clone C48 CDK5 activator-binding protein mRNA, complete cds.
 5 NT2RP3002273//SCD6 PROTEIN.
 NT2RP3002631//Homo sapiens Ran binding protein 11 mRNA, complete cds.
 NT2RP3002682//Homo sapiens CGI-145 protein mRNA, complete cds.
 NT2RP3002770//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116.
 NT2RP3002818//INSERTION ELEMENT IS2A HYPOTHETICAL 48.2 KD PROTEIN.
 10 NT2RP3002948//RING CANAL PROTEIN (KELCH PROTEIN).
 NT2RP3002972//Halocynthia roretzi mRNA for HrPET-1, complete cds.
 NT2RP3003032//Homo sapiens okadaic acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete cds.
 NT2RP3003290//Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds.
 15 NT2RP3003411//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.
 NT2RP3003491//Drosophila melanogaster Pelle associated protein Pellino (Pli) mRNA, complete cds.
 NT2RP3003500//SCY1 PROTEIN.
 NT2RP3003726//Homo sapiens spermatogenesis associated PD1 mRNA, complete cds.
 NT2RP3004348//R. norvegicus mRNA for cytosolic resiniferatoxin-binding protein.
 20 NT2RP3004507//MOB1 PROTEIN (MPS1 BINDER 1).
 NT2RP4000129//Xenopus laevis F-box protein 28 (Fbx28) mRNA, partial cds.
 NT2RP4000498//MOB1 PROTEIN (MPS1 BINDER 1).
 NT2RP4000528//NPL4 PROTEIN.
 NT2RP4000737//Mus musculus F-box protein FBL10 mRNA, partial cds.
 25 NT2RP4000979//Homo sapiens putative HIV-1 infection related protein mRNA, partial cds.
 NT2RP4001010//Rattus norvegicus PSD-95/SAP90-associated protein-4 mRNA, complete cds.
 NT2RP4001207//Homo sapiens Ran binding protein 11 mRNA, complete cds.
 NT2RP4001228//RING CANAL PROTEIN (KELCH PROTEIN).
 NT2RP4001260//Homo sapiens F-box protein Fbx21 (FBX21) mRNA, complete cds.
 30 NT2RP4001339//Homo sapiens mRNA for AMMERC1 protein.
 NT2RP4001351//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.
 NT2RP4001474//Xenopus laevis putative Zic3 binding protein mRNA, complete cds.
 NT2RP4001966//Mus musculus ODZ3 (Odz3) mRNA, partial cds.
 35 NT2RP4002018//RING CANAL PROTEIN (KELCH PROTEIN).
 OVARC1000209//Oryza sativa submergence induced protein 2A mRNA, complete cds.
 OVARC1000876//MOB1 PROTEIN (MPS1 BINDER 1).
 OVARC1001065//Homo sapiens CGI-12 protein mRNA, complete cds.
 OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F1857O7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin)).
 40 OVARC1001419//Homo sapiens GOK (STIM1) mRNA, complete cds.
 OVARC1001555//NGG1-INTERACTING FACTOR 3.
 OVARC1001711//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1 B).
 OVARG1001943//Mus musculus DEBT-91 mRNA, complete cds.
 45 PLACE1000004//Homo sapiens IDN3-B mRNA, complete cds.
 PLACE1000066//SSU72 PROTEIN.
 PLACE1000610//MSN5 PROTEIN.
 PLACE1000636//MALE STERILITY PROTEIN 2.
 PLACE1000769//Homo sapiens CGI-18 protein mRNA, complete cds.
 50 PLACE1000987//Rattus norvegicus late gestation lung 2 protein (Lgl2) mRNA, complete cds.
 PLACE1001036//Homo sapiens mRNA for alpha integrin binding protein 63, partial.
 PLACE1001845//Mus musculus cyclin ania-6a mRNA, complete cds.
 PLACE1001920//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.
 PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.
 55 PLACE1003602//Homo sapiens mRNA expressed in placenta
 PLACE1004256//Mus musculus short coiled coil protein SCOC1 (Scoc) mRNA, complete cds.
 PLACE1004550//Homo sapiens CGI-20 protein mRNA, complete cds.

PLACE1004868//MALE STERILITY PROTEIN 2.

PLACE1004930//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds

PLACE1005052//Homo sapiens CGI-16 protein mRNA, complete cds.

PLACE1005102//RING CANAL PROTEIN (KELCH PROTEIN).

5 PLACE1005176//Homo sapiens hypothalamus protein HT001 mRNA, complete cds.

PLACE1005187//APAG PROTEIN.

PLACE1005331//Homo sapiens 7h3 protein mRNA, partial cds.

PLACE1005727//Homo sapiens STRIN protein (STRIN) mRNA, complete cds.

PLACE1006003//Homo sapiens CGI-94 protein mRNA, complete cds.

10 PLACE1006335//Homo sapiens NY-REN-50 antigen mRNA, partial cds.

PLACE1006385//Homo sapiens epsin 2a mRNA, complete cds.

PLACE1006506//Homo sapiens anaphase-promoting complex subunit 4 (APC4) mRNA, complete cds.

PLACE1007105//Homo sapiens muskellin (MKLN1) mRNA, complete cds.

PLACE1007537//Homo sapiens ankyrin repeat-containing protein ASB-2 mRNA, complete cds.

15 PLACE1007705//Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds.

PLACE1007791//Homo sapiens IDN3-B mRNA, complete cds.

PLACE1007897//Homo sapiens FLASH mRNA, complete cds.

PLACE1008080//Homo sapiens mRNA for HEXIM1 protein, complete cds.

PLACE1008368//RING CANAL PROTEIN (KELCH PROTEIN).

20 PLACE1008398//GENE 33 POLYPEPTIDE.

PLACE1008465//Homo sapiens mRNA for rapa-1 (rapa gene).

PLACE1008627//Homo sapiens mRNA for cysteine-rich protein.

PLACE1009020//NIFS PROTEIN.

PLACE1009060//BRO1 PROTEIN.

25 PLACE1009186//Homo sapiens small zinc finger-like protein (TIM9b) mRNA, complete cds.

PLACE1009443//Mus musculus F-box protein FBL8 mRNA, complete cds.

PLACE1009571//Homo sapiens PTD002 mRNA, complete cds.

PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.

PLACE1010105//RING CANAL PROTEIN (KELCH PROTEIN).

30 PLACE1010261//SEGREGATION DISTORTER PROTEIN.

PLACE1010310//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).

PLACE1010522//Homo sapiens mRNA for DEPP (decidual protein induced by progesterone), complete cds.

PLACE1010579//Homo sapiens CED-6 protein (CED-6) mRNA, complete cds.

35 PLACE1010628//Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds.

PLACE1010661//TESTIS-SPECIFIC PROTEIN PBS13.

PLACE1010761//Homo sapiens mRNA for cisplatin resistance-associated overexpressed protein, complete cds.

PLACE1011185//INSERTION ELEMENT IS1 PROTEIN INSB.

PLACE1011340//Homo sapiens IDN3-B mRNA, complete cds.

40 PLACE1011586//Rattus norvegicus clone C53 CDK5 activator-binding protein mRNA, complete cds.

PLACE2000246//RING CANAL PROTEIN (KELCH PROTEIN).

PLACE2000411//Homo sapiens epsin 2b mRNA, complete cds.

PLACE3000477//Homo sapiens phosphoprotein pp75 mRNA, partial cds.

THYRO1000173//Homo sapiens AP-mu chain family member mu1B (HSMU1B) mRNA, complete cds.

45 THYRO1000401//Human TcD37 homolog (HTcD37) mRNA, partial cds.

THYRO1000666//Mus musculus mRNA for kinesin like protein 9.

THYRO1001033//TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521.

THYRO1001347//Homo sapiens RAN binding protein 16 mRNA, complete cds.

THYRO1001656//Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds.

50 THYRO1001703//NIFR3-LIKE PROTEIN.

THYRO1001721//RING CANAL PROTEIN (KELCH PROTEIN).

Y79AA1000059//Homo sapiens aryl-hydrocarbon interacting protein-like 1 (AIP1) gene, complete cds.

Y79AA1000181//Homo sapiens CGI-01 protein mRNA, complete cds.

Y79AA1000268//Mus musculus Nip2l mRNA, complete cds.

55 Y79AA1000313//CALPHOTIN.

Y79AA1000540//Homo sapiens

Y79AA1000966//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.

Y79AA1000985//Human centrosomal protein kendrin mRNA, complete cds.

Y79AA1001323//Mus musculus mRNA for GSG1, complete cds.

Y79AA1001402//Homo sapiens paraneoplastic cancer-testis-brain antigen (MA4) mRNA, partial cds.

Y79AA1001679//Homo sapiens lambda-crystallin mRNA, complete cds.

Y79AA1001923//Homo sapiens F-box protein Fbx22 (FBX22) gene, partial cds. Y79AA1002083//H. sapiens mRNA for MUF1 protein.

Y79AA1002307//Homo sapiens astrotactin2 (ASTN2) mRNA, complete cds.

Y79AA1002311//R. norvegicus mRNA for cytosolic resiniferatoxin-binding protein.

Y79AA1002487//Homo sapiens chromosome 5 F-box protein Fbx4 (FBX4) mRNA, complete cds.

10 [0292] Among the clones other than the above-mentioned, there were 36 clones that were similarly classified into the functional categories based on the results of functional domain search using the Pfam program. These clones were categorized as follows.

[0293] Clones presumably belonging to the category of secretory or membrane proteins are two clones, MAMMA1002498 and NT2RM4002287; a clone presumably belonging to the category of glycoproteins-associated proteins is a clone MAMMA1002498; clones presumably belonging to the category of signal transduction-associated proteins are 11 clones, HEMBA1001247, NT2RM2001813, NT2RM4001454, NT2RP2005140, NT2RP2005293, NT2RP3000487, NT2RP3003311, PLACE1000972, PLACE1003723, PLACE1005327, and PLACE3000124; clones presumably belonging to the category of transcription-associated proteins are 12 clones, HEMBA1003257, NT2RM2000101, NT2RM2001797, NT2RP1000101, NT2RP2002208, NT2RP3001214, NT2RP3003278, NT2RP4001235, PLACE1000050, PLACE1001716, PLACE1002499, and PLACE1007544; clones presumably belonging to the category of enzymes and/or metabolism-associated proteins are 2 clones, HEMBA1005732 and MAMMA1000402; clones presumably belonging to the category of DNA- and/or RNA-binding proteins are 4 clones, HEMBA1004596, OVARC1000148, PLACE1003334, and THYRO1001661; a clone presumably belonging to the category of protein synthesis- and/or protein transport-associated proteins is a clone, HEMBA1006284.

25 [0294] So far, useful information for presuming the functions is unavailable for the remaining 2511 clones. Their functions will possibly be revealed by further analyses. Names of the clones are listed below.

[0295] So far, useful information for presuming the functions is unavailable for the remaining 2511 clones. Their functions will possibly be revealed by further analyses. Names of the clones are listed below.

30	HEMBA1000042,	HEMBA1000046,	HEMBA1000050,	HEMBA1000076,	HEMBA1000193,	HEMBA1000213,
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	HEMBA1000338,	HEMBA1000351,	HEMBA1000357,	HEMBA1000376,	HEMBA1000387,	HEMBA1000392,
	HEMBA1000396,	HEMBA1000428,	HEMBA1000442,	HEMBA1000456,	HEMBA1000459,	HEMBA1000460,
	HEMBA1000469,	HEMBA1000497,	HEMBA1000501,	HEMBA1000504,	HEMBA1000505,	HEMBA1000508,
35	HEMBA1000519,	HEMBA1000520,	HEMBA1000534,	HEMBA1000545,	HEMBA1000557,	HEMBA1000568,
	HEMBA1000575,	HEMBA1000594,	HEMBA1000604,	HEMBA1000622,	HEMBA1000636,	HEMBA1000655,
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	HEMBA1000727,	HEMBA1000749,	HEMBA1000752,	HEMBA1000769,	HEMBA1000773,	HEMBA1000774,
	HEMBA1000843,	HEMBA1000867,	HEMBA1000869,	HEMBA1000872,	HEMBA1000876,	HEMBA1000908,
40	HEMBA1000918,	HEMBA1000934,	HEMBA1000942,	HEMBA1000943,	HEMBA1000946,	HEMBA1000960,
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45	HEMBA1001213,	HEMBA1001226,	HEMBA1001235,	HEMBA1001281,	HEMBA1001299,	HEMBA1001303,
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50	HEMBA1001533,	HEMBA1001566,	HEMBA1001570,	HEMBA1001581,	HEMBA1001589,	HEMBA1001608,
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10	HEMBA1003078,	HEMBA1003083,	HEMBA1003117,	HEMBA1003129,	HEMBA1003133,	HEMBA1003142,
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15	HEMBA1003463,	HEMBA1003480,	HEMBA1003528,	HEMBA1003531,	HEMBA1003548,	HEMBA1003556,
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25	HEMBA1004241,	HEMBA1004246,	HEMBA1004267,	HEMBA1004272,	HEMBA1004274,	HEMBA1004289,
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35	HEMBA1004944,	HEMBA1004954,	HEMBA1004960,	HEMBA1004977,	HEMBA1004978,	HEMBA1004980,
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40	HEMBA1005331,	HEMBA1005374,	HEMBA1005382,	HEMBA1005403,	HEMBA1005411,	HEMBA1005426,
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50	HEMBA1006252,	HEMBA1006259,	HEMBA1006349,	HEMBA1006364,	HEMBA1006377,	HEMBA1006380,
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55	HEMBA1006639,	HEMBA1006643,	HEMBA1006665,	HEMBA1006674,	HEMBA1006676,	HEMBA1006682,
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5	HEMBA1007342,	HEMBA1007347,	HEMBB1000005,	HEMBB1000008,	HEMBB1000018,	HEMBB1000024,
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45 Homology Search Result Data 1.

[0296] The result of the homology search of the SwissProt using the 5'-end sequence.

[0297] Data include

50 the name of clone,
definition of the top hit data,
the P-value: the length of the compared sequence: identity (%), and
the organism and the Accession No. of the top hit data, as in the order separated by //.

55 [0298] Data are not shown for the clones in which the P-value was higher than 1

299

ences. In general, the smaller P-value reflects the higher similarity. (Altschul, J. D., Gish, W., Miller, W., Myers, E. W., & Lipman, D. J. (1990) "Basic local alignment search tool." J. Mol. Biol. 215 403-410. Gish, W. &

States, D.J. (1993) "Identification of protein coding regions by database similarity search." Nature Genet. 3:266-272).

- 5 F-HEMBA1000005//DNAJ PROTEIN HOMOLOG MTJ1.//1.8e-85:244:75//MUS MUSCULUS (MOUSE)//Q61712
- F-HEMBA1000012//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINETRNA LIGASE) (LEURS)//7.6e-57:231:53//CAENORHABDITIS ELEGANS//Q09996
- F-HEMBA1000020//TUBULIN BETA CHAIN.//1.0e-92:143:80//AJELLOMYCES CAPSULATA (HISTOPLASMA CAPSULATUM)//P41742
- 10 F-HEMBA1000030//CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).//0.021:136:33//PLASMODIUM KNOWLESI (STRAIN NURI)//P04922
- F-HEMBA1000042//METALLOTHIONEIN 10-II (MT-10-II).//0.71:64:32//MYTILUS EDULIS (BLUE MUSSEL)//P80247
- F-HEMBA1000046//PROTEIN Q300.//0.92:40:37//MUS MUSCULUS (MOUSE)//Q02722
- F-HEMBA1000050//COMPETENCE PROTEIN S.//0.50:28:35//BACILLUS SUBTILIS//P80355
- 15 F-HEMBA1000076//ATP SYNTHASE E CHAIN, MITOCHONDRIAL (EC 3.6.1.34)//0.86:41:41//HOMO SAPIENS (HUMAN)//P56385
- F-HEMBA1000111
- F-HEMBA1000129//UVSW PROTEIN (DAR PROTEIN)//0.023:68:33//BACTERIOPHAGE T4//P20703
- 20 F-HEMBA1000141//YSY6 PROTEIN.//0.90:29:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38374
- F-HEMBA1000150//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//8.4e-16:47:70//HOMO SAPIENS (HUMAN)//P39193
- F-HEMBA1000156//IMMEDIATE-EARLY PROTEIN //8.1e-07:143:28//HERPESVIRUS SAIMIRI (STRAIN 11) //Q01042
- 25 F-HEMBA1000158//HYPOTHETICAL PROTEIN KIAA0192 (FRAGMENT)//7.9e-11:129:40//HOMO SAPIENS (HUMAN)//Q93074
- F-HEMBA1000168//INSULIN RECEPTOR SUBSTRATE-2 (IRS-2) (4PS)//0.00055:86:36//MUS MUSCULUS (MOUSE)//P81122
- F-HEMBA1000180//VPU PROTEIN (U ORF PROTEIN)//0.22:73:28//CHIMPANZEE IMMUNODEFICIENCY VIRUS (SIV(CPZ)) (CIV)//P17286
- 30 F-HEMBA1000185//RAS-1 PROTEIN.//5.1e-10:121:29//NEUROSPORA CRASSA//P22126
- F-HEMBA1000193//PROLINE-RICH PEPTIDE P-B//0.00078:56:41//HOMO SAPIENS (HUMAN)//P02814
- F-HEMBA1000201//PROLINE-RICH PROTEIN MP-2 PRECURSOR//0.00061:49:42//MUS MUSCULUS (MOUSE)//P05142
- 35 F-HEMBA1000213
- F-HEMBA1000216//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN)//1.6e-59:115:53//MUS MUSCULUS (MOUSE)//Q61221
- F-HEMBA1000227//SUPPRESSOR PROTEIN SRP40//0.00059:135:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32583
- 40 F-HEMBA1000231//HYPOTHETICAL 60.7 KD PROTEIN C56F8.17C IN CHROMOSOME I.//0.024:60:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10264
- F-HEMBA1000243//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.0038:125:34//HOMO SAPIENS (HUMAN)//P08547
- F-HEMBA1000244//HYPOTHETICAL 123.6 KD PROTEIN IN POR2-COX5B INTERGENIC REGION.//3.1e-17:149:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40480
- 45 F-HEMBA1000251
- F-HEMBA1000264//PROBABLE E5 PROTEIN//1.0:49:36//HUMAN PAPILLOMAVIRUS TYPE 58//P26552
- F-HEMBA1000280//SHORT NEUROTOXIN 1 (TOXIN C-6).//0.98:58:31//NAJA NAJA KAOUTHIA (MONOCLED COBRA) (NAJA NAJA SIAMENSIS)//P14613
- 50 F-HEMBA1000282//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.14:26:65//HOMO SAPIENS (HUMAN)//P39188
- F-HEMBA1000288
- F-HEMBA1000290//HYPOTHETICAL 14 KD PROTEIN IN TVRI-6 REPETITIVE REGION.//3.8e-06:98:39//HOMO SAPIENS (HUMAN)//P10516
- 55 F-HEMBA1000302
- F-HEMBA1000303
- F-HEMBA1000304//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//0.021:18:83//HOMO SAPIENS (HUMAN).//

P39194

F-HEMBA1000307//MYOSIN HEAVY CHAIN, CLONE 203 (FRAGMENT)//7.1e-06:235:25//HYDRA ATTENUATA (HYDRA) (HYDRA VULGARIS)//P39922

F-HEMBA1000327

5 F-HEMBA1000333//SRP1 PROTEIN//1.0:159:30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10193

F-HEMBA1000338//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/8.8e-26:36:83//HOMO SAPIENS (HUMAN)//P39193

F-HEMBA1000351

10 F-HEMBA1000355//BASIC PROLINE-RICH PEPTIDE P-E (IB-9)//0.99:22:50//HOMO SAPIENS (HUMAN)//P02811

F-HEMBA1000356//IMMEDIATE-EARLY PROTEIN IE180//0.11:82:36//PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV)//P11675

15 F-HEMBA1000357//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/2.1e-35:105:74//HOMO SAPIENS (HUMAN)//P39192

F-HEMBA1000366//HYPOTHETICAL TRANSCRIPTIONAL REGULATOR AF1627//1.0:28:42//ARCHAEOGLOBUS FULGIDUS//O28646

F-HEMBA1000369//PRESYNAPTIC DENSITY PROTEIN 95 (PSD-95)//0.013:140:26//HOMO SAPIENS (HUMAN)//P78352

20 F-HEMBA1000376//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE]//6.8e-08:66:42//MUS MUSCULUS (MOUSE)//P11369

F-HEMBA1000387//HYPOTHETICAL 63.2 KD PROTEIN C1F3.09 IN CHROMOSOME I//1.5e-15:177:32//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10414

F-HEMBA1000390//PARATHYMOSIN//0.0071:61:29//HOMO SAPIENS (HUMAN)//P20962

25 F-HEMBA1000392//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.1e-30:92:69//HOMO SAPIENS (HUMAN)//P39194

F-HEMBA1000396//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//3.9e-23:64:57//HOMO SAPIENS (HUMAN)//P08547

F-HEMBA1000411

30 F-HEMBA1000418

F-HEMBA1000422//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/8.3e-10:90:53//HOMO SAPIENS (HUMAN)//P39188

F-HEMBA1000428//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//3.1e-12:72:55//HOMO SAPIENS (HUMAN)//P08547

35 F-HEMBA1000434

F-HEMBA1000442//GENE 11 PROTEIN//1.0:28:46//SPIROPLASMA VIRUS SPV1-R8A2 B//P15902

F-HEMBA1000456//26S PROTEASOME REGULATORY SUBUNIT MTS4 (19S REGULATORY CAP REGION OF 26S PROTEASE SUBUNIT 2)//0.077:118:28//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//P87048

40 F-HEMBA1000459//HEME-REGULATED EUKARYOTIC INITIATION FACTOR EIF-2-ALPHA KINASE (EC 2.7.1.-) (HRI)//4.8e-62:102:78//ORYCTOLAGUS CUNICULUS (RABBIT)//P33279

F-HEMBA1000460//LYSIS PROTEIN (E PROTEIN) (GPE)//1.0:24:50//BACTERIOPHAGE ALPHA-3//P31280

F-HEMBA1000464

F-HEMBA1000469//PILI PROTEIN//1.0:27:44//PSEUDOMONAS AERUGINOSA//P43502

45 F-HEMBA1000488//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN)//1.1e-07:90:38//HOMO SAPIENS (HUMAN)//Q13105

F-HEMBA1000490//PLECTIN//0.74:254:25//RATTUS NORVEGICUS (RAT)//P30427

F-HEMBA1000491//RAS-RELATED PROTEIN M-RAS//3.0e-14:100:36//RATTUS NORVEGICUS (RAT)//P97538

50 F-HEMBA1000501//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.5e-20:81:54//HOMO SAPIENS (HUMAN)//P39194

F-HEMBA1000504

F-HEMBA1000505//NEURON-SPECIFIC X11 PROTEIN (FRAGMENT)//0.00028:128:32//HOMO SAPIENS (HUMAN)//Q02410

55 F-HEMBA1000508//CHITIN SYNTHASE 3 (EC 2.4.1.16) (CHITIN-UDP ACETYL-GLUCOSAMINYL TRANSFERASE 3)//0.61:132:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P29465

F-HEMBA1000514

F-HEMBA1000514//ALU SUBFAMILY J WARNING ENTRY !!!!!/8.3e-10:90:53//HOMO SAPIENS (HUMAN)//P39188

F-HEMBA1000520/////ALU SUBFAMILY SC WARNING ENTRY !!!!!/5.2e-09:75:49//HOMO SAPIENS (HUMAN)//
 P39192
 F-HEMBA1000523//TESTIS-SPECIFIC PROTEIN PBS13//1.5e-35:257:36//MUS MUSCULUS (MOUSE)//
 Q01755
 5 F-HEMBA1000531//HEAT SHOCK PROTEIN 70 B2//1.6e-14:72:44//ANOPHELES ALBIMANUS (NEW WORLD
 MALARIA MOSQUITO)//P41827
 F-HEMBA1000534/////ALU SUBFAMILY SP WARNING ENTRY !!!!!/9.7e-32:96:78//HOMO SAPIENS (HUMAN)//
 P39193
 10 F-HEMBA1000540//LANTIBIOTIC LACTICIN 481 PRECURSOR (LACTOCOCCIN DR)//1.0:12:75//LACTOCOC-
 CUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS)//P36499
 F-HEMBA1000542//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS)//0.0089:79:31//MUS
 MUSCULUS (MOUSE)//P15265
 F-HEMBA1000545//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//9.0e-83:256:66//HOMO SAPIENS (HU-
 MAN)//P08547
 15 F-HEMBA1000555//TRANSLATION INITIATION FACTOR IF-2//3.6e-06:252:22//SACCHAROMYCES CEREVI-
 SIAE (BAKER'S YEAST)//P39730
 F-HEMBA1000557
 F-HEMBA1000561//ZINC FINGER PROTEIN 81 (FRAGMENT)//9.1 e-18:200:28//HOMO SAPIENS (HUMAN)//
 P51508
 20 F-HEMBA1000563
 F-HEMBA1000568
 F-HEMBA1000569//GPI-ANCHORED PROTEIN P137//1.0e-40:137:54//HOMO SAPIENS (HUMAN)//Q14444
 F-HEMBA1000575
 F-HEMBA1000588
 25 F-HEMBA1000591/////ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.1e-17:41:92//HOMO SAPIENS (HU-
 MAN)//P39194
 F-HEMBA1000592//CENTROMERIC PROTEIN E (CENP-E PROTEIN)//0.18:128:23//HOMO SAPIENS (HU-
 MAN)//Q02224
 30 F-HEMBA1000594//HYPOTHETICAL 29.3 KD PROTEIN B0280.6 IN CHROMOSOME III//0.93:24:54//
 CAENORHABDITIS ELEGANS//P41997
 F-HEMBA1000604/////ALU SUBFAMILY J WARNING ENTRY !!!!!/0.00010:49:55//HOMO SAPIENS (HUMAN)//
 P39188
 F-HEMBA1000608//HYPOTHETICAL PROTEIN KIAA0411 (FRAGMENT)//1.8e-55:179:61//HOMO SAPIENS
 (HUMAN)//O43295
 35 F-HEMBA1000622/////ALU SUBFAMILY J WARNING ENTRY !!!!!/1.1e-21:94:62//HOMO SAPIENS (HUMAN)//
 P39188
 F-HEMBA1000636//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)//0.34:73:36//VOLVOX CARTERI//
 P21997
 F-HEMBA1000637//BASIC PROLINE-RICH PEPTIDE IB-1//0.0057:76:38//HOMO SAPIENS (HUMAN)//P04281
 40 F-HEMBA1000655
 F-HEMBA1000657//ZINC FINGER PROTEIN GCS1//1.5e-07:66:37//SACCHAROMYCES CEREVISIAE (BAK-
 ER'S YEAST)//P35197
 F-HEMBA1000662//METALLOTHIONEIN-II (MT-II)//0.79:33:39//CRICETULUS GRISEUS (CHINESE HAM-
 STER)//P02799
 45 F-HEMBA1000673/////ALU SUBFAMILY SP WARNING ENTRY !!!!!/3.1e-17:86:59//HOMO SAPIENS (HUMAN)//
 P39193
 F-HEMBA1000682//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE
 (EC 2.7.7.49); ENDONUCLEASE]//3.0e-13:45:44//MUS MUSCULUS (MOUSE)//P11369
 50 F-HEMBA1000686//HYPOTHETICAL 48.0 KD PROTEIN C1B3.08 IN CHROMOSOME I//4.5e-07:79:34//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//O13873
 F-HEMBA1000702
 F-HEMBA1000705//PROTEIN Q300//0.80:25:44//MUS MUSCULUS (MOUSE)//Q02722
 F-HEMBA1000719//MYOSIN IC HEAVY CHAIN//0.0026:115:44//ACANTHAMOEBA CASTELLANII (AMOEBA)//
 P10569
 55 F-HEMBA1000722
 F-HEMBA1000727//ZINC FINGER PROTEIN C1B2.1151 (PROTEIN) //0.73:26:46//SACCHAROMYCES CER-

EVISIAE (BAKER'S YEAST)//P47977

F-HEMBA1000747

F-HEMBA1000749//HYPOTHETICAL PROTEIN HI1484//1.0:42:35//HAEMOPHILUS INFLUENZAE//P44211

F-HEMBA1000752//RETROVIRUS-RELATED ENV POLYPROTEIN//1.0e-08:84:39//HOMO SAPIENS (HUMAN)//P10267

F-HEMBA1000769

F-HEMBA1000773//PAIRED BOX PROTEIN PAX-4//1.0:107:33//HOMO SAPIENS (HUMAN)//O43316

F-HEMBA1000774//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.3e-23:92:63//HOMO SAPIENS (HUMAN)//P39188

F-HEMBA1000791

F-HEMBA1000817//PROLACTIN RECEPTOR PRECURSOR (PRL-R)//0.079:87:29//CERVUS ELAPHUS (RED DEER)//Q28235

F-HEMBA1000822

F-HEMBA1000827//HYPOTHETICAL 8.4 KD PROTEIN//0.98:48:39//VACCINIA VIRUS (STRAIN COPENHAGEN)//P20546

F-HEMBA1000843//HYPOTHETICAL 7.3 KD PROTEIN D1044.5 IN CHROMOSOME III//0.92:46:34//CAENORHABDITIS ELEGANS//P41953

F-HEMBA1000851//HOMEBOX PROTEIN GBX-2 (GASTRULATION AND BRAIN-SPECIFIC HOMEBOX PROTEIN 2)//0.048:39:51//HOMO SAPIENS (HUMAN)//P52951

F-HEMBA1000852//ARYLSULFATASE D PRECURSOR (EC 3.1.6.-) (ASD)//4.0e-24:29:100//HOMO SAPIENS (HUMAN)//P51689

F-HEMBA1000867

F-HEMBA1000869//PROBABLE E5 PROTEIN//0.99:70:27//HUMAN PAPILLOMAVIRUS TYPE 18//P06792

F-HEMBA1000870//MYOTOXIN 3 PRECURSOR (CROTAMINE 3)//0.79:43:32//CROTALUS DURISSUS TERRIFICUS (SOUTH AMERICAN RATTLESNAKE)//P24333

F-HEMBA1000872//GAR2 PROTEIN//0.89:70:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//P41891

F-HEMBA1000876//DEFENSIN//0.89:34:38//ALLOMYRINA DICHOTOMA//Q10745

F-HEMBA1000908//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)//0.69:43:37//HOMO SAPIENS (HUMAN)//P30808

F-HEMBA1000910//MELANOMA-ASSOCIATED ANTIGEN B3 (MAGE-B3 ANTIGEN)//5.1e-08:44:38//HOMO SAPIENS (HUMAN)//O15480

F-HEMBA1000918//60S RIBOSOMAL PROTEIN L37-A (YL35) (FRAGMENT)//1.0:19:52//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//P22667

F-HEMBA1000919//69 KD PARAFLAGELLAR ROD PROTEIN (69 KD PFR PROTEIN) (PFR-A/PFR-B)//0.29:116:30//TRYPANOSOMA BRUCEI BRUCEI//P22225

F-HEMBA1000934

F-HEMBA1000942//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.85:27:59//HOMO SAPIENS (HUMAN)//P39188

F-HEMBA1000943

F-HEMBA1000946//STO-2 PROTEIN//0.82:82:30//CAENORHABDITIS ELEGANS//Q19958

F-HEMBA1000960//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/0.0097:29:72//HOMO SAPIENS (HUMAN)//P39192

F-HEMBA1000968//METALLOTHIONEIN 20-III ISOFORMS A AND B (MT-20-III A AND MT-20-III B)//0.047:45:37//MYTILUS EDULIS (BLUE MUSSEL)//P80253

F-HEMBA1000971//HYPOTHETICAL BHLF1 PROTEIN//0.038:172:31//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4)//P03181

F-HEMBA1000972

F-HEMBA1000974//HYPOTHETICAL PROTEIN MG441//0.98:66:28//MYCOPLASMA GENITALIUM//P47679

F-HEMBA1000975//COLLAGEN ALPHA 2(VIII) CHAIN (ENDOTHELIAL COLLAGEN) (FRAGMENT)//0.028:57:36//HOMO SAPIENS (HUMAN)//P25067

F-HEMBA1000985

F-HEMBA1000986//SUBMANDIBULAR GLAND SECRETORY GLX-RICH PROTEIN CB PRECURSOR (GRP-CB) (CONTIGUOUS REPEAT POLYPEPTIDE) (CRP)//0.13:91:34//RATTUS NORVEGICUS (RAT)//P08462

F-HEMBA1000991//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHROMOSOME III//0.0001:100:100//HOMO SAPIENS (HUMAN)//P39192

F-HEMBA1001007//HYPOTHETICAL PROTEIN K-AA1179//0.07:20:41//HOMO SAPIENS (HUMAN)//P39192

F-HEMBA1001008//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.4e-25:61:70//HOMO SAPIENS (HUMAN)//P39192

MAN)//P39194

F-HEMBA1001009//CUTICLE COLLAGEN 34//0.044:214:29//CAENORHABDITIS ELEGANS//P34687

F-HEMBA1001017//SYNDECAN-3 PRECURSOR (N-SYNDECAN) (NEUROGLYCAN)//5.0e-85:191:84//RATTUS NORVEGICUS (RAT)//P33671

5 F-HEMBA1001019

F-HEMBA1001020//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/6.7e-24:49:73//HOMO SAPIENS (HUMAN)//P39188

F-HEMBA1001022

10 F-HEMBA1001024//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//3.0e-11:61:59//HOMO SAPIENS (HUMAN)//P08547

F-HEMBA1001026//HYPOTHETICAL PROTEIN BB0073//0.94:63:34//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE)//O51100

F-HEMBA1001043//INVOLUCRIN//0.0036:238:25//SAGUINUS OEDIPUS (COTTON-TOP TAMARIN)//P24712

15 F-HEMBA1001051//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/3.3e-32:95:75//HOMO SAPIENS (HUMAN)//P39189

F-HEMBA1001052//CURROMYCIN RESISTANCE PROTEIN//1.0:31:38//STREPTOMYCES HYGROSCOPICUS//P16961

20 F-HEMBA1001059//N-ACETYLGALACTOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.4) (N-ACETYLGALACTOSAMINE-6-SULFATE SULFATASE) (GALACTOSE-6-SULFATE SULFATASE) (GALNAC6S SULFATASE) (CHONDROITINSULFATASE) (CHONDROITINASE)//3.2e-132:249:94//HOMO SAPIENS (HUMAN)//P34059

F-HEMBA1001060

F-HEMBA1001071//PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR//8.3e-23:51:96//HOMO SAPIENS (HUMAN)//P02461

25 F-HEMBA1001077//AUTOIMMUNE REGULATOR (APECED PROTEIN)//3.4e-06:37:56//HOMO SAPIENS (HUMAN)//O43918

F-HEMBA1001080//INFECTED CELL PROTEIN ICP34.5 (NEUROVIRULENCE FACTOR ICP34.5)//0.0012:70:38//HERPES SIMPLEX VIRUS (TYPE 1 / STRAW MGH-10)//P37319

F-HEMBA1001085//SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PPS) (PROTEIN PHOSPHATASE T) (PPT) (FRAGMENT)//0.00018:76:32//MUS MUSCULUS (MOUSE)//Q60676

30 F-HEMBA1001088//PINCH PROTEIN (PARTICULARLY INTERESTING NEW CYS-HIS PROTEIN)//3.5e-50:176:57//HOMO SAPIENS (HUMAN)//P48059

F-HEMBA1001094

35 F-HEMBA1001099//LIGHT-HARVESTING PROTEIN B800/850/890, ALPHA-2 CHAIN (EHA-ALPHA-2) (ANTENNA PIGMENT PROTEIN, ALPHA-2 CHAIN) (FRAGMENT)//1.0:15:60//ECTOTHIORHODOSPIRA HALOPHILA//P80101

F-HEMBA1001109//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/6.7e-37:102:82//HOMO SAPIENS (HUMAN)//P39189

F-HEMBA1001121//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//0.036:49:46//HOMO SAPIENS (HUMAN)//P08547

40 F-HEMBA1001122

F-HEMBA1001123

F-HEMBA1001133//HYPOTHETICAL 9.4 KD PROTEIN (ORF2)//0.86:29:41//FELINE IMMUNODEFICIENCY VIRUS (ISOLATE SAN DIEGO) (FIV), AND FELINE IMMUNODEFICIENCY VIRUS (ISOLATE PETALUMA) (FIV)//P19033

45 F-HEMBA1001137//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)//2.0e-22:103:52//HOMO SAPIENS (HUMAN)//P51523

F-HEMBA1001140//COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR//0.032:94:36//HOMO SAPIENS (HUMAN)//P53420

F-HEMBA1001172

50 F-HEMBA1001174//ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 5//2.9e-78:179:79//RATTUS NORVEGICUS (RAT)//P51646

F-HEMBA1001197//MAJOR PRION PROTEIN PRECURSOR (PRP) (PRP27-30) (PRP33-35C) (FRAGMENT)//0.051:96:32//CERCOCEBUS ATERRIMUS, AND MACACA SYLVANUS (BARBARY APE)//Q95145

F-HEMBA1001208

55 F-HEMBA1001213

F-HEMBA1001235//FIBRONECTIN (FN) (FRAGMENT)//0.76:50:38//ORYCTOLAGUS CUNICULUS (RABBIT)//P25789

Q28749

F-HEMBA1001247//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)//0.00052:16:81//VOLVOX CART-ERI//P21997

F-HEMBA1001257//2-ARYLPROPIONYL-COA EPIMERASE (EC 5.-.-.-)//1.6e-68:178:77//RATTUS NORVEGI-CUS (RAT)//P70473

F-HEMBA1001265//MANNAN ENDO-1,4-BETA-MANNOSIDASE A PRECURSOR (EC 3.2.1.78) (BETA- MAN-NANASE A) (1,4-BETA-D-MANNAN MANNANOHYDROLASE A)//0.67:23:60//PIROMYCES SP//P55296

F-HEMBA1001281//HYPOTHETICAL 8.9 KD PROTEIN YCF34 (ORF76)//0.83:48:35//PORPHYRA PURPU-REA//P51229

F-HEMBA1001286//COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR//1.3e-07:185:29//CAVIA PORCELLUS (GUINEA PIG)//Q60401

F-HEMBA1001289//METABOTROPIC GLUTAMATE RECEPTOR 3 PRECURSOR//0.00018:159:30//RATTUS NORVEGICUS (RAT)//P31422

F-HEMBA1001294

F-HEMBA1001299//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/5.3e-07:27:77//HOMO SAPIENS (HUMAN)//P39195

F-HEMBA1001302//45 KD CALCIUM-BINDING PROTEIN PRECURSOR (STROMAL CELL-DERIVED FACTOR 4) (SDF-4)//3.3e-61:150:76//MUS MUSCULUS (MOUSE)//Q61112

F-HEMBA1001303

F-HEMBA1001310//HYPOTHETICAL PROTEIN KIAA0161//2.7e-10:170:27//HOMO SAPIENS (HUMAN)//P50876

F-HEMBA1001319

F-HEMBA1001323

F-HEMBA1001326//HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PES4 INTERGENIC REGION//1.1e-39:144:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P43601

F-HEMBA1001327

F-HEMBA1001330

F-HEMBA1001351//VESICLE-ASSOCIATED MEMBRANE PROTEIN/SYNAPTOBREVIN BINDING PROTEIN (VAP-33)//1.9e-37:155:46//APLYSIA CALIFORNICA (CALIFORNIA SEA HARE)//Q16943

F-HEMBA1001361//RUBREDOXIN (RD)//0.95:44:29//ALCALIGENES EUTROPHUS//P31912

F-HEMBA1001375//AEROLYSIN REGULATORY PROTEIN//0.013:45:33//AEROMONAS SOBRIA//P09165

F-HEMBA1001377//SPERM PROTAMINE P1//1.0:22:40//PLANIGALE MACULATA SINUALIS (COMMON PLAN-IGALE)//O18746

F-HEMBA1001383//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN)//0.60:37:29//HUMAN IM-MUNODEFICIENCY VIRUS TYPE 1 (Z2/CDC-Z34 ISOLATE) (HIV-1)//P12506

F-HEMBA1001387//GTP-BINDING PROTEIN TC10//6.6e-43:83:92//HOMO SAPIENS (HUMAN)//P17081

F-HEMBA1001388//HYPOTHETICAL PROTEIN KIAA0136 (FRAGMENT)//0.00088:46:45//HOMO SAPIENS (HUMAN)//Q14149

F-HEMBA1001391

F-HEMBA1001398//CLOACIN (EC 3.1.-.-) (RIBONUCLEASE)//1.0:59:37//ESCHERICHIA COLI//P00645

F-HEMBA1001405//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930)//0.25:41:34//HOMO SAPIENS (HUMAN)//P22531

F-HEMBA1001407//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CON-TAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H]//4.0e-09:129:40//HOMO SAPIENS (HUMAN)//P04280

F-HEMBA1001411//HYPOTHETICAL 34.9 KD PROTEIN IN CYSJ-ENO INTERGENIC REGION (O313)//0.95:88:31//ESCHERICHIA COLI//P55140

F-HEMBA1001413//SOX-12 PROTEIN (FRAGMENT)//0.95:46:32//MUS MUSCULUS (MOUSE)//Q04890

F-HEMBA1001415//HISTONE H5//0.43:95:29//GALLUS GALLUS (CHICKEN)//P02259

F-HEMBA1001432//LANTIBIOTIC NISIN A PRECURSOR//0.77:46:32//LACTOCOCCUS LACTIS (SUBSP. LAC-TIS) (STREPTOCOCCUS LACTIS)//P13068

F-HEMBA1001433//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//4.8e-09:132:31//NYCTICEBUS COU-CANG (SLOW LORIS)//P08548

F-HEMBA1001435//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.2e-31:84:77//HOMO SAPIENS (HUMAN)//P39189

F-HEMBA1001442

F-HEMBA1001443//WINTER HINDRER P22790

F-HEMBA1001450//PROLINE-RICH PROTEIN LAS17//0.13:127:27//SACCHAROMYCES CEREVISIAE (BAK-)

- F-HEMBA1001672//CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)//2.7e-10:216:35//PLASMODIUM CYNOMOLGI (STRAIN BEROK)//P08672
- F-HEMBA1001675//NODULIN 20 PRECURSOR (N-20)//0.98:36:44//GLYCINE MAX (SOYBEAN)//P08960
- 5 F-HEMBA1001678//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/8.2e-13:62:64//HOMO SAPIENS (HUMAN)//P39195
- F-HEMBA1001681//HYPOTHETICAL 41.5 KD PROTEIN IN P6.5-VP48 INTERGENIC REGION (P40) (ORF3) (ORF102)//1.0:51:39//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV)//P24653
- 10 F-HEMBA1001702//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6)//0.017:54:37//TRYPANOSOMA BRUCEI BRUCEI//P24499
- F-HEMBA1001709//HYPOTHETICAL 21.2 KD PROTEIN IN TOR2-MNN4 INTERGENIC REGION//0.59:109:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P36042
- F-HEMBA1001711
- 15 F-HEMBA1001712//HYPOTHETICAL 6.9 KD PROTEIN IN 100 KD PROTEIN REGION//0.54:44:34//HUMAN AD-ENOVIRUS TYPE 41//P23690
- F-HEMBA1001714//ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR//1.2e-19:60:75//RATTUS NORVEGICUS (RAT)//Q03344
- F-HEMBA1001718//HYPOTHETICAL PROTEIN UL63//1.0:54:37//HUMAN CYTOMEGALOVIRUS (STRAIN AD169)//P16820
- 20 F-HEMBA1001723//HYPOTHETICAL 34.0 KD TRP-ASP REPEATS CONTAINING PROTEIN IN SIS1-MRPL2 INTERGENIC REGION//5.1e-26:90:53//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P41318
- F-HEMBA1001731//HYPOTHETICAL 16.6 KD PROTEIN//0.71:49:32//AVIAN INFECTIOUS BURSAL DISEASE VIRUS (STRAIN 52/70) (IBDV)//P25221
- F-HEMBA1001734
- 25 F-HEMBA1001744//SCY1 PROTEIN//2.1e-11:182:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53009
- F-HEMBA1001745//HYPOTHETICAL 11.6 KD PROTEIN IN NUT1-ARO2 INTERGENIC REGION PRECURSOR//1.0:36:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53116
- F-HEMBA1001746//PROTEIN-EXPORT MEMBRANE PROTEIN SEC6 HOMOLOG//0.94:48:35//MYCOBACTERIUM LEPRAE//P38388
- 30 F-HEMBA1001761
- F-HEMBA1001781//ZINC FINGER PROTEIN 19 (ZINC FINGER PROTEIN KOX12) (FRAGMENT)//0.028:47:40//HOMO SAPIENS (HUMAN)//P17023
- F-HEMBA1001784//HYPOTHETICAL 6.1 KD PROTEIN C03B1.10 IN CHROMOSOME X//0.00068:32:46//CAENORHABDITIS ELEGANS //Q11116
- 35 F-HEMBA1001791//METALLOTHIONEIN (MT)//1.0:34:35//PLEURONECTES PLATESSA (PLAICE)//P07216
- F-HEMBA1001800//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT)//1.5e-14:60:48//MUS MUSCULUS (MOUSE)//P16372
- F-HEMBA1001803
- 40 F-HEMBA1001804//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1 PRECURSOR//9.3e-17:56:57//ORYZA SATIVA (RICE)//P25074
- F-HEMBA1001808//PARANEOPLASTIC ENCEPHALOMYELITIS ANTIGEN HUD HOMOLOG (HU-ANTIGEN D)//0.75:97:31//RATTUS NORVEGICUS (RAT)//O09032
- 45 F-HEMBA1001809//IMMEDIATE-EARLY PROTEIN IE180//4.5e-11:206:36//PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV)//P11675
- F-HEMBA1001815//60S RIBOSOMAL PROTEIN L37-B (YL27) (FRAGMENT)//0.34:30:30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//P05733
- F-HEMBA1001819//ZINC FINGER PROTEIN 135//2.6e-102:262:66//HOMO SAPIENS (HUMAN)//P52742
- F-HEMBA1001820
- 50 F-HEMBA1001822//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15)//1.2e-18:251:33//MUS MUSCULUS (MOUSE)//P42567
- F-HEMBA1001824//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN)//4.7e-11:124:37//OVIS ARIES (SHEEP)//P26372
- F-HEMBA1001835
- 55 F-HEMBA1001844//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/4.3e-14:36:63//HOMO SAPIENS (HUMAN) //P11126
- F-HEMBA1001845//HYPOTHETICAL 10.5 KD PROTEIN IN 100 KD PROTEIN REGION//0.54:44:34//HUMAN AD-ENOVIRUS TYPE 41//P23690

F-HEMBA1001861

F-HEMBA1001864//HEAT-STABLE ENTEROTOXIN A3/A4 PRECURSOR (STA3/STA4) (ST-IB) (ST-H)//1.0:31:38//ESCHERICHIA COLI//P07965

F-HEMBA1001866//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT)//9.7e-42:234.41//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q09332

F-HEMBA1001869//HYPOTHETICAL 94.9 KD PROTEIN C22E12.11C IN CHROMOSOME I//5.3e-13:65.47//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10362

F-HEMBA1001888//HYPOTHETICAL 11.4 KD PROTEIN (ORF1)//0.85:62:37//STREPTOMYCES FRADIAE//P26800

F-HEMBA1001896//DIMETHYLGLYCINE DEHYDROGENASE PRECURSOR (EC 1.5.99.2) (ME2GLYDH)//9.8e-20:250:29//RATTUS NORVEGICUS (RAT)//Q63342

F-HEMBA1001910//EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E) (EIF4E) (MRNA CAP-BINDING PROTEIN) (EIF-4F 25 KD SUBUNIT)//0.94:44:38//CAENORHABDITIS ELEGANS//O61955

F-HEMBA1001912//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//8.7e-07:53:62//HOMO SAPIENS (HUMAN)//P39188

F-HEMBA1001913//GCN20 PROTEIN//1.8e-21:68:60//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P43535

F-HEMBA1001915//KLEE PROTEIN (KCRB3 PROTEIN)//0.94:64:21//ESCHERICHIA COLI//Q52280

F-HEMBA1001918

F-HEMBA1001921

F-HEMBA1001939//CHLOROPLAST 50S RIBOSOMAL PROTEIN L24//1.0:47:31//ODONTELLA SINENSIS//P49560

F-HEMBA1001940//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.0017:31:77//HOMO SAPIENS (HUMAN)//P39188

F-HEMBA1001942//HIBERNATION-ASSOCIATED PLASMA PROTEIN HP-27 PRECURSOR (HIBERNATOR-SPECIFIC BLOOD COMPLEX, 27 KD SUBUNIT)//1.0:77:28//TAMIAS ASIATICUS (CHIPMUNK)//Q06577

F-HEMBA1001945//HYPOTHETICAL 4.6 KD PROTEIN IN GP47-AGT INTERGENIC REGION (ORF E)//1.0:35:37//BACTERIOPHAGE T4//P32269

F-HEMBA1001950//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//0.43:18:44//DROSOPHILA YAKUBA (FRUIT FLY)//P03933

F-HEMBA1001960//HOMEBOX PROTEIN HOX-C5 (HOX-3D) (CP11)//0.17:12:66//HOMO SAPIENS (HUMAN)//Q00444

F-HEMBA1001962//HYPOTHETICAL 9.0 KD PROTEIN IN ADH4 5'REGION//1.0:30:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53056

F-HEMBA1001964

F-HEMBA1001967//HYPOTHETICAL PROTEIN UL61//0.027:111:36//HUMAN CYTOMEGALOVIRUS (STRAIN AD169)//P16818

F-HEMBA1001979

F-HEMBA1001987//HYPOTHETICAL 11.2 KD PROTEIN (ORF117)//1.0:83:32//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV)//O10356

F-HEMBA1001991//NEUROTOXIN 1 (TOXIN ATX-I)//0.99:31:45//ANEMONIA SULCATA (SNAKE-LOCKS SEA ANEMONE)//P01533

F-HEMBA1002003//GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, TESTIS-SPECIFIC (EC 1.2.1.12) (GAPDH)//5.5e-07:109:32//MUS MUSCULUS (MOUSE)//Q64467

F-HEMBA1002008

F-HEMBA1002018//EC PROTEIN HOMOLOG 2 (FRAGMENT)//0.83:66:33//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)//Q42377

F-HEMBA1002022//INSULIN//1.0:59:32//SQUALUS ACANTHIAS (SPINY DOGFISH)//P12704

F-HEMBA1002035//MONOCYTIC LEUKEMIA ZINC FINGER PROTEIN//8.3e-15:64:40//HOMO SAPIENS (HUMAN)//Q92794

F-HEMBA1002039//HYPOTHETICAL PROLINE-RICH PROTEIN KIAA0269//0.0070:70:40//HOMO SAPIENS (HUMAN)//Q92558

F-HEMBA1002049//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.5e-07:37:75//HOMO SAPIENS (HUMAN)//P39188

F-HEMBA1002084

F-HEMBA1002085

F-HEMBA1002086

F-HEMBA1002087

F-HEMBA1002102//ANKYRIN.//1.4e-12:106:35//MUS MUSCULUS (MOUSE)//Q02357
F-HEMBA1002113//EARLY NODULIN 20 PRECURSOR (N-20)//0.073:155:32//MEDICAGO TRUNCATULA (BARREL MEDIC)//P93329
F-HEMBA1002119//MALE SPECIFIC SPERM PROTEIN MST84DB//0.85:22:36//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q01643
F-HEMBA1002125//GAG POLYPROTEIN [CONTAINS: CORE PROTEINS P15, P12, P30]//0.35:111:33//FELINE SARCOMA VIRUS (STRAIN SNYDER-THEILEN)//P03338
F-HEMBA1002139//HYPOTHETICAL 12.4 KD PROTEIN IN SEC17-QCR1 INTERGENIC REGION.//0.88:72:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38192
F-HEMBA1002144
F-HEMBA1002150//THROMBOMODULIN (FETOMODULIN) (TM) (FRAGMENT)//4.8e-10:65:46//BOS TAURUS (BOVINE)//P06579
F-HEMBA1002151//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR//0.24:146:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32323
F-HEMBA1002153//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3)//0.93:58:25//APIS MELIFERA (HONEYBEE)//P34859
F-HEMBA1002160//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/5.1e-21:94:65//HOMO SAPIENS (HUMAN)//P39193
F-HEMBA1002161//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM//1.4e-51:180:56//SUS SCROFA (PIG)//P79293
F-HEMBA1002162//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/4.1e-40:102:75//HOMO SAPIENS (HUMAN)//P39193
F-HEMBA1002166//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.8e-13:133:45//HOMO SAPIENS (HUMAN)//P39188
F-HEMBA1002177//ZINC FINGER PROTEIN 142 (KIAA0236) (HA4654)//0.0014:153:26//HOMO SAPIENS (HUMAN)//P52746
F-HEMBA1002185
F-HEMBA1002189//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/0.86:46:45//HOMO SAPIENS (HUMAN)//P39194
F-HEMBA1002191//MALE SPECIFIC SPERM PROTEIN MST84DC//0.037:14:57//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q01644
F-HEMBA1002199
F-HEMBA1002204
F-HEMBA1002212//DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE DSOR1 (EC 2.7.1.-) (DOWNSTREAM OF RAF) (MAPKK)//3.2e-13:201:30//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q24324
F-HEMBA1002215//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)]//1.1e-62:147:84//MUS MUSCULUS (MOUSE)//P47226
F-HEMBA1002226//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.6e-26:168:44//HOMO SAPIENS (HUMAN)//P39188
F-HEMBA1002229//!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!!/6.8e-18:68:72//HOMO SAPIENS (HUMAN)//P39190
F-HEMBA1002237//EAMZP30-47 PROTEIN (FRAGMENT)//0.96:21:61//EIMERIA ACERVULINA//P21959
F-HEMBA1002241//METALLOTHIONEIN (MT)//0.95:25:48//PARACENTROTUS LIVIDUS (COMMON SEA URCHIN)//P80367
F-HEMBA1002253//METALLOTHIONEIN-II (MT-II)//0.97:27:48//MESOCRICETUS AURATUS (GOLDEN HAMSTER)//P17808
F-HEMBA1002257
F-HEMBA1002265//MALE SPECIFIC SPERM PROTEIN MST84DC//0.95:24:50//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q01644
F-HEMBA1002267//NEURONAL PROTEIN 3.1 (P311 PROTEIN)//0.94:33:33//GALLUS GALLUS (CHICKEN)//Q90667
F-HEMBA1002270
F-HEMBA1002321//HYPOTHETICAL IMMUNITY REGION PROTEIN 14//0.99:22:40//BACTERIOPHAGE PHI-105//P10437
F-HEMBA1002322//HYPOTHETICAL IMMUNITY REGION PROTEIN 15//0.99:22:40//BACTERIOPHAGE PHI-105//P10437
F-HEMBA1002323//HYPOTHETICAL IMMUNITY REGION PROTEIN 16//0.99:22:40//BACTERIOPHAGE PHI-105//P10437
F-HEMBA1002324//HYPOTHETICAL IMMUNITY REGION PROTEIN 17//0.99:22:40//BACTERIOPHAGE PHI-105//P10437
F-HEMBA1002325//HYPOTHETICAL IMMUNITY REGION PROTEIN 18//0.99:22:40//BACTERIOPHAGE PHI-105//P10437
F-HEMBA1002326//HYPOTHETICAL IMMUNITY REGION PROTEIN 19//0.99:22:40//BACTERIOPHAGE PHI-105//P10437
F-HEMBA1002327//HYPOTHETICAL IMMUNITY REGION PROTEIN 20//0.99:22:40//BACTERIOPHAGE PHI-105//P10437
F-HEMBA1002328//HYPOTHETICAL IMMUNITY REGION PROTEIN 21//0.99:22:40//BACTERIOPHAGE PHI-105//P10437
F-HEMBA1002329//HYPOTHETICAL IMMUNITY REGION PROTEIN 22//0.99:22:40//BACTERIOPHAGE PHI-105//P10437
F-HEMBA1002330//HYPOTHETICAL IMMUNITY REGION PROTEIN 23//0.99:22:40//BACTERIOPHAGE PHI-105//P10437
F-HEMBA1002331//HYPOTHETICAL IMMUNITY REGION PROTEIN 24//0.99:22:40//BACTERIOPHAGE PHI-105//P10437
F-HEMBA1002332//HYPOTHETICAL IMMUNITY REGION PROTEIN 25//0.99:22:40//BACTERIOPHAGE PHI-105//P10437
F-HEMBA1002333//HYPOTHETICAL IMMUNITY REGION PROTEIN 26//0.99:22:40//BACTERIOPHAGE PHI-105//P10437
F-HEMBA1002334//HYPOTHETICAL IMMUNITY REGION PROTEIN 27//0.99:22:40//BACTERIOPHAGE PHI-105//P10437
F-HEMBA1002335//HYPOTHETICAL IMMUNITY REGION PROTEIN 28//0.99:22:40//BACTERIOPHAGE PHI-105//P10437
F-HEMBA1002336//HYPOTHETICAL IMMUNITY REGION PROTEIN 29//0.99:22:40//BACTERIOPHAGE PHI-105//P10437
F-HEMBA1002337//HYPOTHETICAL IMMUNITY REGION PROTEIN 30//0.99:22:40//BACTERIOPHAGE PHI-105//P10437
F-HEMBA1002338//HYPOTHETICAL IMMUNITY REGION PROTEIN 31//0.99:22:40//BACTERIOPHAGE PHI-105//P10437
F-HEMBA1002339//HYPOTHETICAL IMMUNITY REGION PROTEIN 32//0.99:22:40//BACTERIOPHAGE PHI-105//P10437
F-HEMBA1002340//HYPOTHETICAL IMMUNITY REGION PROTEIN 33//0.99:22:40//BACTERIOPHAGE PHI-105//P10437
F-HEMBA1002341//HYPOTHETICAL IMMUNITY REGION PROTEIN 34//0.99:22:40//BACTERIOPHAGE PHI-105//P10437
F-HEMBA1002342//HYPOTHETICAL IMMUNITY REGION PROTEIN 35//0.99:22:40//BACTERIOPHAGE PHI-105//P10437
F-HEMBA1002343//HYPOTHETICAL IMMUNITY REGION PROTEIN 36//0.99:22:40//BACTERIOPHAGE PHI-105//P10437
F-HEMBA1002344//HYPOTHETICAL IMMUNITY REGION PROTEIN 37//0.99:22:40//BACTERIOPHAGE PHI-105//P10437
F-HEMBA1002345//HYPOTHETICAL IMMUNITY REGION PROTEIN 38//0.99:22:40//BACTERIOPHAGE PHI-105//P10437
F-HEMBA1002346//HYPOTHETICAL IMMUNITY REGION PROTEIN 39//0.99:22:40//BACTERIOPHAGE PHI-105//P10437
F-HEMBA1002347//HYPOTHETICAL IMMUNITY REGION PROTEIN 40//0.99:22:40//BACTERIOPHAGE PHI-105//P10437
F-HEMBA1002348//HYPOTHETICAL IMMUNITY REGION PROTEIN 41//0.99:22:40//BACTERIOPHAGE PHI-105//P10437
F-HEMBA1002349//HYPOTHETICAL IMMUNITY REGION PROTEIN 42//0.99:22:40//BACTERIOPHAGE PHI-105//P10437
F-HEMBA1002350//HYPOTHETICAL IMMUNITY REGION PROTEIN 43//0.99:22:40//BACTERIOPHAGE PHI-105//P10437
F-HEMBA1002351//HYPOTHETICAL IMMUNITY REGION PROTEIN 44//0.99:22:40//BACTERIOPHAGE PHI-105//P10437
F-HEMBA1002352//HYPOTHETICAL IMMUNITY REGION PROTEIN 45//0.99:22:40//BACTERIOPHAGE PHI-105//P10437
F-HEMBA1002353//HYPOTHETICAL IMMUNITY REGION PROTEIN 46//0.99:22:40//BACTERIOPHAGE PHI-105//P10437
F-HEMBA1002354//HYPOTHETICAL IMMUNITY REGION PROTEIN 47//0.99:22:40//BACTERIOPHAGE PHI-105//P10437
F-HEMBA1002355//HYPOTHETICAL IMMUNITY REGION PROTEIN 48//0.99:22:40//BACTERIOPHAGE PHI-105//P10437
F-HEMBA1002356//HYPOTHETICAL IMMUNITY REGION PROTEIN 49//0.99:22:40//BACTERIOPHAGE PHI-105//P10437
F-HEMBA1002357//HYPOTHETICAL IMMUNITY REGION PROTEIN 50//0.99:22:40//BACTERIOPHAGE PHI-105//P10437
F-HEMBA1002358//HYPOTHETICAL IMMUNITY REGION PROTEIN 51//0.99:22:40//BACTERIOPHAGE PHI-105//P10437
F-HEMBA1002359//HYPOTHETICAL IMMUNITY REGION PROTEIN 52//0.99:22:40//BACTERIOPHAGE PHI-105//P10437
F-HEMBA1002360//HYPOTHETICAL IMMUNITY REGION PROTEIN 53//0.99:22:40//BACTERIOPHAGE PHI-105//P10437
F-HEMBA1002361//HYPOTHETICAL IMMUNITY REGION PROTEIN 54//0.99:22:40//BACTERIOPHAGE PHI-105//P10437
F-HEMBA1002362//HYPOTHETICAL IMMUNITY REGION PROTEIN 55//0.99:22:40//BACTERIOPHAGE PHI-105//P10437

(MOUSE)//Q62415
 F-HEMBA1002348//PROBABLE E5 PROTEIN //0.43:30:50//HUMAN PAPILLOMAVIRUS TYPE 35//P27226
 F-HEMBA1002349
 5 F-HEMBA1002363//CHROMOSOME ASSEMBLY PROTEIN XCAP-E//5.7e-105:278:71//XENOPUS LAEVIS
 (AFRICAN CLAWED FROG)//P50533
 F-HEMBA1002381//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.3e-24:69:73//HOMO SAPIENS (HUMAN)//
 P39188
 F-HEMBA1002389//EARLY NODULIN 20 PRECURSOR (N-20)//0.16:110:31//MEDICAGO TRUNCATULA (BAR-
 REL MEDIC)//P93329
 10 F-HEMBA1002417//TIGHT JUNCTION PROTEIN ZO-1 (TIGHT JUNCTION PROTEIN 1)//2.6e-51:187:56//MUS
 MUSCULUS (MOUSE)//P39447
 F-HEMBA1002419//PROLINE-RICH PEPTIDE P-B//1.0:18:61//HOMO SAPIENS (HUMAN)//P02814
 F-HEMBA1002430//HYPOTHETICAL 12.3 KD PROTEIN IN GAP1-NAP1 INTERGENIC REGION//0.042:41:46//
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P36140
 15 F-HEMBA1002439//CHLOROPLAST 50S RIBOSOMAL PROTEIN L27 (FRAGMENT)//0.99:47:29//CALYPTRO-
 SPHAERA SPHAEROIDEA//P41548
 F-HEMBA1002458//OVARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74//4.1e-24:109:55//HOMO SAPI-
 ENS (HUMAN)//Q00994
 F-HEMBA1002460
 20 F-HEMBA1002462//SALIVARY PROLINE-RICH PROTEIN II-1 (FRAGMENT)//0.00025:80:30//HOMO SAPIENS
 (HUMAN)//P81489
 F-HEMBA1002469//PUTATIVE TUMOR SUPPRESSOR LUCA15//0.0012:110:33//HOMO SAPIENS (HUMAN)//
 P52756
 F-HEMBA1002475//PROLINE-RICH PROTEIN MP-3 (FRAGMENT)//0.37:106:33//MUS MUSCULUS
 25 (MOUSE)//P05143
 F-HEMBA1002477//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.3e-34:96:71//HOMO SAPIENS (HU-
 MAN)//P39194
 F-HEMBA1002486
 F-HEMBA1002495//LIGHT-MEDIATED DEVELOPMENT PROTEIN DET1//2.9e-31:110:39//ARABIDOPSIS
 30 THALIANA (MOUSE-EAR CRESS)//P48732
 F-HEMBA1002498//SFT2 PROTEIN//1.0:54:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//
 P38166
 F-HEMBA1002503//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.0e-06:49:63//HOMO SAPIENS (HUMAN)//
 P39188
 35 F-HEMBA1002508//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.6e-22:169:44//HOMO SAPIENS (HU-
 MAN)//P39195
 F-HEMBA1002513//HYPOTHETICAL 89.8 KD PROTEIN F41H10.6 IN CHROMOSOME IV//0.00017:79:35//
 CAENORHABDITIS ELEGANS//Q20296
 F-HEMBA1002515
 40 F-HEMBA1002538//ATP SYNTHASE E CHAIN, MITOCHONDRIAL (EC 3.6.1.34)//1.0:53:37//SACCHAROMY-
 CES CEREVISIAE (BAKER'S YEAST)//P81449
 F-HEMBA1002542//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/5.7e-32:96:75//HOMO SAPIENS (HUMAN)//
 P39188
 F-HEMBA1002547//AGRN PRECURSOR//2.5e-100:218:80//RATTUS NORVEGICUS (RAT)//P25304
 45 F-HEMBA1002552//HEP27 PROTEIN (PROTEIN D)//9.5e-12:29:82//HOMO SAPIENS (HUMAN)//Q13268
 F-HEMBA1002555//COLLAGEN ALPHA 1(III) CHAIN//2.4e-15:207:36//BOS TAURUS (BOVINE)//P04258
 F-HEMBA1002558//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.0:34:50//HOMO SAPIENS (HUMAN)//
 P39193
 F-HEMBA1002561//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//1.5e-05:49:46//NYCTICEBUS COU-
 50 CANG (SLOW LORIS)//P08548
 F-HEMBA1002569//SINGLE-STRANDED DNA-BINDING PROTEIN P12//0.97:60:33//BACTERIOPHAGE
 PRD1//P17637
 F-HEMBA1002583
 F-HEMBA1002590//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/5.6e-15:54:55//HOMO SAPIENS (HUMAN)//
 55 P39188
 F-HEMBA1002604//SMYD4 PROTEIN//1.0:100:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//

P40318

F-HEMBA1002621//CYTOCHROME B6-F COMPLEX 3.5 KD SUBUNIT (CYTOCHROME B6-F COMPLEX SUB-UNIT 6)//1.0:20:55//ZEA MAYS (MAIZE)//P19445

F-HEMBA1002624//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)//0.0035:124:33//NICOTIANA TABACUM (COMMON TOBACCO)//P13983

F-HEMBA1002628

F-HEMBA1002629//IMMEDIATE-EARLY PROTEIN IE180//0.84:80:36//PSEUDORABIES VIRUS (STRAIN KAP-LAN) (PRV)//P33479

F-HEMBA1002645//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.8e-16:57:68//HOMO SAPIENS (HUMAN)//P39193

F-HEMBA1002651

F-HEMBA1002659//CUTICLE COLLAGEN 2//0.0077:77:38//CAENORHABDITIS ELEGANS//P17656

F-HEMBA1002661//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//2.3e-89:116:72//HOMO SAPIENS (HU-MAN)//P08547

F-HEMBA1002666//BETA CRYSTALLIN A4//0.18:58:44//GALLUS GALLUS (CHICKEN)//P49152

F-HEMBA1002678

F-HEMBA1002679//GLUTAMIC ACID-RICH PROTEIN PRECURSOR//5.7e-06:219:27//PLASMODIUM FALCI-PARUM (ISOLATE FC27 / PAPUA NEW GUINEA)//P13816

F-HEMBA1002688//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT)//1.1e-07:198:32//NEPHILA CLA-UIPES (ORB SPIDER)//P46804

F-HEMBA1002696//COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLA-GEN)//0.16:158:33//HOMO SAPIENS (HUMAN)//Q02388

F-HEMBA1002703//HYPOTHETICAL BHLF1 PROTEIN//0.78:147:29//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4)//P03181

F-HEMBA1002712//11.2 KD PROTEIN (ORF 103)//0.029:75:34//BACTERIOPHAGE PF1//P25133

F-HEMBA1002716//50S RIBOSOMAL PROTEIN L28//1.0:44:27//BACILLUS SUBTILIS//P37807

F-HEMBA1002728//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/5.4e-18:56:75//HOMO SAPIENS (HUMAN)//P39195

F-HEMBA1002730//HYPOTHETICAL PROTEIN MJ0316//0.097:84:35//METHANOCOCCUS JANNASCHII//Q57764

F-HEMBA1002742//APOLIPOPROTEIN C-III PRECURSOR (APO-CIII)//0.97:26:50//SUS SCROFA (PIG)//P27917

F-HEMBA1002746//CALPHOTIN//0.35:65:35//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q02910

F-HEMBA1002748//PLATELET GLYCOPROTEIN IB BETA CHAIN PRECURSOR (GP-IB BETA) (GPIBB)//1.0:74:32//MUS MUSCULUS (MOUSE)//P56400

F-HEMBA1002750//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/7.0e-15:49:75//HOMO SAPIENS (HUMAN)//P39188

F-HEMBA1002768//HYPOTHETICAL 72.2 KD PROTEIN C12C2.05C IN CHROMOSOME II//0.00036:197:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09746

F-HEMBA1002770//UTEROGLOBIN PRECURSOR (BLASTOKININ)//0.23:88:27//ORYCTOLAGUS CUNICU-LUS (RABBIT)//P02779

F-HEMBA1002777//HOMEBOX PROTEIN HOX-A4 (HOX-1.4) (MH-3)//0.00018:67:43//MUS MUSCULUS (MOUSE)//P06798

F-HEMBA1002779//HYPOTHETICAL 17.6 KD PROTEIN IN NPR1-RPS3 INTERGENIC REGION//0.70:30:53//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53880

F-HEMBA1002780//OLFACTORY RECEPTOR 3 (K10) (FRAGMENT)//1.0:31:45//MUS MUSCULUS (MOUSE)//Q60879

F-HEMBA1002794//HMG-Y RELATED PROTEIN B (SB16B PROTEIN) (FRAGMENT)//0.0044:66:37//GLYCINE MAX (SOYBEAN)//Q10370

F-HEMBA1002801

F-HEMBA1002810//HYPOTHETICAL 25.9 KD PROTEIN AH6.3 IN CHROMOSOME II//0.0033:116:31//CAENORHABDITIS ELEGANS//Q09202

F-HEMBA1002816//HYPOTHETICAL 47.1 KD PROTEIN C9G1.13C IN CHROMOSOME I//1.0e-17:68:48//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//O14308

F-HEMBA1002818//FIBULIN-2 PRECURSOR//2.1e-27:92:44//MUS MUSCULUS (MOUSE)//P37889

F-HEMBA1002822//FIBULIN-2 PRECURSOR

F-HEMBA1002830

- F-HEMBA1002850//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//1.0:27:37//METRIDIDIUM SENILE (BROWN SEA ANEMONE) (FRILLED SEA ANEMONE)//O47493
- F-HEMBA1002863//PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV (PHOTOSYSTEM I 8.1 KD PROTEIN) (P30 PROTEIN) (PSI-E)//0.84:37:43//SYNECHOCYSTIS SP. (STRAIN PCC 6803)//P12975
- 5 F-HEMBA1002876//OCTAPEPTIDE-REPEAT PROTEIN T2//0.74:58:34//MUS MUSCULUS (MOUSE)//Q06666
- F-HEMBA1002886
- F-HEMBA1002896//HOMEODOMAIN PROTEIN HOX-B3 (HOX-2G) (HOX-2.7)//4.7e-05:84:35//HOMO SAPIENS (HUMAN)//P14651
- 10 F-HEMBA1002921//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN)//0.21:42:42//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (RF/HAT ISOLATE) (HIV-1)//P05908
- F-HEMBA1002924//EC PROTEIN HOMOLOG 2 (FRAGMENT)//0.85:75:22//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)//Q42377
- F-HEMBA1002934//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.4e-31:92:72//HOMO SAPIENS (HUMAN)//P39188
- 15 F-HEMBA1002935//GASTRULA ZINC FINGER PROTEIN XLCGF58.1 (FRAGMENT)//7.7e-06:187:29//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P18730
- F-HEMBA1002937//SUPPRESSOR PROTEIN SRP40//0.00031:150:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32583
- 20 F-HEMBA1002939//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN)//5.2e-25:225:33//HOMO SAPIENS (HUMAN)//P16157
- F-HEMBA1002944
- F-HEMBA1002951//TRICHOHYALIN//0.0011:220:24//HOMO SAPIENS (HUMAN)//Q07283
- F-HEMBA1002954//PROBABLE E8 PROTEIN//0.98:49:32//BOVINE PAPILLOMAVIRUS TYPE 4//P08352
- F-HEMBA1002968//ACCESSORY GLAND PEPTIDE PRECURSOR (PARAGONIAL PEPTIDE B)//0.93:41:34//DROSOPHILA SECHELLIA (FRUIT FLY)//O18417
- 25 F-HEMBA1002970//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//0.00010:35:62//HOMO SAPIENS (HUMAN)//P39193
- F-HEMBA1002971//INSULIN//1.0:31:35//HYDROLAGUS COLLIEI (SPOTTED RATFISH) (PACIFIC RATFISH), AND CHIMAERA MONSTROSA (RABBIT FISH)//P09536
- 30 F-HEMBA1002973//CAMP-DEPENDENT 3',5'-CYCLIC PHOSPHODIESTERASE 4B (EC 3.1.4.17) (DPDE4)//3.0e-29:63:100//RATTUS NORVEGICUS (RAT)//P14646
- F-HEMBA1002997//HYPOTHETICAL 106.5 KD PROTEIN IN CTT1-PRP31 INTERGENIC REGION//1.0e-08:211:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53253
- F-HEMBA1002999//SUPPRESSOR PROTEIN SRP40//0.026:175:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32583
- 35 F-HEMBA1003021//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.3e-36:102:70//HOMO SAPIENS (HUMAN)//P39194
- F-HEMBA1003033//HYPOTHETICAL 23.1 KD PROTEIN CY277.20C//0.029:75:29//MYCOBACTERIUM TUBERCULOSIS//P71779
- 40 F-HEMBA1003034//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//6.3e-23:144:46//HOMO SAPIENS (HUMAN)//P39192
- F-HEMBA1003035//HYPOTHETICAL 13.3 KD PROTEIN IN AROD-COMER INTERGENIC REGION//0.99:55:30//BACILLUS SUBTILIS//P54457
- F-HEMBA1003037//DNA-BINDING PROTEIN INHIBITOR ID-4//0.17:42:40//HOMO SAPIENS (HUMAN)//P47928
- 45 F-HEMBA1003041//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)//0.69:28:46//HOMO SAPIENS (HUMAN)//P30808
- F-HEMBA1003046//MITOCHONDRIAL PROCESSING PROTEASE BETA SUBUNIT PRECURSOR (EC 3.4.24.64) (BETA-MPP) (P-52)//7.9e-124:253:96//HOMO SAPIENS (HUMAN)//O75439
- 50 F-HEMBA1003064//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3)//0.25:263:22//TRYPANOSOMA BRUCEI BRUCEI//P04540
- F-HEMBA1003067//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION//4.1e-05:189:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53214
- F-HEMBA1003071//CUTICLE COLLAGEN 40//6.0e-07:126:38//CAENORHABDITIS ELEGANS//P34804
- 55 F-HEMBA1003077//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN)//2.4e-10:26:34//HOMO SAPIENS (HUMAN) (HUMAN) (HUMAN)
- F-HEMBA1003078//RETRON VIMON-RELATED PROTEIN (CONTAINS REVERSED REPEATS) (P11369)
- F-HEMBA1003079//ENDONUCLEASE//7.2e-05:60:40//MUS MUSCULUS (MOUSE)//P11369

F-HEMBA1003079//PROTEIN Q300./0.0012:16:87/MUS MUSCULUS (MOUSE)//Q02722
F-HEMBA1003083/////ALU SUBFAMILY SB WARNING ENTRY /////3.3e-32:95:75/HOMO SAPIENS (HUMAN)//
P39189
F-HEMBA1003086
F-HEMBA1003096//PROTAMINE IA (IRIDINE IA)/0.36:20:40/SALMO IRIDEUS (RAINBOW TROUT)//P02328
F-HEMBA1003098/////ALU SUBFAMILY J WARNING ENTRY /////4.4e-09:43:72/HOMO SAPIENS (HUMAN)//
P39188
F-HEMBA1003117//PUTATIVE CUTICLE COLLAGEN C09G5.5/1.0:88:38//CAENORHABDITIS ELEGANS//
Q09456
F-HEMBA1003129//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3)/0.61:63:25//APIS MEL-
LIFERA (HONEYBEE)//P34859
F-HEMBA1003133//COLLAGEN ALPHA 2(VIII) CHAIN (ENDOTHELIAL COLLAGEN) (FRAGMENT)/0.48:79:
37//HOMO SAPIENS (HUMAN)//P25067
F-HEMBA1003136//MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP-MANNOSE-1-
PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE)/3.6e-25:190:34//SAC-
CHAROMYCES CEREVISIAE (BAKER'S YEAST)//P41940
F-HEMBA1003142
F-HEMBA1003148//HYPOTHETICAL 56.4 KD PROTEIN IN RPL30-CWH41 INTERGENIC REGION PRECUR-
SOR./0.068:171:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53189
F-HEMBA1003166/////ALU SUBFAMILY SC WARNING ENTRY /////1.8e-13:54:66//HOMO SAPIENS (HUMAN)//
P39192
F-HEMBA1003175//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION/0.015:147:
31//SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53214
F-HEMBA1003179//PROBABLE TRNA (5-METHYLAMINOMETHYL-2-THIOURIDYLATE)-METHYLTRANS-
FERASE (EC 2.1.1.61)/2.6e-51:164:47//BACILLUS SUBTILIS//O35020
F-HEMBA1003197
F-HEMBA1003199//HOMEBOX PROTEIN HOX-A4 (HOX-1D) (HOX-1.4)/0.00049:83:38//HOMO SAPIENS
(HUMAN)//Q00056
F-HEMBA1003202//SPERM PROTAMINE P1/0.98:53:28//PLANIGALE GILESI (FLAT-SKULLED MARSUPIAL
MOUSE)//O18747
F-HEMBA1003204/////ALU SUBFAMILY SQ WARNING ENTRY /////5.2e-22:42:80//HOMO SAPIENS (HU-
MAN)//P39194
F-HEMBA1003212/////ALU SUBFAMILY SP WARNING ENTRY /////1.6e-18:74:71//HOMO SAPIENS (HUMAN)//
P39193
F-HEMBA1003220/////ALU SUBFAMILY SQ WARNING ENTRY /////3.3e-18:56:78//HOMO SAPIENS (HU-
MAN)//P39194
F-HEMBA1003222//HYPOTHETICAL 37.5 KD PROTEIN IN GNTR-HTPG INTERGENIC REGION/0.0018:159:
27//BACILLUS SUBTILIS//P46327
F-HEMBA1003229//DIHYDRODIPICOLINATE SYNTHASE 1 PRECURSOR (EC 4.2.1.52) (DHDPDS)/1.0:85:28//
TRITICUM AESTIVUM (WHEAT)//P24846
F-HEMBA1003235//TROPOMYOSIN/8.3e-07:109:33//SCHIZOSACCHAROMYCES POMBE (FISSION
YEAST)//Q02088
F-HEMBA1003250
F-HEMBA1003257//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT)/1.5e-07:27:74//OWENIA FUSI-
FORMIS//P21260
F-HEMBA1003273
F-HEMBA1003276
F-HEMBA1003278
F-HEMBA1003281//HOMEBOX PROTEIN HOX-A4 (CHOX-1.4)/0.0053:116:36//GALLUS GALLUS (CHICK-
EN)//P17277
F-HEMBA1003286//DNA-DIRECTED RNA POLYMERASE SUBUNIT N (EC 2.7.7.6)/0.96:37:35//SULFOLOBUS
ACIDOCDARIUS//P39472
F-HEMBA1003291//5'-AMP-ACTIVATED PROTEIN KINASE, CATALYTIC ALPHA-2 CHAIN (EC 2.7.1.-) (AMPK
ALPHA-2 CHAIN) (FRAGMENT)/3.3e-15:68:39//SUS SCROFA (PIG)//Q28948
F-HEMBA1003296//PULMONARY SURFACTANT-ASSOCIATED PROTEIN B (SR-B-KD PROTEIN) (PM-
28)
F-HEMBA1003304//MITOCHONDRIA MEMBRANE PROTEIN (MEMBRANE PROTEIN) (MTMP)

F-HEMBA1003304//MITOCHONDRIA MEMBRANE PROTEIN (MEMBRANE PROTEIN) (MTMP) (P46750

- F-HEMBA1003309//HYPOTHETICAL 7.9 KD PROTEIN//0.69:54:37//VACCINIA VIRUS (STRAIN WR), AND VACCINIA VIRUS (STRAIN COPENHAGEN)//P04306
- F-HEMBA1003314//MIXED LINEAGE KINASE 2 (EC 2.7.1.-) (FRAGMENT)//2.3e-06:143:22//HOMO SAPIENS (HUMAN)//Q02779
- 5 F-HEMBA1003322//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.5e-30:53:77//HOMO SAPIENS (HUMAN)//P39194
- F-HEMBA1003327
- F-HEMBA1003328//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT)//0.53:21:42//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BH5 ISOLATE) (HIV-1)//P04612
- 10 F-HEMBA1003330//LONG NEUROTOXIN 3 (TOXIN VN2)//1.0:26:34//DENDROASPIS POLYLEPIS POLYLEPIS (BLACK MAMBA)//P25667
- F-HEMBA1003348//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/6.5e-09:56:66//HOMO SAPIENS (HUMAN)//P39194
- F-HEMBA1003369//ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR//0.0042:97:36//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)//P40602
- 15 F-HEMBA1003370//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/7.0e-18:99:53//HOMO SAPIENS (HUMAN)//P39188
- F-HEMBA1003373
- F-HEMBA1003376//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/4.7e-16:60:75//HOMO SAPIENS (HUMAN)//P39189
- 20 F-HEMBA1003380//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.8e-10:50:68//HOMO SAPIENS (HUMAN)//P39188
- F-HEMBA1003384
- F-HEMBA1003395//PROBABLE E5 PROTEIN//0.62:64:29//HUMAN PAPILLOMAVIRUS TYPE 16//P06927
- 25 F-HEMBA1003402//HYPOTHETICAL 12.0 KD PROTEIN IN TUB1-CPR3 INTERGENIC REGION PRECURSOR//0.89:74:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q04521
- F-HEMBA1003403//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT)//0.0010:69:33//RATTUS NORVEGICUS (RAT)//P10164
- F-HEMBA1003408//WEB1 PROTEIN (PROTEIN TRANSPORT PROTEIN SEC31)//4.8e-06:93:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38968
- 30 F-HEMBA1003417//PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS: CHONDROCALCIN]//0.0021:140:34//MUS MUSCULUS (MOUSE)//P28481
- F-HEMBA1003418//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75)//1.7e-14:188:33//HOMO SAPIENS (HUMAN)//Q08170
- 35 F-HEMBA1003433//DNA REPAIR PROTEIN XRS2//1.0:88:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P33301
- F-HEMBA1003447//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT)//0.0061:69:33//RATTUS NORVEGICUS (RAT)//P10164
- F-HEMBA1003461//SPIDROIN 1 (DRAGLINE SILK FIBROIN 1) (FRAGMENT)//2.3e-09:239:33//NEPHILA CLAVIPES (ORB SPIDER)//P19837
- 40 F-HEMBA1003463//METALLOTHIONEIN-A (MTA) (FRAGMENT)//1.0:40:35//SPHAERECHINUS GRANULARIS (PURPLE SEA URCHIN)//Q26497
- F-HEMBA1003480//FUSARIC ACID RESISTANCE PROTEIN FUSB//0.0043:96:32//BURKHOLDERIA CEPACIA (PSEUDOMONAS CEPACIA)//P24127.
- 45 F-HEMBA1003528//36.4 KD PROLINE-RICH PROTEIN//6.4e-15:167:33//LYCOPERSICON ESCULENTUM (TOMATO)//Q00451
- F-HEMBA1003531//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.2e-18:56:78//HOMO SAPIENS (HUMAN)//P39189
- F-HEMBA1003538//COMPLEMENT C1R COMPONENT PRECURSOR (EC 3.4.21.41)//2.5e-28:136:47//HOMO SAPIENS (HUMAN)//P00736
- 50 F-HEMBA1003545//INSULIN GENE ENHANCER PROTEIN ISL-2 (ISLET-2)//9.2e-105:217:85//RATTUS NORVEGICUS (RAT)//P50480
- F-HEMBA1003548
- F-HEMBA1003555//HYPOTHETICAL 31.9 KD PROTEIN IN BET1-PAN1 INTERGENIC REGION//8.7e-57:180:55//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40558
- 55 F-HEMBA1003556//HYPOTHETICAL 12.0 KD PROTEIN IN TUB1-CPR3 INTERGENIC REGION PRECURSOR//0.89:74:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q04521
- F-HEMBA1003557//BACTERIOPHAGE T4 (FRAGMENT)//1.0:40:35//SPHAERECHINUS GRANULARIS (PURPLE SEA URCHIN)//Q26497
- F-HEMBA1003560//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA 2 SUBUNIT (G GAMMA 2)

F-HEMBA1003742//MALE SPECIFIC SPERM PROTEIN MST84DB//0.066:72:33//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q01643

F-HEMBA1003758

F-HEMBA1003760//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN)//1.5e-51:220:52//MUS MUSCULUS (MOUSE)//Q61221

F-HEMBA1003773

F-HEMBA1003783

F-HEMBA1003784

F-HEMBA1003799//SHORT NEUROTOXIN 1 (TOXIN AA C)//0.95:27:37//ACANTHOPHIS ANTARCTICUS (COMMON DEATH ADDER)//P01434

F-HEMBA1003803//GAG POLYPROTEIN [CONTAINS: CORE PROTEINS P15, P12, P30]//0.46:96:34//FELINE SARCOMA VIRUS (STRAIN SNYDER-THEILEN)//P03338

F-HEMBA1003804//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)//0.019:30:50//HOMO SAPIENS (HUMAN)//P30808

F-HEMBA1003805//HYPOTHETICAL 75.0 KD PROTEIN B0280.11 IN CHROMOSOME III//1.8e-20:109:47//CAENORHABDITIS ELEGANS//P42083

F-HEMBA1003807

F-HEMBA1003827//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT)//2.1e-09:23:78//OWENIA FUSIFORMIS//P21260

F-HEMBA1003836//MOB1 PROTEIN (MPS1 BINDER 1)//2.0e-31:134:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40484

F-HEMBA1003838//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/3.9e-22:39:76//HOMO SAPIENS (HUMAN)//P39192

F-HEMBA1003856

F-HEMBA1003864//HYPOTHETICAL 39.4 KD PROTEIN IN MET1-SIS2 INTERGENIC REGION//1.5e-15:194:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P36151

F-HEMBA1003866//PROTEIN A39//0.0027:72:33//VACCINIA VIRUS (STRAIN COPENHAGEN)//P21062

F-HEMBA1003879//80 KD NUCLEAR CAP BINDING PROTEIN (NCBP 80 KD SUBUNIT) (CBP80)//2.9e-16:22:100//HOMO SAPIENS (HUMAN)//Q09161

F-HEMBA1003880//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//0.99:39:38//FELIS SILVESTRIUS CATUS (CAT)//P48896

F-HEMBA1003885//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/3.5e-28:47:76//HOMO SAPIENS (HUMAN)//P39193

F-HEMBA1003893//HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION//1.7e-57:215:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53215

F-HEMBA1003902

F-HEMBA1003908

F-HEMBA1003926//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.3e-10:60:63//HOMO SAPIENS (HUMAN)//P39188

F-HEMBA1003937//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/8.1e-29:68:64//HOMO SAPIENS (HUMAN)//P39194

F-HEMBA1003939//PROTEIN Q300//0.0025:24:62//MUS MUSCULUS (MOUSE)//Q02722

F-HEMBA1003942//EXCITATORY INSECT TOXIN BJXTR-IT PRECURSOR (BJ-XTRIT)//0.084:67:31//BUTHOTUS JUDAICUS (SCORPION) (HOTTENTOTTA JUDAICA)//P56637

F-HEMBA1003950//HYPOTHETICAL 8.1 KD PROTEIN IN SPEA-METK INTERGENIC REGION (O71)//0.95:26:34//ESCHERICHIA COLI//P46878

F-HEMBA1003953//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT)//2.5e-17:89:46//MUS MUSCULUS (MOUSE)//P16372

F-HEMBA1003958//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//4.2e-23:43:76//HOMO SAPIENS (HUMAN)//P08547

F-HEMBA1003959

F-HEMBA1003976//HYPOTHETICAL PROTEIN KIAA0076 (HA0936)//0.99:88:28//HOMO SAPIENS (HUMAN)//Q14999

F-HEMBA1003978//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930)//0.98:19:57//HOMO SAPIENS (HUMAN)//P22531

F-HEMBA1003980

F-HEMBA1003982//MYCOBACTERIUM THERMOPRAE//P46886

F-HEMBA1003987//HYPOTHETICAL PROTEIN UL66//0.27:65:33//HUMAN CYTOMEGALOVIRUS (STRAIN

AD169)//P16822

F-HEMBA1003989//MALE SPECIFIC SPERM PROTEIN MST84DB//5.2e-05:64:40//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q01643

F-HEMBA1004000//PROTEIN Q300//0.00042:17:82//MUS MUSCULUS (MOUSE)//Q02722

5 F-HEMBA1004011//ALPHA-TYPE CALCITONIN GENE-RELATED PEPTIDE PRECURSOR (CGRP-1)//0.47:106:32//HOMO SAPIENS (HUMAN)//P06881

F-HEMBA1004012//ATP SYNTHASE PROTEIN 9, MITOCHONDRIAL (EC 3.6.1.34) (LIPID-BINDING PROTEIN)//0.96:36:33//PARAMECIUM TETRAURELIA//P16001

10 F-HEMBA1004015//HYPOTHETICAL 29.3 KD PROTEIN B0280.6 IN CHROMOSOME III//0.00018:90:34//CAENORHABDITIS ELEGANS//P41997

F-HEMBA1004024//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/5.1e-34:75:80//HOMO SAPIENS (HUMAN)//P39194

F-HEMBA1004038

F-HEMBA1004042

15 F-HEMBA1004045//40S RIBOSOMAL PROTEIN S27A//1.0:20:55//ASPARAGUS OFFICINALIS (GARDEN ASPARAGUS)//P31753

F-HEMBA1004048//PROLINE-RICH PROTEIN MP-3 (FRAGMENT)//1.3e-06:158:35//MUS MUSCULUS (MOUSE)//P05143

20 F-HEMBA1004049//32 KD HEAT SHOCK PROTEIN (4-1 PROTEIN)//0.098:106:32//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD)//P54658

F-HEMBA1004055//HYPOTHETICAL PROTEIN HI0258/259//0.87:133:23//HAEMOPHILUS INFLUENZAE//P43974

F-HEMBA1004056//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/3.3e-25:39:64//HOMO SAPIENS (HUMAN)//P39191

25 F-HEMBA1004074//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/9.9e-08:35:68//HOMO SAPIENS (HUMAN)//P39188

F-HEMBA1004086

F-HEMBA1004097//IMMEDIATE-EARLY PROTEIN IE4 (IE68) (FRAGMENT)//0.71:95:35//HERPES SIMPLEX VIRUS (TYPE 2)//P14379

30 F-HEMBA1004111//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.7e-26:84:64//HOMO SAPIENS (HUMAN)//P39188

F-HEMBA1004131//SEPTIN 2 HOMOLOG (FRAGMENT)//2.8e-34:108:63//HOMO SAPIENS (HUMAN)//Q14141

F-HEMBA1004132//HYPOTHETICAL PROTEIN HI1736//1.0:44:34//HAEMOPHILUS INFLUENZAE//P44300

35 F-HEMBA1004133//HYPOTHETICAL 8.5 KD PROTEIN CY274.40C//0.89:21:57//MYCOBACTERIUM TUBERCULOSIS//Q10826

F-HEMBA1004138//EARLY NODULIN 75 (N-75) (NGM-75) (FRAGMENT)//0.016:39:41//MEDICAGO SATIVA (ALFALFA)//P11728

40 F-HEMBA1004143//CYTOCHROME C OXIDASE POLYPEPTIDE VIII PRECURSOR (EC 1.9.3.1)//0.93:34:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P04039

F-HEMBA1004146//BASIC PROLINE-RICH PEPTIDE P-E (IB-9)//0.63:52:36//HOMO SAPIENS (HUMAN)//P02811

F-HEMBA1004150//METALLOTHIONEIN-II (MT-II)//1.0:20:45//MUS MUSCULUS (MOUSE)//P02798

45 F-HEMBA1004164//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/3.0e-13:57:71//HOMO SAPIENS (HUMAN)//P39195

F-HEMBA1004168//V-TYPE SODIUM ATP SYNTHASE SUBUNIT F (EC 3.6.1.34) (NA(+)-TRANSLOCATING ATPASE SUBUNIT F)//0.00035:90:34//ENTEROCOCCUS HIRAE//P43437

F-HEMBA1004199//HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III//5.1e-14:115:31//CAENORHABDITIS ELEGANS//P34529

50 F-HEMBA1004200

F-HEMBA1004202//YPT1-RELATED PROTEIN 1//2.5e-24:96:52//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//P11620

F-HEMBA1004203//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/2.2e-09:48:64//HOMO SAPIENS (HUMAN)//P39193

55 F-HEMBA1004207//HYPOTHETICAL 8.7 KD PROTEIN IN BPL22 BPL23 INTERGENIC REGION

F-HEMBA1004225//MELANIN-PRODUCING PROTEIN IN MELANOPHILUS

PRAIA//P15114

F-HEMBA1004227//PUTATIVE PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C) (KIAA0015)//5.9e-06:109:
 33//HOMO SAPIENS (HUMAN)//P49593
 F-HEMBA1004238//VERY HYPOTHETICAL XYLU PROTEIN//0.98:39:38//ESCHERICHIA COLI//P05056
 F-HEMBA1004241//SOX-13 PROTEIN (FRAGMENT)//0.66:36:38//MUS MUSCULUS (MOUSE)//Q04891
 5 F-HEMBA1004246
 F-HEMBA1004248//INSULIN-INDUCED GROWTH RESPONSE PROTEIN CL-6 (IMMEDIATE-EARLY PROTEIN
 CL-6)//1.0e-43:98:84//RATTUS NORVEGICUS (RAT)//Q08755
 F-HEMBA1004264//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT)//0.014:160:28//NEPHILA CLA-
 VIPES (ORB SPIDER)//P46804
 10 F-HEMBA1004267//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.8e-52:56:83//HOMO SAPIENS (HUMAN)//
 P39189
 F-HEMBA1004272
 F-HEMBA1004274//HYPOTHETICAL 13.0 KD PROTEIN F59B2.10 IN CHROMOSOME III//0.00084:33:54//
 CAENORHABDITIS ELEGANS//P34485
 15 F-HEMBA1004275//HYPOTHETICAL 56.5 KD PROTEIN IN CAJ1-HOM3 INTERGENIC REGION//9.3e-06:125:
 27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40034
 F-HEMBA1004276//BETA-ADAPTIN 1 (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN BETA SUBUNIT)
 (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 BETA LARGE CHAIN) (AP105A)//3.7e-30:239:32//HOMO SA-
 PIENS (HUMAN)//Q10567
 20 F-HEMBA1004286//CUTICLE COLLAGEN 34//0.0027:71:38//CAENORHABDITIS ELEGANS//P34687
 F-HEMBA1004289//PTR3 PROTEIN (SSY3 PROTEIN)//1.0:76:28//SACCHAROMYCES CEREVISIAE (BAK-
 ER'S YEAST)//P43606
 F-HEMBA1004295//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)//0.075:58:39//HO-
 MO SAPIENS (HUMAN)//P30808
 25 F-HEMBA1004306//HYPOTHETICAL 29.3 KD PROTEIN (ORF92)//0.020:132:30//ORGYIA PSEUDOTSUGATA
 MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV)//O10341
 F-HEMBA1004312//EARLY PROTEIN I73R//0.99:65:32//AFRICAN SWINE FEVER VIRUS (STRAIN BA71V)
 (ASFV)//P27946
 30 F-HEMBA1004321//ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10)//4.3e-43:133:44//
 MUS MUSCULUS (MOUSE)//Q61967
 F-HEMBA1004323
 F-HEMBA1004327//SMALL PROLINE-RICH PROTEIN 2-1//0.027:48:43//HOMO SAPIENS (HUMAN)//P35326
 F-HEMBA1004330//HOMEBOX PROTEIN ENGRAILED-1 (HU-EN-1)//0.46:70:34//HOMO SAPIENS (HU-
 MAN)//Q05925
 35 F-HEMBA1004334//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//7.7e-05:83:34//HOMO SAPIENS (HU-
 MAN)//P08547
 F-HEMBA1004335//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.0e-24:41:80//HOMO SAPIENS (HUMAN)//
 P39195
 F-HEMBA1004341//PROLINE-RICH PROTEIN MP-3 (FRAGMENT)//2.8e-06:148:35//MUS MUSCULUS
 40 (MOUSE)//P05143
 F-HEMBA1004353//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.2e-29:57:80//HOMO SAPIENS (HUMAN)//
 P39195
 F-HEMBA1004354//CHL1 PROTEIN//0.017:40:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//
 P22516
 45 F-HEMBA1004356
 F-HEMBA1004366//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//0.00045:49:46//HOMO SAPIENS (HU-
 MAN)//P08547
 F-HEMBA1004372//VERY HYPOTHETICAL 20.6 KD PROTEIN C56F8.15 IN CHROMOSOME I//1.0:125:28//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10263
 50 F-HEMBA1004389//HYPOTHETICAL 113.1 KD PROTEIN IN PRE5-FET4 INTERGENIC REGION//0.76:170:25//
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q04893
 F-HEMBA1004394
 F-HEMBA1004396//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//1.2e-10:72:51//HOMO SAPIENS (HU-
 MAN)//P08547
 55 F-HEMBA1004405
 F-HEMBA1004406//HYPOTHETICAL 13.0 KD PROTEIN F59B2.10 IN CHROMOSOME III//0.00084:33:54//
 CAENORHABDITIS ELEGANS//P34485
 F-HEMBA1004429//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/0.0019:47:59//HOMO SAPIENS (HU-

MAN)//P39191

F-HEMBA1004433//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.1e-20:47:68//HOMO SAPIENS (HUMAN)//P39192

F-HEMBA1004460//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/6.2e-64:134:69//HOMO SAPIENS (HUMAN)//P39193

F-HEMBA1004461//METALLOTHIONEIN-LIKE PROTEIN 1//1.0:39:35//PISUM SATIVUM (GARDEN PEA)//P20830

F-HEMBA1004479//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN)//9.7e-43:101:48//MUS MUSCULUS (MOUSE)//Q61221

F-HEMBA1004482//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34)//1.0:41:36//CANDIDA GLABRATA (YEAST) (TORULOPSIS GLABRATA)//P05040

F-HEMBA1004499//TUBULIN BETA CHAIN//0.00021:55:36//CAENORHABDITIS ELEGANS//P52275

F-HEMBA1004502

F-HEMBA1004506//HYPOTHETICAL PROTEIN ORF-1137//5.3-11:119:35//MUS MUSCULUS (MOUSE)//P11260

F-HEMBA1004507//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66)//0.00072:90:37//HOMO SAPIENS (HUMAN)//Q15428

F-HEMBA1004509//HYPOTHETICAL 52.2 KD PROTEIN IN MPR1-GCN20 INTERGENIC REGION//6.3e-28:169:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P43589

F-HEMBA1004534//ENDOTHELIAL ACTIN-BINDING PROTEIN (ABP-280) (NONMUSCLE FILAMIN) (FILAMIN 1)//1.3e-80:226:66//HOMO SAPIENS (HUMAN)//P21333

F-HEMBA1004538//HYPOTHETICAL PROTEIN MJ0764//0.96:28:35//METHANOCOCCUS JANNASCHII//Q58174

F-HEMBA1004542//METALLOTHIONEIN (MT)//0.78:36:41//GADUS MORHUA (ATLANTIC COD)//P51902

F-HEMBA1004554

F-HEMBA1004560//HYPOTHETICAL PROTEIN KIAA0281 (HA6725)//4.2e-15:56:69//HOMO SAPIENS (HUMAN)//Q92556

F-HEMBA1004573//CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)//0.65:31:58//PLASMODIUM BERGHEI//P06915

F-HEMBA1004577//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/3.9e-08:35:80//HOMO SAPIENS (HUMAN)//P39195

F-HEMBA1004586//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/6.6e-08:64:54//HOMO SAPIENS (HUMAN)//P39194

F-HEMBA1004596//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN C (HNRNP C) (HNRNP CORE PROTEIN C) (FRAGMENT)//0.00057:88:31//RATTUS NORVEGICUS (RAT)//P17132

F-HEMBA1004604//COLLAGEN ALPHA 2(XI) CHAIN PRECURSOR (FRAGMENT)//0.045:37:45//MUS MUSCULUS (MOUSE)//Q64739

F-HEMBA1004610//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.3e-11:73:54//HOMO SAPIENS (HUMAN)//P39188

F-HEMBA1004617

F-HEMBA1004629

F-HEMBA1004631//HYPOTHETICAL 7.8 KD PROTEIN IN WAPA-LICT INTERGENIC REGION//1.0:36:38//BACILLUS SUBTILIS//P42303

F-HEMBA1004632//PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING 8.0 KD POLYPEPTIDE)//0.86:48:35//SYNECHOCOCCUS ELONGATUS NAEGELI//P20453

F-HEMBA1004637//HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III//1.7e-32:159:42//CAENORHABDITIS ELEGANS//P34535

F-HEMBA1004638//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT)//2.8e-06:50:46//OWENIA FUSIFORMIS//P21260

F-HEMBA1004666//TOXIN S6C4//1.0:36:30//DENDROASPIS JAMESONI KAIMOSAE (EASTERN JAMESON'S MAMBA)//P25682

F-HEMBA1004669//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75)//1.6e-12:105:42//HOMO SAPIENS (HUMAN)//Q08170

F-HEMBA1004670//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR//2.5e-06:62:45//HOMO SAPIENS (HUMAN)//P02452

F-HEMBA1004671

F-HEMBA1004672

F-HEMBA1004693//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B)

TYPE B) (NMMHC-B)//0.00035:217:23//HOMO SAPIENS (HUMAN)//P35580

F-HEMBA1004697//IMMUNOGLOBULIN G BINDING PROTEIN H PRECURSOR (PROTEIN H)//0.058:118:30//
STREPTOCOCCUS PYOGENES//P50470

F-HEMBA1004705//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/6.8e-09:43:72//HOMO SAPIENS (HUMAN).//
P39188

F-HEMBA1004709//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/8.8e-18:50:84//HOMO SAPIENS (HUMAN).//
P39189

F-HEMBA1004711//ETS-RELATED PROTEIN 71 (ETS TRANSLOCATION VARIANT 2)//0.0027:148:30//HOMO
SAPIENS (HUMAN)//000321

F-HEMBA1004725//CUTICLE COLLAGEN 2.//0.0051:41:41//CAENORHABDITIS ELEGANS.//P17656

F-HEMBA1004730//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.4e-22:210:37//HOMO SAPIENS (HUMAN)//P08547

F-HEMBA1004733//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.7e-07:50:62//HOMO SAPIENS (HUMAN).//
P39188

F-HEMBA1004734//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42)//9.96-39:143:52//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)//P42743

F-HEMBA1004736//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//4.1e-60:210:61//HOMO SAPIENS (HUMAN)//P08547

F-HEMBA1004748

F-HEMBA1004751//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.8e-20:88:63//HOMO SAPIENS (HUMAN).//
P39188

F-HEMBA1004752//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)//0.0043:126:34//
XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P17437

F-HEMBA1004753//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/7.8e-28:47:78//HOMO SAPIENS (HUMAN).//
P39193

F-HEMBA1004756//HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION.//0.22:77:27//
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39981

F-HEMBA1004758

F-HEMBA1004763//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//1.1e-06:58:43//OWENIA FUSIFORMIS.//P21260

F-HEMBA1004768//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//4.7e-65.298.53//HOMO SAPIENS (HUMAN)//P08547

F-HEMBA1004770

F-HEMBA1004771

F-HEMBA1004776//GRANULIN 1//0.78:28.42//CYPRINUS CARPIO (COMMON CARP)//P81013

F-HEMBA1004778

F-HEMBA1004795//CDC4-LIKE PROTEIN (FRAGMENT)//6.9e-20:74:63//HOMO SAPIENS (HUMAN)//P50851

F-HEMBA1004803//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG../1.4e-22:58:86//HOMO SAPIENS (HUMAN)//P08547

F-HEMBA1004806//HYPOTHETICAL 24.3 KD PROTEIN IN PSBH-RPL11 INTERGENIC REGION (ORF182).//
0.72:75:33//CYANOPHORA PARADOXA//P48324

F-HEMBA1004807

F-HEMBA1004816

F-HEMBA1004820//HEMOLYMPH TRYPSIN INHIBITOR A (BPI-TYPE) (FRAGMENT)//1.0:50:38//MANDUCA
SEXTA (TOBACCO HAWKMOTH) (TOBACCO HORNWORM)//P26226

F-HEMBA1004847//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//3.0e-76:171:91//CANIS FAMILIARIS (DOG).//Q00004

F-HEMBA1004850//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS)//3.0e-05:64:43//BOS TAURUS (BOVINE)//P25508

F-HEMBA1004863//TOXIN C13S1C1 PRECURSOR//0.38:52:30//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAMBA)//P18329

F-HEMBA1004864//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT)//0.89:24:50//
HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BH5 ISOLATE) (HIV-1)//P04612

F-HEMBA1004865

1931 1932

EMBL accession number: [U08252.1](https://www.ebi.ac.uk/EMBL/Sequence/Database/seq_fetch?seq_type=genomic&acc=U08252.1&range=1004889..1004902) (HUMAN) P22532

F-HEMBA1004900
 F-HEMBA1004909
 F-HEMBA1004918//CHLOROPLAST 30S RIBOSOMAL PROTEIN S8 (FRAGMENT)//0.56:37:32//SPINACIA OL-
 ERACEA (SPINACH)//P09597
 5 F-HEMBA1004923//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.5e-24:44:68//HOMO SAPIENS (HUMAN)//
 P39188
 F-HEMBA1004929//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//0.97:39:38//STRONGYLOCENTROTUS
 PURPURATUS (PURPLE SEA URCHIN)//P15997
 F-HEMBA1004930//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//6.6e-15:64:59//HOMO SAPIENS (HU-
 10 MAN)//P08547
 F-HEMBA1004933//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP)//0.34:58:41//HOMO SAPIENS
 (HUMAN)//P50552
 F-HEMBA1004934
 F-HEMBA1004944
 15 F-HEMBA1004954//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6.5.3)//0.58:78:30//PARA-
 MECIUM TETRAURELIA//P15579
 F-HEMBA1004956//HYPOTHETICAL 18.8 KD PROTEIN (ORF4)//0.98:57:31//PARAMECIUM TETRAURELIA//
 P15605
 F-HEMBA1004960//HYPOTHETICAL 12.6 KD PROTEIN-(ORFJ) (RETRON EC67)//1.0:58:27//ESCHERICHIA
 20 COLI//P21324
 F-HEMBA1004972
 F-HEMBA1004973//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930)//0.90:55:30//HOMO SAPIENS
 (HUMAN)//P22531
 F-HEMBA1004977
 25 F-HEMBA1004978
 F-HEMBA1004980//MOTILIN PRECURSOR//0.088:79:31//MACACA MULATTA (RHESUS MACAQUE)//018811
 F-HEMBA1004983//10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES)//0.87:51:31//BUCHNERA
 APHIDICOLA//Q59176
 F-HEMBA1004995//MYOCYTE-SPECIFIC ENHANCER FACTOR 2B (SERUM RESPONSE FACTOR-LIKE PRO-
 30 TEIN 2) (XMEF2) (RSRFR2)//0.17:52:40//HOMO SAPIENS (HUMAN)//Q02080
 F-HEMBA1005008//METALLOTHIONEIN (MT)//1.0:52:32//CRASSOSTREA VIRGINICA (EASTERN OYS-
 TER)//P23038
 F-HEMBA1005009//ACTIN//3.5e-27:171:38//CANDIDA ALBICANS (YEAST)//P14235
 F-HEMBA1005019//HYPOTHETICAL PROTEIN HI1222//0.13:58:31//HAEMOPHILUS INFLUENZAE//P44129
 35 F-HEMBA1005029//P2Y PURINOCEPTOR 5 (P2Y5) (PURINERGIC RECEPTOR 5) (6H1)//0.76:72:31//GALLUS
 GALLUS (CHICKEN)//P32250
 F-HEMBA1005035//HOMEBOX PROTEIN HB9//0.0086:60:40//HOMO SAPIENS (HUMAN)//P50219
 F-HEMBA1005039//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N)//0.47:49:32//HOMO SAPIENS
 (HUMAN)//P22532
 40 F-HEMBA1005047//RAS-RELATED PROTEIN RAB-24 (RAB-16)//1.5e-19:39:100//MUS MUSCULUS
 (MOUSE)//P35290
 F-HEMBA1005050//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS)//0.074:34:44//BOS TAURUS (BOVINE)//
 P25508
 F-HEMBA1005062
 45 F-HEMBA1005066//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//2.1e-44:126:65//HOMO SAPIENS (HU-
 MAN)//P08547
 F-HEMBA1005075//SUPPRESSOR PROTEIN SRP40//0.35:96:31//SACCHAROMYCES CEREVISIAE (BAK-
 ER'S YEAST)//P32583
 F-HEMBA1005079//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/3.6e-20:75:64//HOMO SAPIENS (HU-
 50 MAN)//P39191
 F-HEMBA1005083//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS)//0.00015:72:34//BOS TAURUS (BO-
 VINE)//P25508
 F-HEMBA1005101//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN 27C (HNRNP 48) (HRP48.1)//
 4.8e-10:176:25//DROSOPHILA MELANOGASTER (FRUIT FLY)//P48809
 55 F-HEMBA1005113
 F-HEMBA1005114
 F-HEMBA1005115
 F-HEMBA1005116
 F-HEMBA1005117
 F-HEMBA1005118
 F-HEMBA1005119
 F-HEMBA1005120
 F-HEMBA1005121
 F-HEMBA1005122
 F-HEMBA1005123
 F-HEMBA1005124
 F-HEMBA1005125
 F-HEMBA1005126
 F-HEMBA1005127
 F-HEMBA1005128
 F-HEMBA1005129
 F-HEMBA1005130
 F-HEMBA1005131
 F-HEMBA1005132
 F-HEMBA1005133//HYPOTHETICAL 13.5 KD PROTEIN IN MOB1-SGA1 INTERGENIC REGION//0.11:22:54//

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40490

F-HEMBA1005149//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.7e-16:59:71//HOMO SAPIENS (HUMAN)//P39188

5 F-HEMBA1005152//GENOME POLYPROTEIN 2 [CONTAINS: HELPER COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); 70 KD PROTEIN]//1.0:77:27//BARLEY YELLOW MOSAIC VIRUS (JAPANESE STRAIN II-1) (BAYMV)//Q01207

F-HEMBA1005159//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3)//0.40:53:33//APIS MEL-LIFERA (HONEYBEE)//P34859

10 F-HEMBA1005185//MYOSIN IB HEAVY CHAIN//0.011:58:48//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD)//P34092

F-HEMBA1005201//HYPOTHETICAL 56.6 KD PROTEIN C16C9.03 IN CHROMOSOME I//3.9e-67:241:53//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09817

F-HEMBA1005202//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68)//3.8e-124:257:95//CANIS FAMILIARIS (DOG)//Q00004

15 F-HEMBA1005206//CUTICLE COLLAGEN 1//0.010:118:33//CAENORHABDITIS ELEGANS//P08124

F-HEMBA1005219//PTB-ASSOCIATED SPLICING FACTOR (PSF)//0.99:85:40//HOMO SAPIENS (HUMAN)//P23246

F-HEMBA1005223//HYPOTHETICAL GENE 1.05 PROTEIN//0.31:75:28//BACTERIOPHAGE T3//P07715

20 F-HEMBA1005232//HYPOTHETICAL 7.8 KD PROTEIN//0.99:48:29//VACCINIA VIRUS (STRAIN WR), AND VACCINIA VIRUS (STRAIN COPENHAGEN)//P20544

F-HEMBA1005241//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.4e-28:138:55//HOMO SAPIENS (HUMAN)//P39193

F-HEMBA1005244//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930)//0.014:39:41//HOMO SAPIENS (HUMAN)//P22531

25 F-HEMBA1005251//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//0.55:15:46//DICENTRARCHUS LABRAX (EUROPEAN SEA BASS)//Q36362

F-HEMBA1005252//EC PROTEIN HOMOLOG (ZINC-METALLOTHIONEIN CLASS II)//0.088:33:42//ZEA MAYS (MAIZE)//P43401

F-HEMBA1005274

30 F-HEMBA1005275//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.96:42:45//HOMO SAPIENS (HUMAN)//P39188

F-HEMBA1005293//PROBABLE COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'-COP)//0.55:98:30//CAENORHABDITIS ELEGANS//Q20168

35 F-HEMBA1005296//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)//0.095:75:34//HOMO SAPIENS (HUMAN)//Q02817

F-HEMBA1005304//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/5.4e-33:103:74//HOMO SAPIENS (HUMAN)//P39189

F-HEMBA1005311//PERIOD CLOCK PROTEIN (FRAGMENT)//0.99:45:31//DROSOPHILA SALTANS (FRUIT FLY)//Q04536

40 F-HEMBA1005314//HYPOTHETICAL 6.3 KD PROTEIN T19C3.3 IN CHROMOSOME III//0.98:30:30//CAENORHABDITIS ELEGANS//Q10009

F-HEMBA1005315//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//1.1e-05:35:51//HOMO SAPIENS (HUMAN)//P08547

45 F-HEMBA1005318//OLFACTORY RECEPTOR-LIKE PROTEIN COR8 (FRAGMENT)//0.57:44:38//GALLUS GALLUS (CHICKEN)//Q98913

F-HEMBA1005331//IMMEDIATE-EARLY PROTEIN IE180//0.57:106:33//PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV)//P11675

F-HEMBA1005338//CARTIAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1)//1.8e-55:199:59//GALLUS GALLUS (CHICKEN)//P05099

50 F-HEMBA1005353//CHLOROPLAST 30S RIBOSOMAL PROTEIN S17//0.88:33:36//PORPHYRA PURPUREA//P51305

F-HEMBA1005359//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1)//1.1e-68:255:48//HOMO SAPIENS (HUMAN)//P51522

55 F-HEMBA1005367//ALPHA-AMYLASE INHIBITOR AAI//1.0:25:40//AMARANTHUS HYPOCHONDRIACUS (PRINCE'S FEATHER) //P80403

F-HEMBA1005374

F-HEMBA1005374//ALPHA-AMYLASE INHIBITOR AAI//1.0:25:40//AMARANTHUS HYPOCHONDRIACUS (PRINCE'S FEATHER) //P39194

- F-HEMBA1005382//APOLIPOPROTEIN C-II (APO-CII)//0.99:39:33//BOS TAURUS (BOVINE)//P19034
 F-HEMBA1005389//HYPOTHETICAL 70.0 KD PROTEIN IN DNAK 3'REGION (ORF4)//0.82:164:31//LACTO-
 COCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS)//P42377
 5 F-HEMBA1005394//HYPOTHETICAL 8.9 KD PROTEIN IN IE0-IE1 INTERGENIC REGION//0.98:44:38//
 AUTOGRAPHIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV)//P41703
 F-HEMBA1005403//SPERM HISTONE P2 PRECURSOR (PROTAMINE MP2)//0.066:64:29//MUS MUSCULUS
 (MOUSE)//P07978
 F-HEMBA1005408//50S RIBOSOMAL PROTEIN L33//0.77:32:25//BACILLUS SUBTILIS//Q06798
 10 F-HEMBA1005410//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE
 (EC 2.7.7.49); ENDONUCLEASE]//0.0065:38:52//MUS MUSCULUS (MOUSE)//P11369
 F-HEMBA1005411//TOXIN S4C8//0.16:46:28//DENDROASPIS JAMESONI KAIMOSAE (EASTERN JAMES-
 ON'S MAMBA)//P25683
 F-HEMBA1005423//CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) (CYCLIN-DEPENDENT KINASE
 4 INHIBITOR C) (P18-INK4C)//4.3e-09:29:96//HOMO SAPIENS (HUMAN)//P42773
 15 F-HEMBA1005426//TOXIN C10S2C2//0.99:49:34//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAM-
 BA)//P25684
 F-HEMBA1005443//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.9e-16:78:60//HOMO SAPIENS (HUMAN)//
 P39188
 F-HEMBA1005447//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//0.99:57:31//DASYPUS NOVEMCINCTUS
 20 (NINE-BANDED ARMADILLO)//O21329
 F-HEMBA1005468//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3) (FRAGMENTS)//0.68:41:
 31//ARTEMIA SALINA (BRINE SHRIMP)//P19040
 F-HEMBA1005469
 F-HEMBA1005472//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//1.5e-39:142:70//HOMO SAPIENS (HU-
 25 MAN)//P08547
 F-HEMBA1005474//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/5.8e-10:44:68//HOMO SAPIENS (HU-
 MAN)//P39194
 F-HEMBA1005475//U1 SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KD (U1 SNRNP 70 KD) (SNRNP70)//9.2e-
 14:179:33//HOMO SAPIENS (HUMAN)//P08621
 30 F-HEMBA1005497
 F-HEMBA1005500//60S RIBOSOMAL PROTEIN L37//0.11:53:33//SCHISTOSOMA MANSONI (BLOOD
 FLUKE)//044125
 F-HEMBA1005506
 F-HEMBA1005508
 35 F-HEMBA1005511//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.5e-30:92:73//HOMO SAPIENS (HUMAN)//
 P39194
 F-HEMBA1005513//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-)//2.0e-39:95:61//DROSOPHILA
 MELANOGASTER (FRUIT FLY)//O02193
 F-HEMBA1005517//PROLINE-RICH PROTEIN MP-2 PRECURSOR//2.1e-06:56:44//MUS MUSCULUS
 40 (MOUSE)//P05142
 F-HEMBA1005518//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS)//5.8e-05:192:33//BOS TAURUS (BO-
 VINE)//P02453
 F-HEMBA1005520//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.0e-18:87:57//HOMO SAPIENS (HUMAN)//
 P39188
 45 F-HEMBA1005526//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/5.1e-22:77:54//HOMO SAPIENS (HU-
 MAN)//P39191
 F-HEMBA1005528//CCR4-ASSOCIATED FACTOR 1 (CAF1)//1.2e-81:157:98//MUS MUSCULUS (MOUSE)//
 Q60809
 F-HEMBA1005530//POLLEN ALLERGEN AMB P 5-A PRECURSOR (AMB P V-A)//0.98:19:47//AMBROSIA PSI-
 50 LOSTACHYA (WESTERN RAGWEED)//P43174
 F-HEMBA1005548//TRANSCRIPTION FACTOR MAF1//1.4e-72:137:97//RATTUS NORVEGICUS (RAT)//
 P54842
 F-HEMBA1005552//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.7e-29:47:78//HOMO SAPIENS (HUMAN)//
 P39193
 55 F-HEMBA1005558//HYPOTHETICAL 25.6 KD PROTEIN IN ABE2 ORF12 INTERGENIC REGION
 F-HEMBA1005564
 F-HEMBA1005570//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3)//1.0e-80:31:

CAENORHABDITIS ELEGANS//P24885

F-HEMBA1005576//TRANSMEMBRANE PROTEIN SEX PRECURSOR//8.5e-58:152:75//HOMO SAPIENS (HUMAN)//P51805

F-HEMBA1005577//KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A//0.98:57:36//OVIS ARIES (SHEEP)//P02438

F-HEMBA1005581//SLIT PROTEIN PRECURSOR//1.1e-62:254:41//DROSOPHILA MELANOGASTER (FRUIT FLY)//P24014

F-HEMBA1005582//DYNACTIN, 150 KD ISOFORM (150 KD DYNEIN-ASSOCIATED POLYPEPTIDE) (DP-150) (DAP-150) (P150-GLUED)//0.0091:189:29//RATTUS NORVEGICUS (RAT)//P28023

F-HEMBA1005583//HYPOTHETICAL 41.2 KD PROTEIN IN CPS REGION (ORF7)//0.83:119:23//KLEBSIELLA PNEUMONIAE//Q48453

F-HEMBA1005588//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.9e-17:108:53//HOMO SAPIENS (HUMAN)//P39188

F-HEMBA1005593//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N)//0.23:24:54//HOMO SAPIENS (HUMAN)//P22532

F-HEMBA1005595//DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC)//2.7e-39:257:39//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD)//P34036

F-HEMBA1005606

F-HEMBA1005609//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/3.2e-20:27:96//HOMO SAPIENS (HUMAN)//P39192

F-HEMBA1005616//LATE CONTROL GENE B PROTEIN (GPB)//0.48:51:33//BACTERIOPHAGE 186//P08711

F-HEMBA1005621//MITOTIC MAD2 PROTEIN//1.2e-06:137:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40958

F-HEMBA1005627//HYPOTHETICAL 17.1 KD PROTEIN IN PUBS 3'REGION//0.18:100:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38898

F-HEMBA1005631

F-HEMBA1005632//HYPOTHETICAL 7.4 KD PROTEIN//0.32:59:32//VACCINIA VIRUS (STRAIN WR)//P04309

F-HEMBA1005634//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.6e-14:93:58//HOMO SAPIENS (HUMAN)//P39188

F-HEMBA1005666//HYPOTHETICAL PROTEIN KIAA0129//2.1e-05:126:25//HOMO SAPIENS (HUMAN)//Q14142

F-HEMBA1005670

F-HEMBA1005679//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//2.2e-08:40:72//HOMO SAPIENS (HUMAN)//P08547

F-HEMBA1005680//SMALL PROLINE-RICH PROTEIN 2-1//0.015:19:47//HOMO SAPIENS (HUMAN)//P35326

F-HEMBA1005685

F-HEMBA1005699//EPHRIN-B3 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 8) (LERK-8) (EPH-RELATED RECEPTOR TRANSMEMBRANE LIGAND ELK-L3)//4.2e-38:98:81//HOMO SAPIENS (HUMAN)//Q15768

F-HEMBA1005705//PROTEIN Q300//0.11:23:56//MUS MUSCULUS (MOUSE)//Q02722

F-HEMBA1005717

F-HEMBA1005732//BACTENECIN 7 PRECURSOR (BAC7)//0.22:55:41//OVIS ARIES (SHEEP)//P50415

F-HEMBA1005737//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT)//4.5e-18:167:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P25296

F-HEMBA1005746

F-HEMBA1005755//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//7.4e-30:69:65//HOMO SAPIENS (HUMAN)//P08547

F-HEMBA1005765//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.8e-19:60:63//HOMO SAPIENS (HUMAN)//P39194

F-HEMBA1005780//METALLOTHIONEIN-I (MT-1)//1.0:31:38//COLUMBA LIVIA (DOMESTIC PIGEON)//P15786

F-HEMBA1005813

F-HEMBA1005815//CALPAIN, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEUTRAL PROTEINASE) (CANP) (MU/M-TYPE)//1.0e-23:200:31//GALLUS GALLUS (CHICKEN)//P00789

F-HEMBA1005822//PROTEIN Q300//0.0016:21:80//MUS MUSCULUS (MOUSE)//Q02722
F-HEMBA1005823//PROTEIN Q300//0.0016:21:80//MUS MUSCULUS (MOUSE)//Q02722
F-HEMBA1005824//PROTEIN Q300//0.0016:21:80//MUS MUSCULUS (MOUSE)//Q02722

F-HEMBA1005834//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//1.6e-22:103:46//NYCTICEBUS COU-

CANG (SLOW LORIS)//P08548

F-HEMBA1005852//PROLINE-RICH PROTEIN MP-3 (FRAGMENT)//8.8e-06:95:35//MUS MUSCULUS (MOUSE)//P05143

F-HEMBA1005853//HYPOTHETICAL PROTEIN

5 MJ0647//0.39:28:39//METHANOCOCCUS JANNASCHII//Q58063

F-HEMBA1005884

F-HEMBA1005891//HYPOTHETICAL PROTEIN MTH137//0.95:51:27//METHANOBACTERIUM THERMOAUTOTROPHICUM//Q26240

10 F-HEMBA1005894//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.6e-29:81:71//HOMO SAPIENS (HUMAN)//P39195

F-HEMBA1005909//HYPOTHETICAL 8.2 KD PROTEIN B0353.1 IN CHROMOSOME III//0.98:19:52//CAENORHABDITIS ELEGANS//Q10958

F-HEMBA1005911//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.9e-27:86:70//HOMO SAPIENS (HUMAN)//P39188

15 F-HEMBA1005921//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.3e-38:99:81//HOMO SAPIENS (HUMAN)//P39194

F-HEMBA1005931//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1)//2.3e-17:76:51//HOMO SAPIENS (HUMAN)//P51522

20 F-HEMBA1005934//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/0.024:54:40//HOMO SAPIENS (HUMAN)//P39189

F-HEMBA1005962

F-HEMBA1005963//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP)//1.7e-32:89:79//BOS TAURUS (BOVINE)//P53620

25 F-HEMBA1005990//HYPOTHETICAL BHLF1 PROTEIN//3.0e-09:180:36//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4)//P03181

F-HEMBA1005991//HYPOTHETICAL PROTEIN KIAA0032//3.0e-17:107:43//HOMO SAPIENS (HUMAN)//Q15034

F-HEMBA1005999

F-HEMBA1006002

30 F-HEMBA1006005//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1 B)//0.0017:45:44//MUS MUSCULUS (MOUSE)//Q62267

F-HEMBA1006031//BASIC PROLINE-RICH PEPTIDE IB-1//0.00016:84:39//HOMO SAPIENS (HUMAN)//P04281

35 F-HEMBA1006035//DNAK PROTEIN 1 (HEAT SHOCK PROTEIN 70) (HSP70)//0.43:100:27//SYNECHOCYSTIS SP. (STRAIN PCC 6803)//Q55154

F-HEMBA1006036//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/6.2e-64:150:74//HOMO SAPIENS (HUMAN)//P39194

F-HEMBA1006042

40 F-HEMBA1006067//METALLOTHIONEIN A (MT-A)//0.86:34:41//THERMARCES CERBERUS//P52721

F-HEMBA1006081

F-HEMBA1006090//SODIUM/GLUCOSE COTRANSPORTER 3 (NA(+)/GLUCOSE COTRANSPORTER 3) (LOW AFFINITY SODIUM-GLUCOSE COTRANSPORTER)//0.87:35:54//SUS SCROFA (PIG)//P31636

F-HEMBA1006091//EARLY NODULIN 20 PRECURSOR (N-20)//0.027:87:32//MEDICAGO TRUNCATULA (BARREL MEDIC)//P93329

45 F-HEMBA1006100//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/8.1e-09:58:60//HOMO SAPIENS (HUMAN)//P39195

F-HEMBA1006108//HYPOTHETICAL 56.6 KD PROTEIN IN URE2-SSU72 INTERGENIC REGION//5.6e-16:88:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53867

50 F-HEMBA1006121//HOMEBOX PROTEIN CDX-1 (CAUDAL-TYPE HOMEBOX PROTEIN 1)//3.4e-05:106:37//HOMO SAPIENS (HUMAN)//P47902

F-HEMBA1006124//50S RIBOSOMAL PROTEIN L33//1.0:12:83//BACILLUS STEAROTHERMOPHILUS//P23375

F-HEMBA1006130//SEL-10 PROTEIN//7.7e-05:129:28//CAENORHABDITIS ELEGANS//Q93794

55 F-HEMBA1006138//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/7.8e-13:41:73//HOMO SAPIENS (HUMAN)//P39194

F-HEMBA1006155

ANT. PROTEIN

F-HEMBA1006155//GENE 33 POLYPEPTIDE//0.2:70:31//RATTUS NORVEGICUS (RAT)//P05432

5 F-HEMBA1006182//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.37:31:61//HOMO SAPIENS (HUMAN).//
P39188

10 F-HEMBA1006248//MALE SPECIFIC SPERM PROTEIN MST84DB//0.0041:64:37//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q01643

15 F-HEMBA1006253//DISINTEGRIN ERISTICOPHIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).//
0.95:19:47//ERISTOCOPHIS MACMAHONI (LEAF-NOSED VIPER).//P22826

F-HEMBA1006268//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/7.0e-05:32:65//HOMO SAPIENS (HUMAN).//
P39192

F-HEMBA1006278/POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE) (FRAGMENT)//2.5e-71:164:75/HOMO SAPIENS (HUMAN)//P51003

25 F-HEMBA1006284//CUTICLE COLLAGEN 2.//0.36:42:40//CAENORHABDITIS ELEGANS.//P17656

F-HEMBA1006293//MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR//0.20:134:29//RATTUS NORVEGICUS (RAT)//Q63345 F-HEMBA1006309//HYPOTHETICAL 54.2 KD PROTEIN IN ERP5-ORC6 INTER-

(NECTADRIN).//0.71:46:39//RATTUS NORVEGICUS (RAT).//Q07490

35 F-HEMBA1006334//HYPOTHETICAL TRANSCRIPTIONAL REGULATOR AF1627.1/0.98:26:46//ARCHAE-
OGLOBUS FULGIDUS.//028646

40 F-HEMBA1006347//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-)//9.1e-48:149:50//DROSOPHILA
MELANOGASTER (FRUIT FLY)//Q2193

F-HEMBA1006359//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//6.8e-96:261:66//HOMO SAPIENS (HUMAN)//P28160

F-HEMBA1006377//EARLY NODULIN 20 PRECURSOR (N-20)//0.00023:110:35//MEDICAGO TRUNCATULA (BARREL MEDIC)//P93329

50 F-HEMBA1006381//METALLOTHIONEIN-II//1.0:26:38//CANDIDA GLABRATA (YEAST) (TORULOPSIS GLABRATA)//P15114

F-HEMBA1006416

F-HEMBA1006419//III ALL SUBFAMILY SB WARNING ENTRY UNCHANGED
 HEMBA1006421 IV HEAM LANNALANIN
 3818b

- F-HEMBA1006424//HYPOTHETICAL PROTEIN IORF1//0.85:55:30//BOVINE CORONAVIRUS (STRAIN ME-BUS), AND BOVINE CORONAVIRUS (STRAIN QUEBEC)//P22053
F-HEMBA1006426//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.8e-36:78:74//HOMO SAPIENS (HUMAN)//P39195
- 5 F-HEMBA1006438//HYPOTHETICAL 8.1 KD PROTEIN (ORF65)//1.0:38:36//GUILLARDIA THETA (CRYPTO-MONAS PHI)//O78421
F-HEMBA1006445//RAS-LIKE PROTEIN 3//1.9e-06:40:47//RHIZOMUCOR RACEMOSUS (MUCOR CIRCINEL-LOIDES F. LUSITANICUS)//P22280
F-HEMBA1006446
- 10 F-HEMBA1006461//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/4.1e-18:68:67//HOMO SAPIENS (HUMAN)//P39192
F-HEMBA1006467
F-HEMBA1006471
F-HEMBA1006474//40 KD PROTEIN//1.1e-37:231:38//BORNA DISEASE VIRUS (BDV)//Q01552
- 15 F-HEMBA1006483//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/6.1e-38:77:74//HOMO SAPIENS (HUMAN)//P39192
F-HEMBA1006485//HYPOTHETICAL 9.3 KD PROTEIN IN NAD3-NAD7 INTERGENIC REGION (ORF 79)//0.91:30:40//MARCHANTIA POLYMORPHA (LIVERWORT)//P38465
F-HEMBA1006486//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//1.1e-12:78:51//HOMO SAPIENS (HU-MAN)//P08547
- 20 F-HEMBA1006489//FUN34 PROTEIN//0.94:58:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32907
F-HEMBA1006492//NADH-UBIQUINONE OXIDOREDUCTASE MWFE SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-MWFE) (CI-MWFE)//0.87:44:36//HOMO SAPIENS (HUMAN)//O15239
- 25 F-HEMBA1006494//FERREDOXIN-LIKE PROTEIN IN NIF REGION//0.11:46:26//RHIZOBIUM LEGUMINOSA-RUM (BIOVAR TRIFOLIUM)//P42711
F-HEMBA1006497
F-HEMBA1006502//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.15:26:73//HOMO SAPIENS (HUMAN)//P39188
- 30 F-HEMBA1006507//DIAPHANOUS PROTEIN//0.0055:129:28//DROSOPHILA MELANOGASTER (FRUIT FLY)//P48608
F-HEMBA1006521//3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) (3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE)//1.1e-32:177:41//ESCHERICHIA COLI//P25716
F-HEMBA1006530//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT)//0.052:84:26//LEISHMANIA TARENTOLAE (SAUROLEISHMANIA TARENTOLAE)//P15583
- 35 F-HEMBA1006535//INHIBITOR OF APOPTOSIS PROTEIN 1 (MIAP1) (MIAP-1)//6.6e-05:53:39//MUS MUSCU-LUS (MOUSE)//O08863
F-HEMBA1006540//PRESYNAPTIC PROTEIN SAP97 (SYNAPSE-ASSOCIATED PROTEIN 97) (DISCS, LARGE HOMOLOG 1)//2.1e-07:206:23//RATTUS NORVEGICUS (RAT)//Q62696
- 40 F-HEMBA1006546//PROBABLE E5 PROTEIN//0.11:70:32//HUMAN PAPILLOMAVIRUS TYPE 51//P26553
F-HEMBA1006559//SUPPRESSOR PROTEIN SRP40//0.015:221:20//SACCHAROMYCES CEREVISIAE (BAK-ER'S YEAST)//P32583
F-HEMBA1006562//SALIVARY PROLINE-RICH PROTEIN PO PRECURSOR (ALLELE S)//1.5e-07:122:33//HO-MO SAPIENS (HUMAN)//P10163
- 45 F-HEMBA1006566//CELL DIVISION PROTEIN KINASE 2 (EC 2.7.1.-) (CDC2 HOMOLOG EG1 PROTEIN KI-NASE)//0.63:53:37//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P23437
F-HEMBA1006569//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENT)//4.4e-06:88:39//BOS TAURUS (BOVINE)//P02465
F-HEMBA1006579
- 50 F-HEMBA1006583//PROLINE-RICH PROTEIN MP-2 PRECURSOR//0.011:61:40//MUS MUSCULUS (MOUSE)//P05142
F-HEMBA1006595//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/5.6e-34:93:77//HOMO SAPIENS (HU-MAN)//P39194
F-HEMBA1006597//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.9e-26:75:74//HOMO SAPIENS (HUMAN)//P39195
- 55 F-HEMBA1006617//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/6.6e-20:73:63//HOMO SAPIENS (HUMAN)//P39195

P39188

F-HEMBA1006624//HYPOTHETICAL 41.9 KD PROTEIN IN SDS3-THS1 INTERGENIC REGION//2.6e-31:209:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40506

F-HEMBA1006631//HYPOTHETICAL 62.8 KD PROTEIN IN TAF145-YOR1 INTERGENIC REGION//1.5e-15:131:41//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53331

F-HEMBA1006635

F-HEMBA1006639//POLYADENYLATE-BINDING PROTEIN 1 (POLY(A) BINDING PROTEIN 1) (PABP 1)//2.2e-11:48:75//MUS MUSCULUS (MOUSE)//P29341

F-HEMBA1006643//LONG NEUROTOXIN CR1 PRECURSOR (KAPPA NEUROTOXIN)//0.28:48:27//BUNGARUS MULTICINCTUS (MANY-BANDED KRAIT)//P15817

F-HEMBA1006648//ZINC FINGER PROTEIN 12 (ZINC FINGER PROTEIN KOX3) (FRAGMENT)//0.26:17:47//HOMO SAPIENS (HUMAN)//P17014

F-HEMBA1006652//60S RIBOSOMAL PROTEIN L7//2.4e-44:206:47//MUS MUSCULUS (MOUSE)//P14148

F-HEMBA1006653

F-HEMBA1006659
F-HEMBA1006665//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//0.018:43:58//HOMO SAPIENS (HUMAN)//P08547

F-HEMBA1006674//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130)//2.9e-05:154:33//HOMO SAPIENS (HUMAN)//O00268

F-HEMBA1006676//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT)//3.6e-09:52:51//OWENIA FUSIFORMIS//P21260

F-HEMBA1006682

F-HEMBA1006695//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.1e-06:35:65//HOMO SAPIENS (HUMAN)//P39188

F-HEMBA1006696

F-HEMBA1006708//HYPOTHETICAL 46.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMC1-TFG2 INTERGENIC REGION//3.4e-19:104:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53196

F-HEMBA1006709//RETINOIC ACID RECEPTOR RXR-BETA//0.24:111:36//HOMO SAPIENS (HUMAN)//P28702

F-HEMBA1006717

F-HEMBA1006737//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT)//5.8e-09:111:40//HOMO SAPIENS (HUMAN)//Q01485

F-HEMBA1006744//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/1.8e-32:84:78//HOMO SAPIENS (HUMAN)//P39191

F-HEMBA1006754//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//1.3e-75:220:62//HOMO SAPIENS (HUMAN)//P08547

F-HEMBA1006758//VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VECADHERIN) (CADHERIN-5) (7B4 ANTIGEN) (CD144 ANTIGEN)//0.024:110:29//HOMO SAPIENS (HUMAN)//P33151

F-HEMBA1006767

F-HEMBA1006779//MITOCHONDRIAL RIBOSOMAL PROTEIN S12//0.67:19:42//LEISHMANIA TARENTOLAE (SAUROLEISHMANIA TARENTOLAE)//Q34940

F-HEMBA1006780

F-HEMBA1006789//PROLINE-RICH PROTEIN MP-3 (FRAGMENT)//0.056:98:30//MUS MUSCULUS (MOUSE)//P05143

F-HEMBA1006795//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//2.9e-11:143:30//NYCTICEBUS COUCANG (SLOW LORIS)//P08548

F-HEMBA1006796//WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP)//0.16:38:42//MUS MUSCULUS (MOUSE)//P70315

F-HEMBA1006807//HYPOTHETICAL 46.4 KD PROTEIN T16H12.5 IN CHROMOSOME III//4.4e-75:184:77//CAENORHABDITIS ELEGANS//P34568

F-HEMBA1006821//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/0.011:20:85//HOMO SAPIENS (HUMAN)//P39194

F-HEMBA1006824//PROTEIN B11//0.44:27:44//VACCINIA VIRUS (STRAIN WR)//Q01229

F-HEMBA1006832//HYPOTHETICAL 34.6 KD PROTEIN C13G5.2 IN CHROMOSOME III//1.0:46:36//CAENORHABDITIS ELEGANS//P34327

F-HEMBA1006844

F-HEMBA1006865//ACTININ INHIBITORS (ACTININ INHIBITORS) (ACTININ INHIBITORS) (ACTININ INHIBITORS)

F-HEMBA1006877//OXYSTEROL-BINDING PROTEIN//3.7e-26:239:36//ORYZOTOAGUS CUNICULUS (RAB

BIT)//P16258

F-HEMBA1006885//HYPOTHETICAL 27.2 KD PROTEIN F09E5.8 IN CHROMOSOME II//4.5e-38:185:43//
CAENORHABDITIS ELEGANS//P52057

F-HEMBA1006900

5 F-HEMBA1006914//UBIQUITIN-ACTIVATING ENZYME E1-LIKE (POLYMERASE-INTERACTING PROTEIN 2)//
5.2e-27:269:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P52488

F-HEMBA1006921//CYTOTOXIN 3 (COMPONENT 3.20)//0.99:32:37//NAJA MELANOLEUCA (FOREST CO-
BRA) (BLACK-LIPPED COBRA)//P01473

10 F-HEMBA1006926//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN)//0.0024:148:
33//RATTUS NORVEGICUS (RAT)//P54258

F-HEMBA1006929//HYPOTHETICAL PROTEIN MJ0525//0.95:35:20//METHANOCOCCUS JANNASCHII//
Q57945

15 F-HEMBA1006936//SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1 / PRP-
3) (PRP-2 / PRP-4) (PIF-F / PIF-S) (PROTEIN A / PROTEIN C) [CONTAINS: PEPTIDE P-C]//0.074:116:31//HOMO
SAPIENS (HUMAN)//P02810

F-HEMBA1006938

F-HEMBA1006941//THIOREDOXIN H-TYPE 1 (TRX-H1)//2.1e-13:90:33//NICOTIANA TABACUM (COMMON
TOBACCO)//P29449

F-HEMBA1006949

20 F-HEMBA1006973//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS)//0.75:29:55//BOS TAURUS (BOVINE)//
P25508

F-HEMBA1006976//CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANS-
FERASE (EC 2.4.99.-) (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ST3GAL!!!!) (ALPHA 2,3-ST)
(GAL-NAC6S) (STZ) (SIAT4-C) (SAT-3) (ST-4)//3.9e-108:117:95//HOMO SAPIENS (HUMAN)//Q11206

25 F-HEMBA1006993

F-HEMBA1006996//HYPOTHETICAL 8.7 KD PROTEIN IN RPL22-RPL23 INTERGENIC REGION (ORF70)//
0.12:51:33//ASTASIA LONGA (EUGLENOPHYCEAN ALGA)//P34779

F-HEMBA1007002//PLATELET GLYCOPROTEIN IX PRECURSOR (GPIX) (CD42A)//0.00096:60:33//HOMO SA-
PIENS (HUMAN)//P14770

30 F-HEMBA1007017//HYPOTHETICAL 7.2 KD PROTEIN IN CYAY-DAPF INTERGENIC REGION//1.0:25:56//ES-
CHERICHIA COLI//P39166

F-HEMBA1007018//DYNEIN LIGHT INTERMEDIATE CHAIN 1, CYTOSOLIC (LIC57/59) (DYNEIN LIGHT CHAIN
A) (DLC-A)//8.5e-120:278:80//GALLUS GALLUS (CHICKEN)//Q90828

35 F-HEMBA1007045//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)//2.1e-12:158:29//
XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P17437

F-HEMBA1007051

F-HEMBA1007052//60S RIBOSOMAL PROTEIN L37-B (L35) (YP55)//0.94:37:35//SACCHAROMYCES CERE-
VISIAE (BAKER'S YEAST)//P51402

40 F-HEMBA1007062//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//0.93:55:29//RHINOCEROS UNICORNIS
(GREATER INDIAN RHINOCEROS)//Q96063

F-HEMBA1007066//ECLOSION HORMONE PRECURSOR (ECDYSIS ACTIVATOR) (EH)//0.58:49:38//BOM-
BYX MORI (SILK MOTH)//P25331

F-HEMBA1007073//PUTATIVE SMALL MEMBRANE PROTEIN (ORF 4)//0.86:46:34//CANINE ENTERIC
CORONAVIRUS (STRAIN INSAVC-1) (CCV)//P36696

45 F-HEMBA1007078//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/8.6e-29:56:67//HOMO SAPIENS (HUMAN)//
P39193

F-HEMBA1007080//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)//0.028:122:30//XENO-
PUS LAEVIS (AFRICAN CLAWED FROG)//P17437

50 F-HEMBA1007085//RTOA PROTEIN (RATIO-A)//7.4e-11:221:31//DICTYOSTELIUM DISCOIDEUM (SLIME
MOLD)//P54681

F-HEMBA1007087//HYPOTHETICAL PROTEIN MJ0162//3.3e-29:173:36//METHANOCOCCUS JANNASCHII//
Q57626

F-HEMBA1007112

F-HEMBA1007113

55 F-HEMBA1007121//INOSITOL POLYPHOSPHATE 1-PHOSPHATASE (EC 3.1.3.57) (IPP) //5.1e-07:90:38//HOMO
SAPIENS (HUMAN) (P11111)

F-HEMBA1007122//HYPOTHETICAL 12.0 KD PROTEIN IN DST1-HEM2 INTERGENIC REGION//0.92:23:34//

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53182
 F-HEMBA1007149//BACTERIOCIN MICROCIN B17 PRECURSOR (MCB17).//0.0078:17:70//ESCHERICHIA COLI//P05834
 F-HEMBA1007151//WDNM1 PROTEIN PRECURSOR//0.25:45:37//MUS MUSCULUS (MOUSE).//Q62477
 5 F-HEMBA1007174//HYPOTHETICAL 45.1 KD PROTEIN IN RPS5-ZMS1 INTERGENIC REGION//6.9e-18:97:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47160
 F-HEMBA1007178//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//9.8e-06:38:65//HOMO SAPIENS (HUMAN).//P39195
 F-HEMBA1007194//GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHOLOROPLAST ISOFORM PRECURSOR (EC 1.1.1.49) (G6PD).//1.0:80:32//NICOTIANA TABACUM (COMMON TOBACCO).//Q43793
 10 F-HEMBA1007203//PROTEIN A22.//1.0:115:26//VARIOLA VIRUS//P33845
 F-HEMBA1007206
 F-HEMBA1007224//HYPOTHETICAL 35.7 KD PROTEIN C41C4.6 IN CHROMOSOME II//2.4e-05:92:30//CAENORHABDITIS ELEGANS//Q09275
 15 F-HEMBA1007243//HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) (HGPRT) (HGPRTASE) (HPRT B).//3.1e-74:205:67//MUS MUSCULUS (MOUSE).//P00493
 F-HEMBA1007251//VITELLINE MEMBRANE PROTEIN VM26AB PRECURSOR (PROTEIN TU-4) (PROTEIN SV23).//0.52:108:30//DROSOPHILA MELANOGASTER (FRUIT FLY).//P13238
 F-HEMBA1007256
 20 F-HEMBA1007267//CALICIN (FRAGMENT).//0.060:88:31//HOMO SAPIENS (HUMAN).//Q13939
 F-HEMBA1007273//HYPOTHETICAL 8.1 KD PROTEIN (ORF65).//0.95:40:37//GUILLARDIA THETA (CRYPTOMONAS PHI).//O78421
 F-HEMBA1007279//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//4.6e-24:98:64//HOMO SAPIENS (HUMAN).//P39188
 25 F-HEMBA1007281
 F-HEMBA1007288//HYPOTHETICAL 13.5 KD PROTEIN IN ZMS1-MNS1 INTERGENIC REGION.//0.88:11:54//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47162
 F-HEMBA1007300//CGMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE (EC 3.1.4.17) (CGB-PDE).//2.7e-43:220:41//BOS TAURUS (BOVINE).//Q28156
 30 F-HEMBA1007301//PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR.//3.3e-22:115:33//HOMO SAPIENS (HUMAN).//P02461
 F-HEMBA1007319
 F-HEMBA1007320//HYPOTHETICAL 28.0 KD PROTEIN IN GLOB-RNHA INTERGENIC REGION.//1.0:48:37//ESCHERICHIA COLI//P75672
 35 F-HEMBA1007322//THREONINE DEHYDRATASE OPERON ACTIVATOR PROTEIN.//1.0:59:33//ESCHERICHIA COLI//P11866
 F-HEMBA1007327
 F-HEMBA1007341//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//9.1e-12:37:62//HOMO SAPIENS (HUMAN).//P39188
 40 F-HEMBA1007342//PROBABLE E5 PROTEIN.//0.89:96:29//PYGMY CHIMPANZEE PAPILLOMAVIRUS TYPE 1.//Q02268
 F-HEMBA1007347//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 PRECURSOR (IGFBP-2) (IBP-2) (IGF-BINDING PROTEIN 2).//0.92:62:43//OVIS ARIES (SHEEP).//Q29400
 F-HEMBA1000005//WEAK NEUROTOXIN 5.//0.98:30:33//NAJA NAJA (INDIAN COBRA).//P29179
 45 F-HEMBA1000008//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//2.7e-35:73:84//HOMO SAPIENS (HUMAN).//P39195
 F-HEMBA1000018//HYPOTHETICAL BHLF1 PROTEIN.//0.39:90:37//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181
 F-HEMBA1000024//VIRE LOCUS 9 KD VIRULENCE PROTEIN.//0.66:36:41//AGROBACTERIUM TUMEFACIENS//P08061
 50 F-HEMBA1000025//MUSCARINIC TOXIN ALPHA (MT-ALPHA).//0.46:32:40//DENDROASPIS POLYLEPIS POLYLEPIS (BLACK MAMBA).//P80494
 F-HEMBA1000030//SUPPRESSOR PROTEIN SRP40.//6.7e-07:50:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583
 55 F-HEMBA1000036//HYPOTHETICAL 43.2 KD PROTEIN C34E10.1 IN CHROMOSOME III.//2.5e-07:120:28//CAENORHABDITIS ELEGANS.//P46573
 F-HEMBA1000037//HYPOTHETICAL 38.4 KD PROTEIN IN ZMS1-MNS1 INTERGENIC REGION.//0.88:11:54//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40492

F-HEMBB1000048//HYPOTHETICAL 15.7 KD PROTEIN IN IDH-DEOR INTERGENIC REGION.//1.0:63:31//BACILLUS SUBTILIS //P54942

F-HEMBB1000050//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/9.0e-14:34:79//HOMO SAPIENS (HUMAN)//P39194

F-HEMBB1000054//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/5.9e-31:45:73//HOMO SAPIENS (HUMAN).//
P39193

F-HEMBB1000055//MUSCARINIC TOXIN ALPHA (MT-ALPHA)//1.0:14:57//DENDROASPIS POLYLEPIS
POLYLEPIS (BLACK MAMBA)//P80494

F-HEMBB1000059//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.0e-21:82:59//HOMO SAPIENS (HUMAN).//
P39195

F-HEMBB1000083//CHROMOGRANIN A PRECURSOR (CGA) [CONTAINS: PANCREASTATIN; BETA-GRANIN; WE-14]//0.87:172:28//RATTUS NORVEGICUS (RAT)//P10354

F-HEMBB1000089//HYPOTHETICAL 9.5 KD PROTEIN IN SPEA-METK INTERGENIC REGION (F83)//1.0:42:33//ESCHERICHIA COLI//P46879

F-HEMBB1000099/////ALU SUBFAMILY SB WARNING ENTRY /////7.7e-08:31:87//HOMO SAPIENS (HUMAN).//
P39189

F-HEMBB1000103/LINE-1 REVERSE TRANSCRIPTASE HOMOLOG./1.4e-38:136:58/HOMO SAPIENS (HUMAN)//P08547

F-HEMBB1000113//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.9e-13:57:64//HOMO SAPIENS (HUMAN).//
P39188

F-HEMBB1000136//HYPOTHETICAL 12.7 KD PROTEIN IN PCS60-ABD1 INTERGENIC REGION.//0.65:71:32//
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38327

F-HEMBB1000141//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD)//0.00014:34:64//HOMO SAPIENS (HUMAN).//P20931

F-HEMBB1000144/////ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/2.0e-26:81:69//HOMO SAPIENS (HUMAN)//P39191

F-HEMBB1000173//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/9.2e-29:91:71//HOMO SAPIENS (HUMAN).//
P39188

F-HEMBB1000175//ANTIMICROBIAL PEPTIDE ENAP-1 (FRAGMENT)//0.97:41:36//EQUUS CABALLUS (HORSE)//P80930

F-HEMBB1000198//HYPOTHETICAL 7.7 KD PROTEIN YCF33 (ORF67)//0.91:21:52//PORPHYRA PURPUREA//P51329

F-HEMBB1000215//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/3.4e-08:39:76//HOMO SAPIENS (HUMAN)//
P39192

F-HEMBB1000217//DNA DAMAGE TOLERANCE PROTEIN RHC31 (RAD31 HOMOLOG)//2.9e-32:174:40//
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q06624

F-HEMBB1000218//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//0.73:31:38//MICROTUS PENNSYLVANICUS (MEADOW VOLE)//P24949

F-HEMBB1000226//HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II.//6.5e-26:191:34//
CAENORHABDITIS ELEGANS//Q09217

F-HEMBB1000244//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.9e-05:44:61//HOMO SAPIENS (HUMAN)//
P39188

F-HEMBB1000258

F-HEMBB1000264//CUTICLE COLLAGEN SQT-1.//0.15:89:33//CAENORHABDITIS ELEGANS.//P12114

F-HEMBB1000266//TRANSLATION INITIATION FACTOR IF-2//2.7e-06:167:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P39730

F-HEMBB1000272//CYTOCHROME C OXIDASE POLYPEPTIDE VIB (EC 1.9.3.1) (AED)//0.75:30:43//BOS TAURUS (BOVINE)//P00429

F-HEMBB1000274//CORNFILIN (SMALL PROLINE RICH PROTEIN) N (SPR N) (SMALL PROLINE RICH PROTEIN) N

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- F-HEMBB1000307
F-HEMBB1000312
F-HEMBB1000317//THROMBOSPONDIN 1 PRECURSOR//3.2e-32:135:43//HOMO SAPIENS (HUMAN)//P07996
- 5 F-HEMBB1000318//PUTATIVE SMALL MEMBRANE PROTEIN (NONSTRUCTURAL PROTEIN NS3) (NON-STRUCTURAL 9.5 KD PROTEIN)//0.41:51:31//HUMAN CORONAVIRUS (STRAIN OC43)//Q04854
F-HEMBB1000335//ZINC FINGER PROTEIN 13 (ZFP-13) (KROX-8 PROTEIN) (FRAGMENT)//0.82:33:45//MUS MUSCULUS (MOUSE)//P10754
F-HEMBB1000336//ALDEHYDE OXIDASE (EC 1.2.3.1) (FRAGMENTS)//0.80:44:40//ORYCTOLAGUS CUNICULUS (RABBIT)//P80456
- 10 F-HEMBB1000337//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75)//0.94:118:22//HOMO SAPIENS (HUMAN)//Q08170
F-HEMBB1000338//MALE SPECIFIC SPERM PROTEIN MST84DA//0.042:33:39//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q01642
- 15 F-HEMBB1000339//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.2e-14:54:55//HOMO SAPIENS (HUMAN)//P39188
F-HEMBB1000341//GENE 74 PROTEIN (GP74)//1.0:39:33//MYCOBACTERIOPHAGE L5//Q05289
F-HEMBB1000343
F-HEMBB1000354//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.1e-15:83:56//HOMO SAPIENS (HUMAN)//P39188
- 20 F-HEMBB1000369//PROTEIN Q300//0.99:27:40//MUS MUSCULUS (MOUSE)//Q02722
F-HEMBB1000374//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/4.7e-34:56:78//HOMO SAPIENS (HUMAN)//P39189
F-HEMBB1000376
- 25 F-HEMBB1000391//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS)//0.0013:79:35//BOS TAURUS (BOVINE)//P25508
F-HEMBB1000399//CHECKPOINT PROTEIN RAD17//2.8e-15:187:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//P50531
F-HEMBB1000402//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT)//0.027:60:38//LEISHMANIA TARENTOLAE (SAUROLEISHMANIA TARENTOLAE)//P15583
- 30 F-HEMBB1000404//CYANELLE 50S RIBOSOMAL PROTEIN L28//0.94:29:27//CYANOPHORA PARADOXA//P48129
F-HEMBB1000420//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53)//0.023:97:35//HOMO SAPIENS (HUMAN)//Q15427
- 35 F-HEMBB1000434//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/4.8e-20:111:54//HOMO SAPIENS (HUMAN)//P39194
F-HEMBB1000438//HYPOTHETICAL 7.9 KD PROTEIN IN GP55-NRDG INTERGENIC REGION//0.93:24:50//BACTERIOPHAGE T4//P07076
F-HEMBB1000441//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.4e-23:85:70//HOMO SAPIENS (HUMAN)//P39188
- 40 F-HEMBB1000449//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.88:27:51//HOMO SAPIENS (HUMAN)//P39195
F-HEMBB1000455
F-HEMBB1000472
- 45 F-HEMBB1000480//PROTEIN STBC//1.0:52:30//ESCHERICHIA COLI//P11905
F-HEMBB1000487//SHORT NEUROTOXIN 1 (NEUROTOXIN ALPHA) (NEUROTOXIN II)//0.93:29:34//NAJA OXIANA (CENTRAL ASIAN COBRA) (OXUS COBRA)//P01427
F-HEMBB1000490//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.3e-16:50:80//HOMO SAPIENS (HUMAN)//P39195
- 50 F-HEMBB1000491
F-HEMBB1000493//3A PROTEIN//1.0:51:35//AVIAN INFECTIOUS BRONCHITIS VIRUS (STRAIN BEAUDETTE) (IBV)//P30237
F-HEMBB1000510//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//9.7e-27:132:45//HOMO SAPIENS (HUMAN)//P08547
- 55 F-HEMBB1000518//CYTOCHROME C OXIDASE POLYPEPTIDE III (EC 1.2.3.4) (CYTOCHROME C OXIDASE POLYPEPTIDE III)
F-HEMBB1000520
F-HEMBB1000530//COLLAGEN ALPHA 1(XIV) CHAIN PRECURSOR (UNDULIN)//9.8e-14:43:83//GALLUS

GALLUS (CHICKEN)//P32018

F-HEMBB1000550//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3)//0.19:97:30//TRYPANO-SOMA BRUCEI BRUCEI//P04540

F-HEMBB1000554//MATERNAL B9.10 PROTEIN (P30 B9.10)//0.94:82:25//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P40744

F-HEMBB1000556//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130)//0.043:201:29//HOMO SAPIENS (HUMAN)//000268

F-HEMBB1000564//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//1.0:5:2:34//METRIDIDIUM SENILE (BROWN SEA ANEMONE) (FRILLED SEA ANEMONE)//O47493

F-HEMBB1000573//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/2.3e-10:52:73//HOMO SAPIENS (HUMAN)//P39191

F-HEMBB1000575//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.8e-26:76:76//HOMO SAPIENS (HUMAN)//P39192

F-HEMBB1000586//NADH-UBIQUINONE OXIDOREDUCTASE MLRQ SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-MLRQ) (CI-MLRQ)//0.74:23:52//HOMO SAPIENS (HUMAN)//O00483

F-HEMBB1000589//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/2.9e-25:61:75//HOMO SAPIENS (HUMAN)//P39193

F-HEMBB1000591//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//1.0:34:35//PETROMYZON MARINUS (SEA LAMPREY)//Q35537

F-HEMBB1000592//SMALL PROLINE-RICH PROTEIN 2-1//0.0016:49:42//HOMO SAPIENS (HUMAN)//P35326

F-HEMBB1000593//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENTS)//0.0070:189:32//GALLUS GALLUS (CHICKEN)//P12105

F-HEMBB1000598//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//5.7e-10:110:41//NYCTICEBUS COUCANG (SLOW LORIS)//P08548

F-HEMBB1000623//HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III//0.0022:98:28//CAENORHABDITIS ELEGANS//P34284

F-HEMBB1000630

F-HEMBB1000631//ALPHA-2C-1 ADRENERGIC RECEPTOR (ALPHA-2C-1 ADRENOCEPTOR) (SUBTYPE C4)//8.8e-06:59:40//HOMO SAPIENS (HUMAN)//P18825

F-HEMBB1000632//GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP)//7.3e-13:173:28//MUS MUSCULUS (MOUSE)//P27671

F-HEMBB1000637//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/4.6e-41:94:82//HOMO SAPIENS (HUMAN)//P39193

F-HEMBB1000638//INVOLUCRIN//1.9e-06:144:29//HOMO SAPIENS (HUMAN)//P07476

F-HEMBB1000643//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/8.3e-30:77:76//HOMO SAPIENS (HUMAN)//P39195

F-HEMBB1000649//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/2.5e-37:58:81//HOMO SAPIENS (HUMAN)//P39189

F-HEMBB1000652//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/2.2e-37:61:77//HOMO SAPIENS (HUMAN)//P39193

F-HEMBB1000665//HYPOTHETICAL PROTEIN BBD24//0.83:38:36//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE)//P70845

F-HEMBB1000671//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//6.8e-51:74:71//HOMO SAPIENS (HUMAN)//P08547

F-HEMBB1000673//HEAT-STABLE ENTEROTOXIN A3/A4 PRECURSOR (STA3/STA4) (ST-IB) (ST-H)//0.012:37:37//ESCHERICHIA COLI//P07965

F-HEMBB1000684//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/3.1e-21:66:72//HOMO SAPIENS (HUMAN)//P39193

F-HEMBB1000693//HUNTINGTIN ASSOCIATED PROTEIN 1 (HAP1)//5.2e-26:121:49//RATTUS NORVEGICUS (RAT)//P54256

F-HEMBB1000705

F-HEMBB1000706

F-HEMBB1000709//HYPOTHETICAL 5.8 KD PROTEIN//1.0:29:44//CLOVER YELLOW MOSAIC VIRUS (CYMV)//P16485

F-HEMBB1000725//RAS-RELATED PROTEIN RAB-8B//7.4e-105:205:98//RATTUS NORVEGICUS (RAT)

F-HEMBB1000726//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.1e-26:76:76//HOMO SAPIENS (HUMAN)//P39194

F-HEMBB1000738//50S RIBOSOMAL PROTEIN L33.//1.0:41:31//THERMUS AQUATICUS (SUBSP. THERMOPHILUS).//P35871

F-HEMBB1000749//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.3e-29:42:85//HOMO SAPIENS (HUMAN)//P39194

5 F-HEMBB1000763//NIFU PROTEIN.//0.089:63:36//FRANKIA ALNI.//P46045

F-HEMBB1000770//CALTRIN-LIKE PROTEIN II.//0.98:13:69//CAVIA PORCELLUS (GUINEA PIG).//P22075

F-HEMBB1000774//HIGH MOBILITY GROUP PROTEIN HMG-Y.//0.029:53:32//MUS MUSCULUS (MOUSE).//P17095

10 F-HEMBB1000781//MAPK/ERK KINASE KINASE 2 (EC 2.7.1.-) (MEK KINASE 2) (MEKK 2).//3.5e-75:144:98//MUS MUSCULUS (MOUSE).//Q61083

F-HEMBB1000789//PUTATIVE 90.2 KD ZINC FINGER PROTEIN IN CCA1-ADK2 INTERGENIC REGION.//2.6e-49:232:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39956

F-HEMBB1000790//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.9e-16:93:51//HOMO SAPIENS (HUMAN).//P39188

15 F-HEMBB1000794

F-HEMBB1000807//MUSCARINIC ACETYLCHOLINE RECEPTOR M3.//0.54:111:27//GALLUS GALLUS (CHICKEN).//P49578

F-HEMBB1000810

F-HEMBB1000821

20 F-HEMBB1000822//HYPOTHETICAL 10 KD PROTEIN (ORF 6).//0.10:50:34//NARCISSUS MOSAIC VIRUS (NMV).//P15099

F-HEMBB1000826//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//0.00025:73:39//HOMO SAPIENS (HUMAN).//P20931

25 F-HEMBB1000827//HYPOTHETICAL 7.4 KD PROTEIN.//0.89:23:52//THERMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1).//P19302

F-HEMBB1000831//MALE SPECIFIC SPERM PROTEIN MST87F.//0.98:35:40//DROSOPHILA MELANOGASTER (FRUIT FLY).//P08175

F-HEMBB1000835//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.8e-31:96:46//HOMO SAPIENS (HUMAN).//P08547

30 F-HEMBB1000840//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.00012:102:36//NYCTICEBUS COUCANG (SLOW LORIS).//P08548

F-HEMBB1000848//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.3e-97:239:70//HOMO SAPIENS (HUMAN).//P08547

F-HEMBB1000852

35 F-HEMBB1000870

F-HEMBB1000876//METALLOTHIONEIN (MT).//0.99:14:64//PERCA FLUVIATILIS (PERCH).//P52725

F-HEMBB1000883//HYPOTHETICAL 7.8 KD PROTEIN (ORF62).//0.34:60:33//GUILLARDIA THETA (CRYPTOMONAS PHI).//O78459

40 F-HEMBB1000887//HISTIDINE-RICH, METAL BINDING POLYPEPTIDE.//1.0:26:42//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//Q48251

F-HEMBB1000888

F-HEMBB1000890

F-HEMBB1000893

F-HEMBB1000908//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.0074:45:51//HOMO SAPIENS (HUMAN).//P39188

45 F-HEMBB1000910//PROBABLE E5 PROTEIN.//1.0:49:36//HUMAN PAPILLOMAVIRUS TYPE 58.//P26552

F-HEMBB1000913//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.29:56:46//HOMO SAPIENS (HUMAN).//P39195

F-HEMBB1000915//CYTOCHROME B (EC 1.10.2.2).//2.5e-24:62:90//HOMO SAPIENS (HUMAN).//P00156

50 F-HEMBB1000917//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/5.9e-26:53:66//HOMO SAPIENS (HUMAN).//P39193

F-HEMBB1000927//NEURONAL CALCIUM SENSOR 1 (NCS-1) (FREQUENIN).//3.9e-44:182:45//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//Q91614

F-HEMBB1000947//SMALL PROLINE-RICH PROTEIN 2-1.//0.24:69:27//HOMO SAPIENS (HUMAN).//P35326

55 F-HEMBB1000959//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.0e-31:89:68//HOMO SAPIENS (HUMAN).//P39195

F-HEMBB1000973//NINE T-CELL-ASSOCIATED PROTEIN 1 (NINTEPP1) (NINTEPP1).//1.0:10:10//HOMO SAPIENS (HUMAN).//P01873

- F-HEMBB1000975//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR (HISTIDINE-PROLINE RICH GLYCOPROTEIN) (HPRG)//0.00042:77:41//HOMO SAPIENS (HUMAN)//P04196
F-HEMBB1000981
F-HEMBB1000985//MIPP PROTEIN (MURINE IAP-PROMOTED PLACENTA-EXPRESSED PROTEIN)//1.0e-18:
5 178:30//MUS MUSCULUS (MOUSE)//P28575
F-HEMBB1000991
F-HEMBB1000996//HYPOTHETICAL 10.1 KD PROTEIN IN RHSD-GCL INTERGENIC REGION (ORFD3)//0.58:
34:35//ESCHERICHIA COLI//P33669
F-HEMBB1001004//PROBABLE E4 PROTEIN//0.24:110:35//HUMAN PAPILLOMAVIRUS TYPE 5B//P26550
10 F-HEMBB1001008
F-HEMBB1001011//ZINC FINGER PROTEIN 7 (ZINC FINGER PROTEIN KOX4) (ZINC FINGER PROTEIN HF
16)//3.2e-17:104:47//HOMO SAPIENS (HUMAN)//P17097
F-HEMBB1001014//EOTAXIN PRECURSOR (EOSINOPHIL CHEMOTACTIC PROTEIN)//1.0:58:39//RATTUS
NORVEGICUS (RAT)//P97545
15 F-HEMBB1001020//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.4e-07:36:75//HOMO SAPIENS (HUMAN)//
P39189
F-HEMBB1001024
F-HEMBB1001037//FERREDOXIN//1.0:52:25//MOORELLA THERMOACETICA (CLOSTRIDIUM THER-
MOACETICUM)//P00203
20 F-HEMBB1001047
F-HEMBB1001051//PROTEIN FAN (FACTOR ASSOCIATED WITH N-SMASE ACTIVATION)//3.4e-21:50:100//
HOMO SAPIENS (HUMAN)//Q92636
F-HEMBB1001056//HYPOTHETICAL 29.3 KD PROTEIN (ORF92)//0.0099:115:35//ORGYIA PSEUDOTSUGATA
MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV)//O10341
25 F-HEMBB1001058//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.1e-33:95:76//HOMO SAPIENS (HUMAN)//
P39192
F-HEMBB1001060//HYPOTHETICAL 8.2 KD PROTEIN ZC21.7 IN CHROMOSOME III//1.0:38:36//
CAENORHABDITIS ELEGANS//P34591
F-HEMBB1001063
30 F-HEMBB1001068
F-HEMBB1001096//NOXIUSTOXIN (NTX) (TOXIN II.11)//0.99:36:38//CENTRUROIDES NOXIUS (MEXICAN
SCORPION)//P08815
F-HEMBB1001102//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I//1.1e-27:115:36//
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09701
35 F-HEMBB1001105//CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN PRECURSOR//0.80:70:40//
HOMO SAPIENS (HUMAN)//P28067
F-HEMBB1001112//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT//1.1e-126:287:85//RATTUS
NORVEGICUS (RAT)//P38378
F-HEMBB1001114//HYPOTHETICAL 9.6 KD PROTEIN (ORF2)//0.84:62:27//BACTERIOPHAGE L2//P42537
40 F-HEMBB1001117
F-HEMBB1001119//COLLAGEN ALPHA 1(XII) CHAIN PRECURSOR//1.6e-21:50:98//HOMO SAPIENS (HU-
MAN)//Q99715
F-HEMBB1001126//HYPOTHETICAL 55.9 KD PROTEIN EEED8.6 IN CHROMOSOME II//1.7e-50:184:53//
CAENORHABDITIS ELEGANS//Q09296
45 F-HEMBB1001133//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.4e-09:53:62//HOMO SAPIENS (HUMAN)//
P39192
F-HEMBB1001137//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAG-
MENT)//2.0e-05:206:27//CRICETULUS GRISEUS (CHINESE HAMSTER)//P11414
F-HEMBB1001142//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/4.1e-05:46:56//HOMO SAPIENS (HUMAN)//
50 P39193
F-HEMBB1001151//HYPOTHETICAL 33.5 KD PROTEIN C1D4.02C IN CHROMOSOME I//2.3e-23:109:44//
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10149
F-HEMBB1001153//PROCOLLAGEN ALPHA 2(IV) CHAIN PRECURSOR//0.75:76:34//ASCARIS SUUM (PIG
ROUNDWORM) (ASCARIS LUMBRICOIDES)//P27393
55 F-HEMBB1001169//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.4e-16:71:59//HOMO SAPIENS (HUMAN)//
P39194
F-HEMBB1001170//ANKYRIN 2//1.6e-16:184:184//MUS MUSCULUS (MOUSE)//P22281
F-HEMBB1001171//PERIODIC TRYPTOPHAN PROTEIN 2 HOMOLOG//9.4e-07:148:27//HOMO SAPIENS (HU-
MAN)//P39195

MAN)//Q15269

F-HEMBB1001182//HYPOTHETICAL 36.0 KD PROTEIN//1.3e-09:110:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P54858

F-HEMBB1001199

5 F-HEMBB1001208//HYPOTHETICAL PROTEIN LAMBDA-SP5//0.053:23:47//MUS MUSCULUS (MOUSE)//P15974

F-HEMBB1001209

F-HEMBB1001210//HYPOTHETICAL PROTEIN LAMBDA-SP5//0.14:40:37//MUS MUSCULUS (MOUSE)//P15974

10 F-HEMBB1001218//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.4e-19:49:67//HOMO SAPIENS (HUMAN)//P39194

F-HEMBB1001221//CYTOCHROME C OXIDASE POLYPEPTIDE VIIA-LIVER PRECURSOR (EC 1.9.3.1)//0.11:44:38//HOMO SAPIENS (HUMAN)//P14406

15 F-HEMBB1001234//65 KD YES-ASSOCIATED PROTEIN (YAP65)//2.0e-45:192:53//MUS MUSCULUS (MOUSE)//P46938

F-HEMBB1001242//HYPOTHETICAL 143.3 KD TRP-ASP REPEATS CONTAINING PROTEIN C12G12.13C IN CHROMOSOME I//5.5e-37:226:41//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09876

F-HEMBB1001249//OXALOACETATE DECARBOXYLASE GAMMA CHAIN (EC 4.1.1.3)//1.0:23:43//KLEBSIELLA PNEUMONIAE//P13155

20 F-HEMBB1001253//METALLOTHIONEIN-IH (MT-1H) (METALLOTHIONEIN-0) (MT-0)//0.14:16:43//HOMO SAPIENS (HUMAN)//P80294

F-HEMBB1001254//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.4e-12:40:75//HOMO SAPIENS (HUMAN)//P39195

25 F-HEMBB1001267//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.0e-12:33:78//HOMO SAPIENS (HUMAN)//P39193

F-HEMBB1001271//HYPOTHETICAL 25.1 KD PROTEIN B0302.5 IN CHROMOSOME X//1.0:58:37//CAENORHABDITIS ELEGANS//Q10928

F-HEMBB1001282//ANKYRIN HOMOLOG PRECURSOR//9.5e-13:206:31//CHROMATIUM VINOSUM//Q06527

30 F-HEMBB1001288//COPPER HOMEOSTASIS PROTEIN CUTC//4.6e-42:163:51//ESCHERICHIA COLI//P46719

F-HEMBB1001289//HYPOTHETICAL PROTEIN ORF-1137//1.0e-05:106:26//MUS MUSCULUS (MOUSE)//P11260

F-HEMBB1001294//GTP-BINDING PROTEIN TC10//1.3e-34:58:94//HOMO SAPIENS (HUMAN)//P17081

35 F-HEMBB1001302//HOMEBOX PROTEIN CDX-2 (CAUDAL-TYPE HOMEBOX PROTEIN 2) (CDX-3)//0.24:49:46//HOMO SAPIENS (HUMAN)//Q99626

F-HEMBB1001304//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1) (FRAGMENT)//1.0:17:70//LYCOPERSICON ESCULENTUM (TOMATO)//Q01157

F-HEMBB1001314//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR//0.21:104:27//DROSOPHILA ERECTA (FRUIT FLY)//P13730

40 F-HEMBB1001315//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.3e-24:53:71//HOMO SAPIENS (HUMAN)//P39195

F-HEMBB1001317//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I//0.24:90:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09782

45 F-HEMBB1001326//HYPOTHETICAL PROTEIN LAMBDA-SP5//0.36:26:50//MUS MUSCULUS (MOUSE)//P15974

F-HEMBB1001331//HYPOTHETICAL BHLF1 PROTEIN//1.0:127:33//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4)//P03181

F-HEMBB1001335//ESCARGOT/SLAIL PROTEIN HOMOLOG (FRAGMENT)//0.85:44:29//SCIARA CO-PROPHILA (FUNGUS GNAT)//Q01799

50 F-HEMBB1001337//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/4.2e-20:62:62//HOMO SAPIENS (HUMAN)//P39194

F-HEMBB1001339//HYPOTHETICAL 17.3 KD PROTEIN CY1A11.16C//8.2e-07:123:34//MYCOBACTERIUM TUBERCULOSIS//Q50606

55 F-HEMBB1001346//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//4.2e-14:60:45//HOMO SAPIENS (HUMAN)//P08547

F-HEMBB1001347

F-HEMBB1001348

F-HEMBB1001356

F-HEMBB1001364

F-HEMBB1001366/HISTIDINE-RICH PROTEIN//0.87:26:42//PLASMODIUM FALCIPARUM (ISOLATE FCM17 / SENEGAL)//P14586

F-HEMBB1001367/////ALU SUBFAMILY SC WARNING ENTRY /////8.6e-40:146:61//HOMO SAPIENS (HUMAN)//P39192

F-HEMBB1001369

F-HEMBB1001380/////ALU SUBFAMILY SP WARNING ENTRY /////1.9e-25:49:83//HOMO SAPIENS (HUMAN)//P39193

F-HEMBB1001384//BH3 INTERACTING DOMAIN DEATH AGONIST (BID)//0.80:95:29//MUS MUSCULUS (MOUSE)//P70444

F-HEMBB1001387//PEA2 PROTEIN (PPF2 PROTEIN)//0.022:117:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40091

F-HEMBB1001394//ALPHA-ADAPTIN A (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-A LARGE CHAIN) (100 KD COATED VESICLE PROTEIN A) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA A SUBUNIT)//0.38:85:31//MUS MUSCULUS (MOUSE)//P17426

F-HEMBB1001410

F-HEMBB1001424//PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECURSOR//0.99:37:21//ORYZA SATIVA (RICE)//P12162

F-HEMBB1001426/////ALU SUBFAMILY SX WARNING ENTRY /////0.0035:40:60//HOMO SAPIENS (HUMAN)//P39195

F-HEMBB1001429//CYTOSOL AMINOPEPTIDASE (EC 3.4.11.1) (LEUCINE AMINOPEPTIDASE) (LAP) (LEUCYL AMINOPEPTIDASE) (PROLINE AMINOPEPTIDASE) (EC 3.4.11.5) (PROLYL AMINOPEPTIDASE)//1.1e-99:21:86//BOS TAURUS (BOVINE)//P00727

F-HEMBB1001436/////ALU SUBFAMILY SX WARNING ENTRY /////3.4e-30:57:78//HOMO SAPIENS (HUMAN)//P39195

F-HEMBB1001443//[PYRUVATE DEHYDROGENASE (LIPOAMIDE)]-PHOSPHATASE PRECURSOR (PDP) (EC 3.1.3.43) (PYRUVATE DEHYDROGENASE PHOSPHATASE, CATALYTIC SUBUNIT (PDPC))//2.5e-79:155:97//BOS TAURUS (BOVINE)//P35816

F-HEMBB1001449

F-HEMBB1001454//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) [CONTAINS: PEPTIDE P-D] (FRAGMENT)//1.1e-05:196:31//HOMO SAPIENS (HUMAN)//P10161

F-HEMBB1001458//24 KD ANTIGEN (FRAGMENT)//0.94:18:50//PLASMODIUM CHABAUDI//P14592

F-HEMBB1001463

F-HEMBB1001464//PPF2L ANTIGEN (FRAGMENT)//1.0:45:28//PLASMODIUM FALCIPARUM (ISOLATE PALO ALTO / UGANDA)//P07765

F-HEMBB1001482//GASTRULA ZINC FINGER PROTEIN XLCGF16.1 (FRAGMENT)//4.2e-10:37:43//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P18712 F-HEMBB1001500

F-HEMBB1001521/////ALU SUBFAMILY J WARNING ENTRY /////2.4e-39:59:72//HOMO SAPIENS (HUMAN)//P39188

F-HEMBB1001527//HOMEBOX PROTEIN HOX-B5 (XLHBOX-4) (XHOX-1B) (FRAGMENT)//0.21:131:25//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P09019

F-HEMBB1001531//GENE 32 PROTEIN (GP32)//0.88:95:30//MYCOBACTERIOPHAGE L5//Q05241

F-HEMBB1001535//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//1.0:31:38//LUMBRICUS TERRESTRIS (COMMON EARTHWORM)//Q34942

F-HEMBB1001536

F-HEMBB1001537/////ALU SUBFAMILY SB2 WARNING ENTRY /////0.0063:52:50//HOMO SAPIENS (HUMAN)//P39191

F-HEMBB1001555/////ALU SUBFAMILY J WARNING ENTRY /////4.9e-23:69:63//HOMO SAPIENS (HUMAN)//P39188

F-HEMBB1001562//RABPHILIN-3A//0.087:147:27//RATTUS NORVEGICUS (RAT)//P47709

F-HEMBB1001564//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//5.9e-27:107:54//HOMO SAPIENS (HUMAN)//P08547

F-HEMBB1001565/////ALU SUBFAMILY SQ WARNING ENTRY /////1.9e-12:51:54//HOMO SAPIENS (HUMAN)//P39194

F-HEMBB1001585

F-HEMBB1001586

F-HEMBB1001588//HISTIDINE-RICH PROTEIN//0.87:26:42//PLASMODIUM FALCIPARUM (ISOLATE FCM17 / SENEGAL)//P14586
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P36140

F-HEMBB1001603

F-HEMBB1001618//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE]//0.00076:47:44//MUS MUSCULUS (MOUSE)//P11369

F-HEMBB1001619//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930)//1.0:52:32//HOMO SAPIENS (HUMAN)//P22531

F-HEMBB1001630

F-HEMBB1001635//METALLOTHIONEIN-LIKE PROTEIN TYPE 2 A//1.0:27:44//LYCOPERSICON ESCULENTUM (TOMATO)//Q40157

F-HEMBB1001637//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.0042:26:73//HOMO SAPIENS (HUMAN)//P39188

F-HEMBB1001641

F-HEMBB1001653//SURVIVAL MOTOR NEURON PROTEIN 1//0.51:36:47//CANIS FAMILIARIS (DOG)//O02771

F-HEMBB1001665//HOMEBOX PROTEIN ENGRAILED-1 (HU-EN-1)//0.0030:135:34//HOMO SAPIENS (HUMAN)//Q05925

F-HEMBB1001668//PROBABLE 60S RIBOSOMAL PROTEIN L39//0.99:25:44//CAENORHABDITIS ELEGANS//P52814

F-HEMBB1001673//HYPOTHETICAL 46.1 KD PROTEIN IN ERP5-ORC6 INTERGENIC REGION//0.0054:128:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38823

F-HEMBB1001684//SUPPRESSOR PROTEIN SRP40//0.56:81:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32583

F-HEMBB1001685//CYTOCHROME C OXIDASE POLYPEPTIDE VIII-HEART PRECURSOR (EC 1.9.3.1) (VIIIb) (IX)//1.0:21:47//BOS TAURUS (BOVINE)//P10175

F-HEMBB1001695//MYOSIN IC HEAVY CHAIN//8.9e-05:86:40//ACANTHAMOEBA CASTELLANII (AMOEBA)//P10569

F-HEMBB1001704//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/9.0e-08:35:71//HOMO SAPIENS (HUMAN)//P39195

F-HEMBB1001706//CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUAMOUS CELL MARKER) (SRP) //0.91:39:41//SUS SCROFA (PIG)//P35323

F-HEMBB1001707//FERREDOXIN-LIKE PROTEIN IN NIF REGION//1.0:43:23//BRADYRHIZOBIUM JAPONICUM//P27394

F-HEMBB1001717//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.3) (FRAGMENT)//1.0:71:25//LEMUR CATTA (RING-TAILED LEMUR)//Q34878

F-HEMBB1001735//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/9.0e-35:97:74//HOMO SAPIENS (HUMAN)//P39194

F-HEMBB1001736//EUKARYOTIC TRANSLATION INITIATION FACTOR 3 BETA SUBUNIT (EIF-3 BETA) (EIF3 P116) (EIF3 P110)//0.00069:180:28//HOMO SAPIENS (HUMAN)//P55884

F-HEMBB1001747

F-HEMBB1001749//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.8e-43:75:70//HOMO SAPIENS (HUMAN)//P39195

F-HEMBB1001753//PROTEIN Q300//0.00091:16:81//MUS MUSCULUS (MOUSE)//Q02722

F-HEMBB1001756//CYCLIN-DEPENDENT KINASES REGULATORY SUBUNIT 2 (XE-P9)//0.94:35:42//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//Q91879

F-HEMBB1001760

F-HEMBB1001762//GENE 35 PROTEIN (GP35)//0.76:21:47//MYCOBACTERIOPHAGE L5//Q05245

F-HEMBB1001785

F-HEMBB1001797//CHLOROPLAST 50S RIBOSOMAL PROTEIN L35//0.99:41:31//PORPHYRA PURPUREA//P51270

F-HEMBB1001802

F-HEMBB1001812//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/2.2e-39:54:77//HOMO SAPIENS (HUMAN)//P39193

F-HEMBB1001816//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.1e-19:97:57//HOMO SAPIENS (HUMAN)//P39194

F-HEMBB1001831//HYPOTHETICAL 45.6 KD PROTEIN IN COX5A-ALG11 INTERGENIC REGION//0.62:204:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53951

F-HEMBB1001832//HYPOTHETICAL 45.6 KD PROTEIN IN COX5A-ALG11 INTERGENIC REGION//0.62:204:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53951

F-HEMBB1001833//SORGHUM//Q99064

F-HEMBB1001836//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/7.1e-14:85:61//HOMO SAPIENS (HUMAN)

MAN)//P39191

F-HEMBB1001839//PROBABLE E4 PROTEIN//0.61:49:34//HUMAN PAPILLOMAVIRUS TYPE 6C//P20969

F-HEMBB1001850

F-HEMBB1001863//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.7e-30:57:68//HOMO SAPIENS (HUMAN)//P39194

F-HEMBB1001867

F-HEMBB1001868//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)//0.00036:47:53//NICOTIANA TABACUM (COMMON TOBACCO)//P13983

F-HEMBB1001869//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/7.0e-11:95:45//HOMO SAPIENS (HUMAN)//P39188

F-HEMBB1001872//HYPOTHETICAL 8.2 KD PROTEIN IN LEF8-FP INTERGENIC REGION//1.0:34:38//AUTOGRAPHAL CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV)//P41459

F-HEMBB1001874

F-HEMBB1001875

F-HEMBB1001880

F-HEMBB1001899//GENE 11 PROTEIN//1.0:45:31//SPIROPLASMA VIRUS SPV1-R8A2 B//P15902

F-HEMBB1001905//HYPOTHETICAL 81.7 KD PROTEIN IN MOL1-NAT2 INTERGENIC REGION//8.8e-54:216:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P48234

F-HEMBB1001906

F-HEMBB1001908//MONOCYTIC LEUKEMIA ZINC FINGER PROTEIN//6.3e-51:138:80//HOMO SAPIENS (HUMAN)//Q92794

F-HEMBB1001910

F-HEMBB1001911

F-HEMBB1001915//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME 64E)//2.3e-27:71:70//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q24574

F-HEMBB1001921//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//9.8e-13:75:53//HOMO SAPIENS (HUMAN)//P08547

F-HEMBB1001922

F-HEMBB1001925//EPITHELIAL MEMBRANE PROTEIN-1 (EMP-1) (TUMOR-ASSOCIATED MEMBRANE PROTEIN)//1.0:55:30//MUS MUSCULUS (MOUSE)//P47801

F-HEMBB1001930//HYPOTHETICAL 9.6 KD PROTEIN K10D2.7 IN CHROMOSOME III//0.43:49:26//CAENORHABDITIS ELEGANS//Q09412

F-HEMBB1001944//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/5.1e-34:63:85//HOMO SAPIENS (HUMAN)//P39189

F-HEMBB1001945//NONSPECIFIC LIPID-TRANSFER PROTEIN (LTP) (PHOSPHOLIPID TRANSFER PROTEIN) (PLTP)//0.28:45:40//AMARANTHUS CAUDATUS (LOVE-LIES-BLEEDING) (INCA-WHEAT)//P80450

F-HEMBB1001947//PROTEIN UL24//0.48:42:47//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)//P10208

F-HEMBB1001950//HYPOTHETICAL 42.6 KD PROTEIN IN GSHB-ANSB INTERGENIC REGION (O378)//1.6e-24:162:36//ESCHERICHIA COLI//P52062

F-HEMBB1001952

F-HEMBB1001953

F-HEMBB1001957//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.7e-11:51:60//HOMO SAPIENS (HUMAN)//P39188

F-HEMBB1001962//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/7.6e-24:163:42//HOMO SAPIENS (HUMAN)//P39188

F-HEMBB1001967//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/2.1e-35:55:80//HOMO SAPIENS (HUMAN)//P39189

F-HEMBB1001973//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/2.1e-37:108:75//HOMO SAPIENS (HUMAN)//P39192

F-HEMBB1001983//LYSIS PROTEIN (E PROTEIN) (GPE)//0.84:45:37//BACTERIOPHAGE ALPHA-3//P31280

F-HEMBB1001988

F-HEMBB1001990

F-HEMBB1001996//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//1.4e-14:98:40//HOMO SAPIENS (HUMAN)//P08547

F-HEMBB1002002

P39188

F-HEMBB1002002//CYTOCHROME C BIOGENESIS PROTEIN CCSA//1.0:150:25//PORPHYRA PURPUREA//

P51369

F-HEM BB1002005//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/7.6e-12:94:40//HOMO SAPIENS (HUMAN)//
P39195

F-HEM BB1002009

5 F-HEM BB1002015//HYPOTHETICAL 7.7 KD PROTEIN IN MRR-TSR INTERGENIC REGION (F67)//1.0:17:47//
ESCHERICHIA COLI//P39395F-HEM BB1002042//CYTOCHROME P450 4C1 (EC 1.14.14.1) (CYP1VC1)//2.4e-50:139:55//BLABERUS DIS-
COIDALIS (TROPICAL COCKROACH)//P2998110 F-HEM BB1002043//HYPOTHETICAL 9.5 KD PROTEIN IN DHFR 3'REGION (ORF3)//0.052:40:42//HERPESVI-
RUS SAIMIRI (SUBGROUP C / STRAIN 488)//P22577F-HEM BB1002044//CELLULOSE COMPLEMENTING PROTEIN//0.45:87:33//ACETOBACTER XYLINUM (AC-
ETOBACTER PASTEURIANUS)//P37697F-HEM BB1002045//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//0.78:18:55//HOMO SAPIENS (HUMAN)//
P03928

15 F-HEM BB1002049

F-HEM BB1002050//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CONTAINS: BASIC
PEPTIDE P-F] (FRAGMENT)//1.0e-06:188:27//HOMO SAPIENS (HUMAN)//P02812F-HEM BB1002068//HOMEBOX PROTEIN HOX-A4 (CHOX-1.4)//0.0023:56:44//GALLUS GALLUS (CHICK-
EN)//P1727720 F-HEM BB1002069//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)//
0.0074:134:33//NICOTIANA TABACUM (COMMON TOBACCO)//P13983F-HEM BB1002092//ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN) [CONTAINS: OUTER MEM-
BRANE PROTEIN CP70; TRANSMEMBRANE PROTEIN P20E]//2.4e-07:75:40//BABOON ENDOGENOUS VI-
RUS (STRAIN M7)//P1026925 F-HEM BB1002094//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/1.9e-24:63:82//HOMO SAPIENS (HU-
MAN)//P39191F-HEM BB1002115//EC PROTEIN HOMOLOG (ZINC-METALLOTHIONEIN CLASS II)//0.94:26:42//ZEA MAYS
(MAIZE)//P4340130 F-HEM BB1002134//ZINC-FINGER PROTEIN NEURO-D4//4.6e-57:176:67//RATTUS NORVEGICUS (RAT)//
P56163F-HEM BB1002139//CHLOROPLAST 50S RIBOSOMAL PROTEIN L35//1.0:17:52//PORPHYRA PURPUREA//
P51270F-HEM BB1002142//EARLY NODULIN 20 PRECURSOR (N-20)//0.087:52:36//MEDICAGO TRUNCATULA (BAR-
REL MEDIC)//P9332935 F-HEM BB1002152//HYPOTHETICAL 12.3 KD PROTEIN IN RPL3-RPL33 INTERGENIC REGION (ORF102)//
5.8e-05:61:37//CYANOPHORA PARADOXA//P15811F-HEM BB1002189//HYPOTHETICAL PROTEIN UL125//1.0:77:32//HUMAN CYTOMEGALOVIRUS (STRAIN
AD169)//P16835

F-HEM BB1002190

40 F-HEM BB1002193//TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR (TYROSINE-PROTEIN
KINASE RSE) (TYROSINE-PROTEIN KINASE SKY) (TYROSINE-PROTEIN KINASE DTK)//1.2e-27:59:100//
HOMO SAPIENS (HUMAN)//Q06418F-HEM BB1002217//ZINC FINGER PROTEIN 184 (FRAGMENT)//6.6e-22:106:50//HOMO SAPIENS (HUMAN)//
Q99676

45 F-HEM BB1002218//PROTEIN Q300//0.85:19:52//MUS MUSCULUS (MOUSE)//Q02722

F-HEM BB1002232//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/9.6e-21:56:71//HOMO SAPIENS (HUMAN)//
P39195

F-HEM BB1002247

50 F-HEM BB1002249//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/7.2e-29:93:69//HOMO SAPIENS (HU-
MAN)//P39194F-HEM BB002254//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.0e-29:101:67//HOMO SAPIENS (HU-
MAN)//P39194F-HEM BB1002255//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6.5.3)//1.0:73:28//PARA-
MECIUM TETRAURELIA//P1557955 F-HEM BB1002266//GLUTAMIC ACID RICH PROTEIN PRECURSOR (CLONE CP7) [CONTAINS: BASIC
PEPTIDE P-F] (FRAGMENT)//1.0e-06:188:27//HOMO SAPIENS (HUMAN)//P02812F-HEM BB1002280//LINE REVERSE TRANSCRIPTASE (CLONE CP7) [CONTAINS: BASIC
PEPTIDE P-F] (FRAGMENT)//1.0e-06:188:27//HOMO SAPIENS (HUMAN)//P02812

GANG (SLOW LORIS)//P08548

F-HEMBB1002300

F-HEMBB1002306/////ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.00011:26:84//HOMO SAPIENS (HUMAN)//P39195

F-HEMBB1002327/////ALU SUBFAMILY SB WARNING ENTRY !!!!!/4.1e-11:41:85//HOMO SAPIENS (HUMAN)//P39189

F-HEMBB1002329//HYPOTHETICAL 74.0 KD PROTEIN IN CAJ1-HOM3 INTERGENIC REGION//9.9e-17:232:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40032

F-HEMBB1002340

F-HEMBB1002342//HYPOTHETICAL 32.5 KD PROTEIN IN MSH6-BMH2 INTERGENIC REGION//3.6e-40:102:57//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q03835

F-HEMBB1002358//THYMIDYLATE KINASE (EC 2.7.4.9) (DTMP KINASE)//6.1e-30:63:96//HOMO SAPIENS (HUMAN)//P23919

F-HEMBB1002359//HYPOTHETICAL 7.1 KD PROTEIN C6G9.01C IN CHROMOSOME I//0.97:28:46//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q92346

F-HEMBB1002364//RETROVIRUS-RELATED POL POLYPROTEIN (FRAGMENT)//0.47:119:25//HOMO SAPIENS (HUMAN)//P12895

F-HEMBB1002371//HYPOTHETICAL 15.5 KD PROTEIN C2F7.12 IN CHROMOSOME I PRECURSOR//3.0e-05:111:30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09703

F-HEMBB1002381//PUTATIVE CUTICLE COLLAGEN C09G5.4//0.34:105:34//CAENORHABDITIS ELEGANS//Q09455

F-HEMBB1002383//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6)//0.049:103:32//AQUIFEX AEOLICUS//066566

F-HEMBB1002387//10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES) (HEAT SHOCK PROTEIN 11)//0.18:75:28//RICKETTSIA TSUTSUGAMUSHI//P16626

F-HEMBB1002409//HIGH MOBILITY GROUP PROTEIN HMG-Y//0.014:61:36//MUS MUSCULUS (MOUSE)//P17095

F-HEMBB1002415

F-HEMBB1002425/////ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.8e-18:55:70//HOMO SAPIENS (HUMAN)//P39194

F-HEMBB1002442//LIN-10 PROTEIN//5.1e-15:121:31//CAENORHABDITIS ELEGANS//P34692

F-HEMBB1002453/////ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.2e-32:54:75//HOMO SAPIENS (HUMAN)//P39189

F-HEMBB1002457/////ALU SUBFAMILY J WARNING ENTRY !!!!!/1.5e-07:31:64//HOMO SAPIENS (HUMAN)//P39188

F-HEMBB1002458//MALE SPECIFIC SPERM PROTEIN MST84DA//0.92:28:53//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q01642

F-HEMBB1002477//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT)//0.0066:198:27//CRICETULUS GRISEUS (CHINESE HAMSTER)//P11414

F-HEMBB1002489//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53)//0.030:182:28//HOMO SAPIENS (HUMAN)//Q15427

F-HEMBB1002492

F-HEMBB1002495/////ALU SUBFAMILY SC WARNING ENTRY !!!!!/2.1e-08:41:75//HOMO SAPIENS (HUMAN)//P39192

F-HEMBB1002502//RETROVIRUS-RELATED POL POLYPROTEIN (FRAGMENT)//0.00030:31:77//HOMO SAPIENS (HUMAN)//P12895

F-HEMBB1002509

F-HEMBB1002510

F-HEMBB1002520//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//6.8e-36:162:50//NYCTICEBUS COUCANG (SLOW LORIS)//P08548

F-HEMBB1002522//7 KD PROTEIN (ORF 4)//0.77:32:40//CHRYSANTHEMUM VIRUS B (CVB)//P37990

F-HEMBB1002531

F-HEMBB1002534/////ALU SUBFAMILY SX WARNING ENTRY !!!!!/3.1e-36:80:73//HOMO SAPIENS (HUMAN)//P39195

F-HEMBB1002545

F-HEMBB1002550//HOMEBOX PROTEIN HOX D11 (HOX 4.6) (HOX 5.5)//3.8e-05:83:34//MUS MUSCULUS (MOUSE) P17095

F-HEMBB1002556

F-HEMBB1002579//SPLICING FACTOR U2AF 35 KD SUBUNIT (U2 AUXILIARY FACTOR 35 KD SUBUNIT) (U2

SNRNP AUXILIARY FACTOR SMALL SUBUNIT) (FRAGMENT).//5.0e-06:27:77//SUS SCROFA (PIG).//Q29350
F-HEMBB1002582//PROTEINASE INHIBITOR.//1.0:27:40//SOLANUM MELONGENA (EGGPLANT) (AUBER-
GINE).//P01078

F-HEMBB1002590//HYPOTHETICAL PROTEIN IN MMSB 3'REGION (ORF1) (FRAGMENT).//1.9e-20:90:54//
PSEUDOMONAS AERUGINOSA.//P28812

F-HEMBB1002596

F-HEMBB1002600//NOVEL ANTIGEN 2 (NAG-2).//1.9e-60:187:59//HOMO SAPIENS (HUMAN).//O14817

F-HEMBB1002601//M PROTEIN, SEROTYPE 6 PRECURSOR.//1.0:71:35//STREPTOCOCCUS PYOGENES.//
P08089

F-HEMBB1002603

F-HEMBB1002607//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAG-
MENT).//0.0032:142:33//HOMO SAPIENS (HUMAN).//P10162

F-HEMBB1002610//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.0e-11:79:49//HOMO SAPIENS (HU-
MAN).//P08547

F-HEMBB1002613//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.9e-08:41:60//HOMO SAPIENS (HUMAN).//
P39188

F-HEMBB1002614//HYPOTHETICAL 9.5 KD PROTEIN.//1.0:40:35//VACCINIA VIRUS (STRAIN COPENHA-
GEN).//P20553

F-HEMBB1002617//INSECT TOXIN 1 (BOT IT1).//1.0:44:29//BUTHUS OCCITANUS TUNETANUS (COMMON
EUROPEAN SCORPION).//P55902

F-HEMBB1002623//HYPOTHETICAL 9.7 KD PROTEIN (ORF88) (PUTATIVE DNA-BINDING PROTEIN).//0.42:
31:54//BACTERIOPHAGE P4.//P12552

F-HEMBB1002635//STRESS-ACTIVATED PROTEIN KINASE JNK3 (EC 2.7.1 -) (C-JUN N-TERMINAL KINASE
3) (MAP KINASE P49 3F12).//6.2e-17:44:95//HOMO SAPIENS (HUMAN).//P53779

F-HEMBB1002664//SMALL NUCLEAR RIBONUCLEOPROTEIN ASSOCIATED PROTEIN B (SM-B) (SNRNP-B)
(SM11) (FRAGMENT).//1.0:57:36//RATTUS NORVEGICUS (RAT).//P17136

F-HEMBB1002677//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.9e-06:194:34//NYCTICEBUS COU-
CANG (SLOW LORIS).//P08548

F-HEMBB1002683//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).//0.96:56:
35//LEMUR CATTA (RING-TAILED LEMUR).//Q34879

F-HEMBB1002684//SILLUCIN.//1.0:16:50//RHIZOMUCOR PUSILLUS.//P02885

F-HEMBB1002686

F-HEMBB1002692

F-HEMBB1002697//HELIX-DESTABILIZING PROTEIN (SINGLE-STRANDED DNA BINDING PROTEIN) (GPV).//
0.57:36:38//BACTERIOPHAGE FD, BACTERIOPHAGE F1, AND BACTERIOPHAGE M13.//P03669

F-HEMBB1002699

F-HEMBB1002702

F-HEMBB1002705//HYPOTHETICAL 34.8 KD PROTEIN C4H3.04C IN CHROMOSOME I.//3.6e-40:180:37//
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10212

F-HEMBB1002712

F-MAMMA1000009//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//1.2e-32:95:75//HOMO SAPIENS (HU-
MAN).//P39189

F-MAMMA1000019

F-MAMMA1000020//DIMETHYLANILINE MONOOXYGENASE [N-OXIDE FORMING] 5 (EC 1.14.13.8) (HEPATIC
FLAVIN-CONTAINING MONOOXYGENASE 5) (FMO 5) (DIMETHYLANILINE OXIDASE 5).//5.2e-12:24:100//HO-
MO SAPIENS (HUMAN).//P49326

F-MAMMA1000025//BETA-2-MICROGLOBULIN PRECURSOR.//1.0:73:26//BRACHYDANIO RERIO (ZE-
BRA FISH) (ZEBRA DANIO).//Q04475

F-MAMMA1000043//HYPOTHETICAL PXBL-I PROTEIN (FRAGMENT).//0.057:130:31//BOVINE LEUKEMIA VI-
RUS (JAPANESE ISOLATE BLV-1) (BLV).//P03412

F-MAMMA1000045

F-MAMMA1000055//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//7.5e-44:138:55//MUS MUSCULUS
(MOUSE).//P47226

F-MAMMA1000057//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.2e-39:92:69//HOMO SAPIENS (HU-
MAN).//P39194

F-MAMMA1000061

F-MAMMA1000061//CAPSID PROTEIN PROSIS VIRUS (PMNPV).//Q1034

F-MAMMA1000084// ALU SUBFAMILY SX WARNING ENTRY !!!!!//5.4e-28:94:73//HOMO SAPIENS (HU-
MAN).//P39194

MAN)//P39195

F-MAMMA1000085//PUTATIVE CYSTEINYL-TRNA SYNTHETASE C29E6.06C (EC 6.1.1.16) (CYSTEINE--TRNA LIGASE) (CYSRS)//6.6e-38:90:51//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09860

F-MAMMA1000092//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//6.4e-30:43:86//HOMO SAPIENS (HUMAN)//P39192

F-MAMMA1000103//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930)//0.038:17:52//HOMO SAPIENS (HUMAN)//P22531

F-MAMMA1000117//50S RIBOSOMAL PROTEIN L24E (HL21/HL22)//0.90:25:48//HALOARcula MARISMORTUI (HALOBACTERIUM MARISMORTUI)//P14116

F-MAMMA1000129//HYPOTHETICAL BHLF1 PROTEIN//0.0016:75:40//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4)//P03181

F-MAMMA1000133

F-MAMMA1000134//HYPOTHETICAL PROTEIN MJ0647//1.0:41:41//METHANOCOCCUS JANNASCHII//Q58063

F-MAMMA1000139//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-3 SUBUNIT//0.99:69:28//BOS TAURUS (BOVINE), AND MUS MUSCULUS (MOUSE)//P29798

F-MAMMA1000143//CALPAIN INHIBITOR (CALPASTATIN) (FRAGMENT)//0.023:111:27//MUS MUSCULUS (MOUSE)//P51125

F-MAMMA1000155//PUTATIVE CUTICLE COLLAGEN C09G5.5//0.018:125:34//CAENORHABDITIS ELEGANS//Q09456

F-MAMMA1000163//MERCURIC TRANSPORT PROTEIN PERIPLASMIC COMPONENT PRECURSOR (PERIPLASMIC MERCURY ION BINDING PROTEIN) (MERCURY SCAVENGER PROTEIN)//0.11:88:25//SHEWANELLA PUTREFACIENS (PSEUDOMONAS PUTREFACIENS)//Q54463

F-MAMMA1000171

F-MAMMA1000173//DREBRIN E//7.6e-41:197:43//HOMO SAPIENS (HUMAN)//Q16643

F-MAMMA1000175//GAMMA-THIONIN HOMOLOG PPT PRECURSOR//0.92:39:38//PETUNIA INTEGRIFOLIA (VIOLET-FLOWERED PETUNIA) (PETUNIA INFLATA)//Q40901

F-MAMMA1000183//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)//2.4e-106:249:61//HOMO SAPIENS (HUMAN)//P51523

F-MAMMA1000198//MALE SPECIFIC SPERM PROTEIN MST84DD//0.0014:35:42//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q01645

F-MAMMA1000221

F-MAMMA1000227//6.8 KD MITOCHONDRIAL PROTEOLIPID//1.0:30:40//MUS MUSCULUS (MOUSE)//P56379

F-MAMMA1000241//PHOTOSYSTEM I REACTION CENTRE SUBUNIT X (PSI-K)//1.0:40:37//PORPHYRA PURPUREA//P51370

F-MAMMA1000251//HYPOTHETICAL 6.8 KD PROTEIN IN FIC-PPIA INTERGENIC REGION//0.99:29:48//SALMONELLA TYPHIMURIUM//P37771

F-MAMMA1000254//HYPOTHETICAL 6.0 KD PROTEIN IN THI12 5'REGION//1.0:20:50//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53820

F-MAMMA1000257//HYPOTHETICAL 50.0 KD PROTEIN IN HEML 3'REGION (ORF2)//0.22:50:44//PSEUDOMONAS AERUGINOSA//Q51470

F-MAMMA1000264//GASTRIN-RELEASING PEPTIDE RECEPTOR (GRP-R) (GRP-PREFERRING BOMBESIN RECEPTOR)//0.80:39:43//HOMO SAPIENS (HUMAN)//P30550

F-MAMMA1000266

F-MAMMA1000270//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//9.5e-42:95:84//HOMO SAPIENS (HUMAN)//P39189

F-MAMMA1000277//PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS: CHONDROCALCIN]//0.0062:90:34//MUS MUSCULUS (MOUSE)//P28481

F-MAMMA1000278//C-HORDEIN (CLONE PC HOR1-3) (FRAGMENT)//0.00096:59:33//HORDEUM VULGARE (BARLEY)//P17991

F-MAMMA1000279//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//8.4e-17:56:76//HOMO SAPIENS (HUMAN)//P39195

F-MAMMA1000284//ARYL HYDROCARBON RECEPTOR NUCLEAR TRANSLOCATOR 2 (ARNT PROTEIN 2)//0.017:146:30//MUS MUSCULUS (MOUSE)//Q61324

F-MAMMA1000285//ALU SUBFAMILY SC WARNING ENTRY !!!!//P39184

F-MAMMA1000302//C-HORDEIN (CLONE PC-919) (FRAGMENT)//1.0:42:33//HORDEUM VULGARE (BAR-

LEY).//P17992

F-MAMMA1000307//PROBABLE E4 PROTEIN.//0.21:71:30//RHESUS PAPILLOMAVIRUS TYPE 1 (RHPV 1).//P24832

F-MAMMA1000309//COLLAGEN ALPHA 1(VIII) CHAIN PRECURSOR (ENDOTHELIAL COLLAGEN).//0.0026:141:36//HOMO SAPIENS (HUMAN).//P27658

F-MAMMA1000312

F-MAMMA1000313//DNA REPAIR PROTEIN RAD51 HOMOLOG (25 KD PROTEIN) (FRAGMENT).//0.76:52:32//STAPHYLOCOCCUS AUREUS.//P31337

F-MAMMA1000331

F-MAMMA1000339//50S RIBOSOMAL PROTEIN L29P.//0.78:32:46//METHANOBACTERIUM THERMAUTOTROPHICUM.//Q26117

F-MAMMA1000340//HYPOTHETICAL 29.4 KD PROTEIN IN STE6-LOS1 INTERGENIC REGION.//1.0:29:58//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36039

F-MAMMA1000348//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//7.5e-09:63:60//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1000356//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.3e-05:42:52//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1000360

F-MAMMA1000361//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//4.4e-33:84:72//HOMO SAPIENS (HUMAN).//P39189

F-MAMMA1000372//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//6.6e-21:53:71//HOMO SAPIENS (HUMAN).//P39193

F-MAMMA1000385

F-MAMMA1000388//OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY ACTIVATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).//0.40:72:36//HOMO SAPIENS (HUMAN).//P43489

F-MAMMA1000395//RABPHILIN-3A (FRAGMENT).//0.032:125:25//MUS MUSCULUS (MOUSE).//P47708

F-MAMMA1000402//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//3.1e-28:266:40//HOMO SAPIENS (HUMAN).//P08547

F-MAMMA1000410//NADH-UBIQUINONE OXIDOREDUCTASE 13 KD-B SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-13KD-B) (CI-13KD-B) (B13).//5.9e-06:32:68//HOMO SAPIENS (HUMAN).//Q16718

F-MAMMA1000413//RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//6.7e-05:93:31//MUS MUSCULUS (MOUSE).//P11369

F-MAMMA1000414

F-MAMMA1000416//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III.//4.1e-28:119:53//CAENORHABDITIS ELEGANS.//Q09232

F-MAMMA1000421//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.7e-23:68:76//HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1000422//METALLOTHIONEIN (MT).//0.037:42:42//GADUS MORHUA (ATLANTIC COD).//P51902

F-MAMMA1000423

F-MAMMA1000424//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//0.048:23:73//HOMO SAPIENS (HUMAN).//P39189

F-MAMMA1000429//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS5.//2.7e-05:110:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q92331

F-MAMMA1000431//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//9.4e-15:85:58//HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1000444//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//4.3e-25:65:76//HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1000446//ZYXIN.//0.79:155:29//GALLUS GALLUS (CHICKEN).//Q04584

F-MAMMA1000458//HYPOTHETICAL 37.7 KD PROTEIN C18B11.06 IN CHROMOSOME I.//0.0048:46:43//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09713

F-MAMMA1000468//PERIOD CLOCK PROTEIN (FRAGMENT).//0.50:20:55//DROSOPHILA ROBUSTA (FRUIT FLY).//Q03296

F-MAMMA1000472//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.5e-17:106:55//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1000478//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.9e-35:80:68//HOMO SAPIENS (HUMAN).//P39193

F-MAMMA1000483//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//4.4e-33:84:72//HOMO SAPIENS (HUMAN).//P39189

F-MAMMA1000490//TYROSINE-PROTEIN KINASE TXK (EC 2.7.1.112) (PTK-RL-18) (RESTING LYMPHOCYTE KINASE)//0.43:21:57//MUS MUSCULUS (MOUSE)//P42682

F-MAMMA1000500//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN)//0.61:33:54//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z2/CDC-Z34 ISOLATE) (HIV-1)//P12506

5 F-MAMMA1000501//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.1e-32:43:83//HOMO SAPIENS (HUMAN)//P39194

F-MAMMA1000516

F-MAMMA1000522//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//0.0015:113:32//HOMO SAPIENS (HUMAN)//P08547

10 F-MAMMA1000524//HYPOTHETICAL HOST RANGE 8.5 KD PROTEIN//1.0:63:31//VACCINIA VIRUS (STRAIN WR)//P17359

F-MAMMA1000559//METALLOTHIONEIN-I (MT-I) (MT-IB/MT-IA)//0.31:16:50//CALLINECTES SAPIDUS (BLUE CRAB)//P55949

F-MAMMA1000565//FERREDOXIN-TYPE PROTEIN NAPF//0.98:37:35//ESCHERICHIA COLI//P33939

15 F-MAMMA1000567//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/5.5e-37:95:76//HOMO SAPIENS (HUMAN)//P39195

F-MAMMA1000576//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/4.1e-07:34:64//HOMO SAPIENS (HUMAN)//P39191

F-MAMMA1000583

20 F-MAMMA1000585//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.5e-28:89:75//HOMO SAPIENS (HUMAN)//P39194

F-MAMMA1000594//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/4.8e-24:38:71//HOMO SAPIENS (HUMAN)//P39195

F-MAMMA1000597//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.1e-25:74:77//HOMO SAPIENS (HUMAN)//P39195

25 F-MAMMA1000605//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.1e-18:83:50//HOMO SAPIENS (HUMAN)//P39195

F-MAMMA1000612//HYPOTHETICAL 34.0 KD TRP-ASP REPEATS CONTAINING PROTEIN IN SIS1-MRPL2 INTERGENIC REGION//4.0e-42:166:48//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P41318

30 F-MAMMA1000616

F-MAMMA1000621

F-MAMMA1000623//METALLOTHIONEIN-IK (MT-1K)//0.0045:25:48//HOMO SAPIENS (HUMAN)//P80296

F-MAMMA1000625//PROLINE-RICH PROTEIN MP-3 (FRAGMENT)//0.00078:79:35//MUS MUSCULUS (MOUSE)//P05143

35 F-MAMMA1000643//HYPOTHETICAL 9.3 KD PROTEIN//1.0:25:28//MAGUARI VIRUS//P16607

F-MAMMA1000664

F-MAMMA1000669//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//4.2e-05:186:30//HOMO SAPIENS (HUMAN)//P08547

F-MAMMA1000670//PROLINE-RICH PROTEIN MP-3 (FRAGMENT)//1.6e-06:195:30//MUS MUSCULUS (MOUSE)//P05143

40 F-MAMMA1000672//VITELLOGENIC CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.-)//3.8e-28:184:35//AEDES AEGYPTI (YELLOWFEVER MOSQUITO)//P42660

F-MAMMA1000684//DNA-BINDING PROTEIN (VMW21)//1.1e-07:55:56//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)//P04487

45 F-MAMMA1000696//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.2e-31:97:74//HOMO SAPIENS (HUMAN)//P39194

F-MAMMA1000707//METALLOTHIONEIN-II (MT-II) (MT-IIB/MT-IIA)//0.31:19:42//CALLINECTES SAPIDUS (BLUE CRAB)//P55950

F-MAMMA1000713//XYLULOSE KINASE (EC 2.7.1.17) (XYLULOKINASE)//1.6e-05:88:35//LACTOBACILLUS PENTOSUS//P21939

50 F-MAMMA1000714//PROTEIN-LYSINE 6-OXIDASE PRECURSOR (EC 1.4.3.13) (LYSYL OXIDASE)//0.44:126:30//RATTUS NORVEGICUS (RAT)//P16636

F-MAMMA1000718//METALLOTHIONEIN-IIIE (MT-2E)//1.0:51:31//ORYCTOLAGUS CUNICULUS (RABBIT)//P80292

55 F-MAMMA1000720//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/3.3e-28:60:71//HOMO SAPIENS (HUMAN)//P39194

F-MAMMA1000723//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//0.0015:113:32//HOMO SAPIENS (HUMAN)//P08547

F-MAMMA1000731//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)//1.8e-43:258:43//HOMO SAPIENS (HUMAN)//O14647

F-MAMMA1000732//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/9.9e-12:76:55//HOMO SAPIENS (HUMAN)//P39188

5 F-MAMMA1000733

F-MAMMA1000734//NPL1 PROTEIN (SEC63 PROTEIN)//2.5e-18:181:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P14906

F-MAMMA1000738//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I//5.4e-52:196:58//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//P87115

10 F-MAMMA1000744//!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!!/6.3e-36:144:47//HOMO SAPIENS (HUMAN)//P39190

F-MAMMA1000746

F-MAMMA1000752

15 F-MAMMA1000760//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/6.6e-29:75:72//HOMO SAPIENS (HUMAN)//P39195

F-MAMMA1000761//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.6e-09:59:64//HOMO SAPIENS (HUMAN)//P39194

F-MAMMA1000775

20 F-MAMMA1000776//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/3.3e-35:99:74//HOMO SAPIENS (HUMAN)//P39193

F-MAMMA1000778//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.1e-19:65:70//HOMO SAPIENS (HUMAN)//P39195

F-MAMMA1000782

25 F-MAMMA1000798//HYPOTHETICAL PROTEIN ORF-1137//0.015:59:37//MUS MUSCULUS (MOUSE)//P11260

F-MAMMA1000802//MYOSIN IC HEAVY CHAIN//0.35:94:41//ACANTHAMOEBA CASTELLANII (AMOEBA)//P10569

F-MAMMA1000824//ACTIN 1//0.046:60:31//ZEA MAYS (MAIZE)//P02582

30 F-MAMMA1000831//PROBABLE NI/FE-HYDROGENASE 1 B-TYPE CYTOCHROME SUBUNIT//1.0:30:46//ESCHERICHIA COLI//P19929

F-MAMMA1000839//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.1e-28:80:58//HOMO SAPIENS (HUMAN)//P39188

F-MAMMA1000841//PUTATIVE AMIDASE (EC 3.5.1.4)//1.5e-39:130:36//METHANOBACTERIUM THERMOAUTOTROPHICUM//O27540

35 F-MAMMA1000842//C-HORDEIN (CLONE PC-919) (FRAGMENT)//0.064:43:41//HORDEUM VULGARE (BARLEY)//P17992

F-MAMMA1000843

F-MAMMA1000845//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 (EC 1.6.5.3)//0.43:58:34//DROSOPHILA YAKUBA (FRUIT FLY)//P03895

40 F-MAMMA1000851//CUTICLE COLLAGEN 34//0.019:107:29//CAENORHABDITIS ELEGANS//P34687

F-MAMMA1000855//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66)//0.00098:149:32//HOMO SAPIENS (HUMAN)//Q15428

F-MAMMA1000856//METALLOTHIONEIN (MT)//0.63:39:41//POTAMON POTAMIOS//P55952

45 F-MAMMA1000859//GLYCOPROTEIN X PRECURSOR//0.014:192:28//EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1)//P28968

F-MAMMA1000862//DISINTEGRIN KISTRIN (PLATELET AGGREGATION ACTIVATION INHIBITOR)//1.0:66:27//AGKISTRODON RHODOSTOMA (MALAYAN PIT VIPER) (CALLOSELASMA RHODOSTOMA)//P17494

F-MAMMA1000863//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/5.4e-16:41:68//HOMO SAPIENS (HUMAN)//P39188

50 F-MAMMA1000865//SALIVARY PROUNE-RICH PROTEIN II-1 (FRAGMENT)//0.030:100:32//HOMO SAPIENS (HUMAN)//P81489

F-MAMMA1000867//APTOTOXIN IX (PARALYTIC PEPTIDE IX) (PP IX)//0.98:43:32//APTOSTICHUS SCHLINGERI (TRAP-DOOR SPIDER)//P49272

F-MAMMA1000875//PROLINE-RICH PEPTIDE P-B//0.18:21:47//HOMO SAPIENS (HUMAN)//P02814

55 F-MAMMA1000876//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.5e-22:85:71//HOMO SAPIENS (HUMAN)//P39188

F-MAMMA1000877//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.5e-22:85:71//HOMO SAPIENS (HUMAN)//P39188

MAMMA1001073/HEPATOCYTE NECROSIS FACTOR WORKHEAVY DOMAINS
US NORVEGICUS (RAT) //Q63244

- F-MAMMA1001074//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//0.00067:163:32//HOMO SAPIENS (HUMAN)//P08547
- F-MAMMA1001075//RETINOBLASTOMA BINDING PROTEIN 1 (RBBP-1)//0.53:72:34//HOMO SAPIENS (HUMAN)//P29374
- 5 F-MAMMA1001078//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//5.0e-79:184:73//HOMO SAPIENS (HUMAN)//P08547
- F-MAMMA1001080//IG HEAVY CHAIN PRECURSOR V-III REGION (VH26)//1.7e-27:82:71//HOMO SAPIENS (HUMAN)//P01764
- F-MAMMA1001082
- 10 F-MAMMA1001091//HYPOTHETICAL BHLF1 PROTEIN//3.1e-05:198:32//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4)//P03181
- F-MAMMA1001092//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//7.1e-21:65:72//HOMO SAPIENS (HUMAN)//P08547
- F-MAMMA1001105//OVO PROTEIN (SHAVEN BABY PROTEIN)//1.0e-18:68:48//DROSOPHILA MELANOGASTER (FRUIT FLY)//P51521
- 15 F-MAMMA1001110//PROCOLLAGEN ALPHA 1(IV) CHAIN PRECURSOR//0.080:108:37//MUS MUSCULUS (MOUSE)//P02463
- F-MAMMA1001126/////ALU SUBFAMILY SB WARNING ENTRY /////2.3e-07:66:45//HOMO SAPIENS (HUMAN)//P39189
- 20 F-MAMMA1001133//HYPOTHETICAL 13.2 KD PROTEIN IN RPS4A-BAT2 INTERGENIC REGION//0.96:43:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P47174
- F-MAMMA1001139//HYPOTHETICAL 36.7 KD PROTEIN AH6.2 IN CHROMOSOME II//5.4e-42:81:62//CAENORHABDITIS ELEGANS//Q09201
- F-MAMMA1001143/////ALU SUBFAMILY J WARNING ENTRY /////0.00014:36:66//HOMO SAPIENS (HUMAN)//P39188
- 25 F-MAMMA1001145
- F-MAMMA1001154//CSBA PROTEIN//1.0:39:38//BACILLUS SUBTILIS//P37953
- F-MAMMA1001161/////ALU SUBFAMILY J WARNING ENTRY /////5.2e-23:53:64//HOMO SAPIENS (HUMAN)//P39188
- 30 F-MAMMA1001162//CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27)//0.69:86:31//MUS MUSCULUS (MOUSE)//P41272
- F-MAMMA1001181//HYPOTHETICAL 81.0 KD PROTEIN C35D10.4 IN CHROMOSOME III//0.00010:74:47//CAENORHABDITIS ELEGANS//Q18486
- F-MAMMA1001186/////ALU SUBFAMILY SQ WARNING ENTRY /////9.0e-32:44:86//HOMO SAPIENS (HUMAN)//P39194
- 35 F-MAMMA1001191//OCTAMER-BINDING TRANSCRIPTION FACTOR 1 (OTF-1) (NF-A1) (FRAGMENT)//0.096:40:40//MACROPUS EUGENII (TAMMAR WALLABY)//Q28466
- F-MAMMA1001198//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN)//2.5e-75:204:70//HOMO SAPIENS (HUMAN)//P42566
- 40 F-MAMMA1001202//METALLOTHIONEIN-II (MT-II) (MT-IIB/MT-IIA)//0.52:46:32//CALLINECTES SAPIDUS (BLUE CRAB)//P55950
- F-MAMMA1001203/////ALU SUBFAMILY SC WARNING ENTRY /////7.3e-11:82:58//HOMO SAPIENS (HUMAN)//P39192
- F-MAMMA1001206/////ALU SUBFAMILY J WARNING ENTRY /////1.9e-17:67:71//HOMO SAPIENS (HUMAN)//P39188
- 45 F-MAMMA1001215//9 KD PROTEIN//1.0:51:33//HOMO SAPIENS (HUMAN)//P13994
- F-MAMMA1001220/////ALU SUBFAMILY SB WARNING ENTRY /////3.4e-37:55:87//HOMO SAPIENS (HUMAN)//P39189
- F-MAMMA1001222//HYPOTHETICAL 73.6 KD PROTEIN CY49.21//3.7e-06:168:38//MYCOBACTERIUM TUBERCULOSIS//Q10690
- 50 F-MAMMA1001243
- F-MAMMA1001244//TRP OPERON LEADER PEPTIDE//1.0:18:55//SERRATIA MARCESCENS//P03055
- F-MAMMA1001249//HYPOTHETICAL 7.2 KD PROTEIN IN RPS2 3'REGION (ORF57)//0.57:23:34//ASTASIA LONGA (EUGLENOPHYCEAN ALGA)//P34774
- 55 F-MAMMA1001256/////ALU SUBFAMILY J WARNING ENTRY /////2.3e-07:79:44//HOMO SAPIENS (HUMAN)//P39188
- F-MAMMA1001259//HYPOTHETICAL 13.2 KD PROTEIN IN RPS4A-BAT2 INTERGENIC REGION//0.96:43:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P47174

F-MAMMA1001260//MYOSIN HEAVY CHAIN, PERINATAL SKELETAL MUSCLE //2.7e-05:219:27//HOMO SAPIENS (HUMAN)//P13535

F-MAMMA1001268//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG //9.7e-27:89:67//HOMO SAPIENS (HUMAN)//P08547

5 F-MAMMA1001271//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN) //4.0e-06:126:38//HOMO SAPIENS (HUMAN)//P54259

F-MAMMA1001274/////ALU SUBFAMILY SQ WARNING ENTRY /////7.4e-29:57:66//HOMO SAPIENS (HUMAN)//P39194

10 F-MAMMA1001280//BACTERIOCIN MICROCIN B17 PRECURSOR (MCB17) //0.27:24:54//ESCHERICHIA COLI//P05834

F-MAMMA1001292//HYPOTHETICAL PROTEIN KIAA0176 (FRAGMENT) //1.3e-73:208:69//HOMO SAPIENS (HUMAN)//Q14681

F-MAMMA1001296/////ALU SUBFAMILY SP WARNING ENTRY /////6.9e-22:41:80//HOMO SAPIENS (HUMAN)//P39193

15 F-MAMMA1001298//HYPOTHETICAL PROTEIN HI0371 //0.99:29:37//HAEMOPHILUS INFLUENZAE//P44668

F-MAMMA1001305//GTPASE-ACTIVATING PROTEIN RHOGAP (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP) //9.9e-62:222:54//HOMO SAPIENS (HUMAN)//Q07960

20 F-MAMMA1001322//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD) //2.1e-09:46:60//HOMO SAPIENS (HUMAN)//P20931

F-MAMMA1001324//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)] //2.5e-43:128:50//FRIEND MURINE LEUKEMIA VIRUS (ISOLATE PVC-211) (F-MULV) //P26808

25 F-MAMMA1001330//HEMOGLOBIN ZETA CHAIN (FRAGMENTS) //0.30:51:37//MACROPUS EUGENII (TAMMAR WALLABY) //P81044

F-MAMMA1001341//TRISTETRAPROLINE (TTP) (TIS11A) (TIS11) (ZFP-36) (GROWTH FACTOR-INDUCIBLE NUCLEAR PROTEIN NUP475) //0.024:89:39//HOMO SAPIENS (HUMAN)//P26651

F-MAMMA1001343//PROBABLE E5 PROTEIN //0.60:64:29//HUMAN PAPILLOMAVIRUS TYPE 16 //P06927

30 F-MAMMA1001346//PROTEINASE INHIBITOR IIB (FRAGMENTS) //0.97:33:45//SOLANUM TUBEROSUM (POTATO) //P01082

F-MAMMA1001383/////ALU SUBFAMILY SQ WARNING ENTRY /////1.2e-30:86:77//HOMO SAPIENS (HUMAN)//P39194

F-MAMMA1001388//LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG) //9.2e-91:195:92//HOMO SAPIENS (HUMAN)//P02750

35 F-MAMMA1001397/////ALU SUBFAMILY J WARNING ENTRY /////3.5e-19:55:69//HOMO SAPIENS (HUMAN) //P39188

F-MAMMA1001408//SALIVARY GLUE PROTEIN SGS-7 PRECURSOR //0.60:45:35//DROSOPHILA MELANOGASTER (FRUIT FLY) //P02841

40 F-MAMMA1001411//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE) //5.8e-06:153:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P08640

F-MAMMA1001419/////ALU SUBFAMILY SQ WARNING ENTRY /////2.3e-16:99:51//HOMO SAPIENS (HUMAN) //P39194

45 F-MAMMA1001420/////ALU SUBFAMILY SB1 WARNING ENTRY /////0.0018:23:65//HOMO SAPIENS (HUMAN) //P39190

F-MAMMA1001435/////ALU SUBFAMILY SX WARNING ENTRY /////1.7e-22:60:58//HOMO SAPIENS (HUMAN) //P39195

F-MAMMA1001442

50 F-MAMMA1001446/////ALU SUBFAMILY SQ WARNING ENTRY /////1.2e-23:48:75//HOMO SAPIENS (HUMAN) //P39194

F-MAMMA1001452//GENE 35 PROTEIN (GP35) //0.61:31:45//MYCOBACTERIOPHAGE L5 //Q05245

F-MAMMA1001465//HYPOTHETICAL PROTEIN E-115 //0.0026:68:38//HUMAN ADENOVIRUS TYPE 2 //P03290

55 F-MAMMA1001476//URIDINE KINASE (EC 2.7.1.48) (URIDINE MONOPHOSPHOKINASE) (FRAGMENT) //3.7e-94:201:92//MUS MUSCULUS (MOUSE) //P52623

F-MAMMA1001477//ANG (SLOW) (RIS) //P08548

F-MAMMA1001501//CALPAIN 1, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEU-

TRAL PROTEINASE) (CANP) (MU-TYPE).//6.2e-59:86:97//HOMO SAPIENS (HUMAN).//P07384
 F-MAMMA1001502//HYPOTHETICAL 11.4 KD PROTEIN (ORF1).//0.21:79:30//STREPTOMYCES FRADIAE.//
 P26800
 F-MAMMA1001510
 5 F-MAMMA1001522//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.67:98:31//STREPTO-
 MYCES FRADIAE.//P20186
 F-MAMMA1001547//PROBABLE MOLYBDENUM-PTERIN BINDING PROTEIN.//0.97:35:42//HAEMOPHILUS
 INFLUENZAE.//P45183
 F-MAMMA1001551//HYPOTHETICAL PROTEIN MJ0458.1.//0.038:31:41//METHANOCOCCUS JANNASCHII.//
 10 P81308
 F-MAMMA1001575
 F-MAMMA1001576//TUBULIN GAMMA CHAIN.//1.6e-86:162:99//XENOPUS LAEVIS (AFRICAN CLAWED
 FROG).//P23330
 F-MAMMA1001590/////ALU SUBFAMILY SX WARNING ENTRY /////0.0035:38:55//HOMO SAPIENS (HUMAN).//
 15 P39195
 F-MAMMA1001600//CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR.//0.85:53:33//HOMO SAPIENS
 (HUMAN).//P29279
 F-MAMMA1001604//HYPOTHETICAL 11.1 KD PROTEIN C30D11.02C IN CHROMOSOME I.//0.14:82:29//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09902
 20 F-MAMMA1001606//HIGH MOBILITY GROUP PROTEIN HMGI-C.//8.2e-05:77:37//HOMO SAPIENS (HUMAN).//
 P52926
 F-MAMMA1001620/////ALU SUBFAMILY SX WARNING ENTRY /////5.5e-05:24:66//HOMO SAPIENS (HU-
 MAN).//P39195
 F-MAMMA1001627//CUTICLE COLLAGEN 40.//0.82:131:31//CAENORHABDITIS ELEGANS.//P34804
 25 F-MAMMA1001630/////ALU SUBFAMILY SQ WARNING ENTRY /////8.6e-26:57:78//HOMO SAPIENS (HU-
 MAN).//P39194
 F-MAMMA1001633//ZINC FINGER PROTEIN 165.//6.9e-38:160:55//HOMO SAPIENS (HUMAN).//P49910
 F-MAMMA1001635
 F-MAMMA1001649//SPERM PROTAMINE P1.//0.39:31:41//TACHYGLOSSUS ACULEATUS ACULEATUS (AUS-
 30 TRALIAN ECHIDNA).//P35311
 F-MAMMA1001654//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE- PRO-
 TEIN KINASE 1).//5.6e-06:99:28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P18160
 F-MAMMA1001663//VERY HYPOTHETICAL XYLU PROTEIN.//0.99:27:37//ESCHERICHIA COLI.//P05056
 F-MAMMA1001670//CUTICLE COLLAGEN 1.//0.033:97:37//CAENORHABDITIS ELEGANS.//P08124
 35 F-MAMMA1001671
 F-MAMMA1001679//PROCOLLAGEN ALPHA 2(IV) CHAIN PRECURSOR.//0.92:32:50//HOMO SAPIENS (HU-
 MAN).//P08572
 F-MAMMA1001683//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.00026:147:34//STREP-
 TOMYCES FRADIAE.//P20186
 40 F-MAMMA1001686
 F-MAMMA1001692//SMALL HYDROPHOBIC PROTEIN (SMALL PROTEIN 1A).//1.0:34:26//BOVINE RESPIRA-
 TORY SYNCYTIAL VIRUS (STRAIN A51908) (BRS).//P24616
 F-MAMMA1001711/////ALU SUBFAMILY SQ WARNING ENTRY /////1.1e-28:56:69//HOMO SAPIENS (HU-
 MAN).//P39194
 45 F-MAMMA1001715/////ALU SUBFAMILY J WARNING ENTRY /////1.6e-08:39:71//HOMO SAPIENS (HUMAN).//
 P39188
 F-MAMMA1001730//METALLOTHIONEIN-B (MTB).//1.0:17:64//STRONGYLOCENTROTUS PURPURATUS
 (PURPLE SEA URCHIN).//Q27287
 F-MAMMA1001735//TUBULIN BETA-5 CHAIN (CLASS-V).//5.1e-121:213:97//GALLUS GALLUS (CHICKEN).//
 50 P09653
 F-MAMMA1001740
 F-MAMMA1001743/////ALU SUBFAMILY SX WARNING ENTRY /////1.3e-09:100:42//HOMO SAPIENS (HU-
 MAN).//P39195
 F-MAMMA1001744//POU DOMAIN PROTEIN 2.//0.97:59:38//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA
 55 DANIO).//Q90270
 F-MAMMA1001751//TWK-8 PROTEIN.//2.9e-15 77:36//CAENORHABDITIS ELEGANS.//P34410

F-MAMMA1001754//MALE SPECIFIC SPERM PROTEIN MST84DD//0.019:20:45//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q01645
 F-MAMMA1001757//HYPOTHETICAL 9.2 KD PROTEIN IN RNPA 3'REGION//0.94:30:43//PSEUDOMONAS PUTIDA//P25753
 5 F-MAMMA1001760//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/4.6e-34:103:59//HOMO SAPIENS (HUMAN)//P39191
 F-MAMMA1001764
 F-MAMMA1001768//HYPOTHETICAL PROTEIN UL61//0.042:167:33//HUMAN CYTOMEGALOVIRUS (STRAIN AD169)//P16818
 10 F-MAMMA1001769//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.0e-29:97:69//HOMO SAPIENS (HUMAN)//P39194
 F-MAMMA1001771//TRANSMEMBRANE PROTEIN SEX PRECURSOR//3.3e-09:123:32//HOMO SAPIENS (HUMAN)//P51805
 F-MAMMA1001783//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.1e-09:55:61//HOMO SAPIENS (HUMAN)//P39188
 15 F-MAMMA1001785//RAS-RELATED PROTEIN RABC//1.9e-06:120:25//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD)//P34143
 F-MAMMA1001788//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//9.3e-29:46:76//HOMO SAPIENS (HUMAN)//P08547
 20 F-MAMMA1001790//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.7e-24:69:69//HOMO SAPIENS (HUMAN)//P39188
 F-MAMMA1001806//HYPOTHETICAL 21.2 KD PROTEIN IN TOR2-MNN4 INTERGENIC REGION//0.95:58:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P36042
 F-MAMMA1001812//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/8.8e-12:53:69//HOMO SAPIENS (HUMAN)//P39195
 25 F-MAMMA1001815//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//0.11:30:70//HOMO SAPIENS (HUMAN)//P08547
 F-MAMMA1001817//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.9e-16:86:55//HOMO SAPIENS (HUMAN)//P39188
 30 F-MAMMA1001818
 F-MAMMA1001820//VITTELLINE MEMBRANE PROTEIN VM26AB PRECURSOR (PROTEIN TU-4) (PROTEIN SV23)//0.0030:63:42//DROSOPHILA MELANOGASTER (FRUIT FLY)//P13238
 F-MAMMA1001824//APTOTOXIN VII (PARALYTIC PEPTIDE VII) (PP VII)//0.99:26:34//APTOSTICHUS SCHLINGERI (TRAP-DOOR SPIDER)//P49271
 35 F-MAMMA1001836//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.6e-35:77:88//HOMO SAPIENS (HUMAN)//P39195
 F-MAMMA1001837//ZINC FINGER PROTEIN 191//1.3e-27:106:58//HOMO SAPIENS (HUMAN)//O14754
 F-MAMMA1001848//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.0e-19:92:58//HOMO SAPIENS (HUMAN)//P39188
 40 F-MAMMA1001851
 F-MAMMA1001854
 F-MAMMA1001858//ISOTOCIN-NEUROPHYSIN IT1 PRECURSOR//0.93:42:38//CATOSTOMUS COMMERSONI (WHITE SUCKER)//P15210
 F-MAMMA1001864//PROBABLE ABC TRANSPORTER PERMEASE PROTEIN MG189//0.77:161:27//MYCOPLASMA GENITALIUM//P47435
 45 F-MAMMA1001868//FK506-BINDING NUCLEAR PROTEIN (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PPIASE) (EC 5.2.1.8) (PROLINE ROTAMASE) (NUCLEOLAR PROLINE ISOMERASE) (FKBP-70)//0.00013:219:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38911
 F-MAMMA1001874//SPERM HISTONE P2 PRECURSOR (PROTAMINE MP2)//0.0075:76:31//MUS MUSCULUS (MOUSE)//P07978
 50 F-MAMMA1001878//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1) (FRAGMENT)//0.020:10:80//LYCOPERSICON ESCULENTUM (TOMATO)//Q01157
 F-MAMMA1001880
 F-MAMMA1001890//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/5.1e-34:56:83//HOMO SAPIENS (HUMAN)//P39192
 55 F-MAMMA1001908//HYPOTHETICAL 16.2 KD PROTEIN IN PRP24-RRN9 INTERGENIC REGION//0.00013:77

37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q03525

F-MAMMA1001931//HYPOTHETICAL 118.2 KD PROTEIN F43C1.1 IN CHROMOSOME III//0.41:106:29//
CAENORHABDITIS ELEGANS//Q09564

F-MAMMA1001956//OCTAPEPTIDE-REPEAT PROTEIN T2//0.00053:149:30//MUS MUSCULUS (MOUSE)//
Q06666

F-MAMMA1001963//HYPOTHETICAL PROTEIN IN NAC 5'REGION (ORF X) (FRAGMENT)//1.0:46:28//KLEBSIELLA AEROGENES//Q08600

F-MAMMA1001969//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//1.7e-34:97:68//HOMO SAPIENS (HUMAN)//P08547

F-MAMMA1001970//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//6.2e-07:67:37//HOMO SAPIENS (HUMAN)//P08547

F-MAMMA1001992//PROTEIN Q300//0.53:14:71//MUS MUSCULUS (MOUSE)//Q02722

F-MAMMA1002009//PROBABLE E5 PROTEIN//0.17:56:32//HUMAN PAPILLOMAVIRUS TYPE 31//P17385

F-MAMMA1002011//MYRISTOYLATED ALANINE-RICH C-KINASE SUBSTRATE (MARCKS) (PROTEIN KINASE C SUBSTRATE, 80 KD PROTEIN, LIGHT CHAIN) (PKCSL) (80K-L PROTEIN)//1.0:100:31//HOMO SAPIENS (HUMAN)//P29966

F-MAMMA1002032//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.1e-21:86:65//HOMO SAPIENS (HUMAN)//P39188

F-MAMMA1002033//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/8.5e-20:67:58//HOMO SAPIENS (HUMAN)//P39188

F-MAMMA1002041//MALE SPECIFIC SPERM PROTEIN MST84DC//1.0:17:52//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q01644

F-MAMMA1002042//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/0.19:45:46//HOMO SAPIENS (HUMAN)//P39192

F-MAMMA1002047//TYROSINE AMINOTRANSFERASE (EC 2.6.1.5) (L-TYROSINE:2-OXOGLUTARATE AMINOTRANSFERASE) (TAT)//0.0017:50:46//RATTUS NORVEGICUS (RAT)//P04694

F-MAMMA1002056//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.2e-37:70:77//HOMO SAPIENS (HUMAN)//P39194

F-MAMMA1002058//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.1e-08:26:76//HOMO SAPIENS (HUMAN)//P39188

F-MAMMA1002068//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//2.0e-11:78:46//HOMO SAPIENS (HUMAN)//P08547

F-MAMMA1002078//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//0.96:26:46//COTURNIX JAPONICA (JAPANESE QUAIL)//P50682

F-MAMMA1002082//SUPPRESSOR PROTEIN SRP40//0.23:95:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32583

F-MAMMA1002084//HYPOTHETICAL 7.5 KD PROTEIN//1.0:40:35//VACCINIA VIRUS (STRAIN COPENHAGEN)//P20520

F-MAMMA1002093

F-MAMMA1002108//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556//0.00079:143:33//STREPTOMYCES FRADIAE//P20186

F-MAMMA1002118//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//1.0:43:34//METRIDIDIUM SENILE (BROWN SEA ANEMONE) (FRILLED SEA ANEMONE)//O47493

F-MAMMA1002125//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.9e-14:60:68//HOMO SAPIENS (HUMAN)//P39192

F-MAMMA1002132

F-MAMMA1002140//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.4e-24:69:65//HOMO SAPIENS (HUMAN)//P39188

F-MAMMA1002143//SERUM PROTEIN MSE55//2.1e-16:166:43//HOMO SAPIENS (HUMAN)//Q00587

F-MAMMA1002145//36.4 KD PROLINE-RICH PROTEIN//0.00014:84:29//LYCOPERSICON ESCULENTUM (TOMATO)//Q00451

F-MAMMA1002153

F-MAMMA1002155

F-MAMMA1002156//METALLOPROTEINASE INHIBITOR PRECURSOR//0.90:58:34//STREPTOMYCES NIGRESCENS//P01077

F-MAMMA1002170

F-MAMMA1002170//40S RIBOSOMAL PROTEIN L16//0.00014:84:29//HOMO SAPIENS (HUMAN)//P15880

F-MAMMA1002174//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/6.5e-25:56:64//HOMO SAPIENS (HUMAN)//P39188

F-MAMMA1002198//THIOREDOXIN PEROXIDASE 1 (THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE 1) (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) (TSA) (PRP) (NATURAL KILLER CELL ENHANCING FACTOR B) (NKEF-B)//9.0e-09:28:100//HOMO SAPIENS (HUMAN)//P32119

5 F-MAMMA1002209//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130)//0.0023:132:33//HOMO SAPIENS (HUMAN)//O00268

F-MAMMA1002215//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR//0.00032:68:35//HOMO SAPIENS (HUMAN)//P02452

10 F-MAMMA1002219//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1//0.0079:224:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P25386

F-MAMMA1002230

F-MAMMA1002236//TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR)//1.4e-118:151:94//RATTUS NORVEGICUS (RAT)//P70541

15 F-MAMMA1002243//WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP)//0.028:112:33//MUS MUSCULUS (MOUSE)//P70315

F-MAMMA1002250//T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11)//0.0012:80:32//ORYCTOLAGUS CUNICULUS (RABBIT)//P06333

F-MAMMA1002267//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6)//0.17:139:28//TRYPANOSOMA BRUCEI BRUCEI//P24499

20 F-MAMMA1002268//60S RIBOSOMAL PROTEIN L22//0.00026:163:30//DROSOPHILA MELANOGASTER (FRUIT FLY)//P50887

F-MAMMA1002269//HISTIDINE-RICH, METAL BINDING POLYPEPTIDE//0.35:14:57//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI)//Q48251

25 F-MAMMA1002282//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/6.1e-05:32:65//HOMO SAPIENS (HUMAN)//P39192

F-MAMMA1002292//TROPOMYOSIN 2//1.4e-05:100:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40414

F-MAMMA1002293//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/6.8e-25:127:44//HOMO SAPIENS (HUMAN)//P39188

30 F-MAMMA1002294//ALPHA TRANS-INDUCING PROTEIN (ALPHA-TIF)//0.00011:138:38//BOVINE HERPESVIRUS TYPE 1 (STRAIN P8-2)//P30020

F-MAMMA1002297//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR//0.15:144:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32323

35 F-MAMMA1002298//PROLINE-RICH PROTEIN MP-3 (FRAGMENT)//1.0e-05:40:50//MUS MUSCULUS (MOUSE)//P05143

F-MAMMA1002299//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3)//0.84:65:32//STRUTHIO CAMELUS (OSTRICH)//O21405

F-MAMMA1002308//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.3e-29:61:73//HOMO SAPIENS (HUMAN)//P39188

40 F-MAMMA1002310//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS)//0.00016:70:38//MUS MUSCULUS (MOUSE)//P15265

F-MAMMA1002311//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/9.4e-09:84:54//HOMO SAPIENS (HUMAN)//P39189

45 F-MAMMA1002312//HYPOTHETICAL 10.8 KD PROTEIN IN GP30-RIII INTERGENIC REGION (URF Y)//0.48:48:33//BACTERIOPHAGE T4//P33084

F-MAMMA1002317

F-MAMMA1002319//RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE]//0.011:128:27//MUS MUSCULUS (MOUSE)//P11369

50 F-MAMMA1002322//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/5.2e-20:92:57//HOMO SAPIENS (HUMAN)//P39195

F-MAMMA1002329//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//0.051:33:36//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P03931

F-MAMMA1002332//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//6.5e-20:116:51//HOMO SAPIENS (HUMAN)//P08547

55 F-MAMMA1002333//COPPER-METALLOTHIONEIN (CU-MT)//0.59:42:38//HELIX POMATIA (ROMAN SNAIL)

(EDIBLE SNAIL).//P55947

F-MAMMA1002347//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.43:26:61//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1002351//HYPOTHETICAL PROTEIN MJ0304.//2.3e-07:139:25//METHANOCOCCUS JANNAS-CHII.//Q57752

F-MAMMA1002352

F-MAMMA1002353//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.00028:31:80//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1002355//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/4.2e-28:87:73//HOMO SAPIENS (HUMAN).//P39193

F-MAMMA1002356//RELAXIN.//0.95:31:35//SQUALUS ACANTHIAS (SPINY DOGFISH).//P11953

F-MAMMA1002359//CHLOROPLAST 50S RIBOSOMAL PROTEIN L33.//0.93:44:36//GUILLARDIA THETA (CRYPTOMONAS PHI).//O78487

F-MAMMA1002360//LATE L2 MU CORE PROTEIN PRECURSOR (PROTEIN X).//0.94:30:43//BOVINE ADENOVIRUS TYPE 2 (MASTADENOVIRUS BOS2).//Q96626

F-MAMMA1002361//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.0e-08:45:68//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1002362//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.58:23:26//LUMBRICUS TERRESTRIS (COMMON EARTHWORM).//Q34942

F-MAMMA1002380//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.23:100:27//DROSOPHILA SIMULANS (FRUIT FLY).//P13729

F-MAMMA1002384

F-MAMMA1002385//HYPOTHETICAL 40.9 KD PROTEIN IN ORC2-TIP1 INTERGENIC REGION.//3.8e-14:125:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38241

F-MAMMA1002392//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:17:58//BRANCHIOSTOMALANCEOLATUM (COMMON LANCELET) (AMPHIOXUS).//O21003

F-MAMMA1002411//30S RIBOSOMAL PROTEIN S17.//0.85:49:32//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//P73311

F-MAMMA1002413//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3) (FRAGMENT).//0.97:41:39//DROSOPHILA AFFINIS (FRUIT FLY).//P51926

F-MAMMA1002417//RFBJ PROTEIN.//0.99:31:35//SHIGELLA FLEXNERI.//P37786

F-MAMMA1002427//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.6e-33:135:59//HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1002428//HYPOTHETICAL PROTEIN C18.//0.97:34:44//SWINEPOX VIRUS (STRAIN KASZA) (SPV).//P32217

F-MAMMA1002434//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/3.1e-36:56:78//HOMO SAPIENS (HUMAN).//P39189

F-MAMMA1002446

F-MAMMA1002454//EARLY NODULIN 20 PRECURSOR (N-20).//0.77:57:45//MEDICAGO TRUNCATULA (BARREL MEDIC).//P93329

F-MAMMA1002461//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP).//1.3e-05:193:32//CANIS FAMILIARIS (DOG).//P50551

F-MAMMA1002470//HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION.//1.0e-75:231:60//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38795

F-MAMMA1002475//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L4 (SNF2-BETA) (BRG-1 PROTEIN) (MITOTIC GROWTH AND TRANSCRIPTION ACTIVATOR) (BRAHMA PROTEIN HOMOLOG 1).//0.013:99:30//HOMO SAPIENS (HUMAN).//P51532

F-MAMMA1002480//NONSTRUCTURAL PROTEIN 5B.//1.0:23:43//HUMAN CORONAVIRUS (STRAIN 229E).//P19741

F-MAMMA1002485//STANNIOCALCIN PRECURSOR.//2.1e-23:88:46//HOMO SAPIENS (HUMAN).//P52823

F-MAMMA1002494//MOLT-INHIBITING HORMONE (MIH).//1.0:32:37//PROCAMBARUS CLARKII (RED SWAMP CRAYFISH).//P55848

F-MAMMA1002498//6.7 KD PROTEIN (ORF 5).//1.0:26:42//BARLEY YELLOW DWARF VIRUS (ISOLATE PAV) (BYDV).//P09517

F-MAMMA1002524//HYPOTHETICAL 117.8 KD PROTEIN IN STE2-ERS2 INTERGENIC REGION.//5.0e-28:707:100//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38795

F-MAMMA1002530//CYTOSOLIC PHOSPHOLIPASE A₂ (EC 3.1.1.42) (PHOSPHATIDYLCHOLINE ACYLHYDROLASE).//LYSOPHOSPHOLIPASE (EC 3.1.1.5).//4.5e-12:88:44//HOMO SAPIENS (HUMAN).//P51532

P47712

F-MAMMA1002545/////ALU SUBFAMILY SX WARNING ENTRY !!!!!/4.3e-29:97:71//HOMO SAPIENS (HUMAN)//P39195

F-MAMMA1002554//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT)//0.46:54:40//CRICETULUS GRISEUS (CHINESE HAMSTER)//P11414

F-MAMMA1002556//METALLOTHIONEIN 20-I ISOFORMS A AND B (MT-20-IA AND MT-20-IB)//0.99:21:47//MYTILUS EDULIS (BLUE MUSSEL)//P80251

F-MAMMA1002566//TRANSCRIPTION FACTOR P65 (NUCLEAR FACTOR NF-KAPPA-B P65 SUBUNIT)//0.70:130:30//MUS MUSCULUS (MOUSE)//Q04207

F-MAMMA1002571//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (FRAGMENT)//0.54:45:51//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD)//P35084

F-MAMMA1002573//PARATHYMOSIN//1.5e-07:69:46//HOMO SAPIENS (HUMAN)//P20962

F-MAMMA1002585//MYOSIN LIGHT CHAIN 1, SLOW-TWITCH MUSCLE B/VENTRICULAR ISOFORM (FRAGMENT)//0.38:36:36//MUS MUSCULUS (MOUSE)//P09542

F-MAMMA1002590/////ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.99:22:77//HOMO SAPIENS (HUMAN)//P39195

F-MAMMA1002597/////ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.1e-18:44:70//HOMO SAPIENS (HUMAN)//P39194

F-MAMMA1002598//60S RIBOSOMAL PROTEIN L7//1.8e-16:40:100//HOMO SAPIENS (HUMAN)//P18124

F-MAMMA1002603

F-MAMMA1002612//30S RIBOSOMAL PROTEIN S16 (FRAGMENT)//1.0:29:37//THERMUS AQUATICUS//O07348

F-MAMMA1002617//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT)//0.00041:81:34//RATTUS NORVEGICUS (RAT)//P10164

F-MAMMA1002618//ESCARGOT/SNAIL PROTEIN HOMOLOG (FRAGMENT)//0.11:18:50//PSYCHODA CINE-REA//Q02027

F-MAMMA1002619//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME)//1.8e-13:110:40//CAENORHABDITIS ELEGANS//Q09931

F-MAMMA1002622/////ALU SUBFAMILY J WARNING ENTRY !!!!!/8.4e-05:53:58//HOMO SAPIENS (HUMAN)//P39188

F-MAMMA1002623//PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR (EC 1.14.17.3) (PAM)//2.6e-07:37:78//HOMO SAPIENS (HUMAN)//P19021

F-MAMMA1002625

F-MAMMA1002629/////ALU SUBFAMILY J WARNING ENTRY !!!!!/4.4e-19:49:73//HOMO SAPIENS (HUMAN)//P39188

F-MAMMA1002636//COLLAGEN ALPHA 2(VI) CHAIN (FRAGMENT)//1.7e-07:189:32//HOMO SAPIENS (HUMAN)//P12110

F-MAMMA1002637//KINESIN LIGHT CHAIN (KLC)//7.7e-54:227:52//RATTUS NORVEGICUS (RAT)//P37285

F-MAMMA1002646//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H)//0.034:199:25//MUS MUSCULUS (MOUSE)//P19246

F-MAMMA1002650//TRANSCRIPTION REGULATOR PROTEIN BACH2 (BTB AND CNC HOMOLOG 2)//1.7e-07:104:32//MUS MUSCULUS (MOUSE)//P97303

F-MAMMA1002655//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N)//1.0:25:44//HOMO SAPIENS (HUMAN)//P22532

F-MAMMA1002662

F-MAMMA1002665/////ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.3e-07:54:57//HOMO SAPIENS (HUMAN)//P39194

F-MAMMA1002671//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME)//1.4e-10:144:31//ESCHERICHIA COLI//P27550

F-MAMMA1002673//BREVICAN CORE PROTEIN PRECURSOR//0.76:64:39//BOS TAURUS (BOVINE)//Q28062

F-MAMMA1002684//HYPOTHETICAL 11.8 KD PROTEIN IN GP55-NRDG INTERGENIC REGION//0.094:77:27//BACTERIOPHAGE T4//P07079

F-MAMMA1002685//COLLAGEN ALPHA 1(I) CHAIN FRAGMENTS (K02C17.3) (P00017) (P00018) (P00019) (P00020) (P00021) (P00022) (P00023) (P00024) (P00025) (P00026) (P00027) (P00028) (P00029) (P00030) (P00031) (P00032) (P00033) (P00034) (P00035) (P00036) (P00037) (P00038) (P00039) (P00040) (P00041) (P00042) (P00043) (P00044) (P00045) (P00046) (P00047) (P00048) (P00049) (P00050) (P00051) (P00052) (P00053) (P00054) (P00055) (P00056) (P00057) (P00058) (P00059) (P00060) (P00061) (P00062) (P00063) (P00064) (P00065) (P00066) (P00067) (P00068) (P00069) (P00070) (P00071) (P00072) (P00073) (P00074) (P00075) (P00076) (P00077) (P00078) (P00079) (P00080) (P00081) (P00082) (P00083) (P00084) (P00085) (P00086) (P00087) (P00088) (P00089) (P00090) (P00091) (P00092) (P00093) (P00094) (P00095) (P00096) (P00097) (P00098) (P00099) (P00100) (P00101) (P00102) (P00103) (P00104) (P00105) (P00106) (P00107) (P00108) (P00109) (P00110) (P00111) (P00112) (P00113) (P00114) (P00115) (P00116) (P00117) (P00118) (P00119) (P00120) 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47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P47160
 F-MAMMA1002701//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.0:14:92//HOMO SAPIENS (HUMAN)//
 P39188
 F-MAMMA1002708//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/7.9e-27:52:65//HOMO SAPIENS (HU-
 5 MAN)//P39193
 F-MAMMA1002711//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.7e-24:54:75//HOMO SAPIENS (HUMAN)//
 P39188
 F-MAMMA1002721
 F-MAMMA1002727//SOX-13 PROTEIN (FRAGMENT)//0.70:36:38//MUS MUSCULUS (MOUSE)//Q04891
 10 F-MAMMA1002728//HYPOTHETICAL 6.0 KD PROTEIN//1.0:25:44//THERMOPROTEUS TENAX VIRUS 1
 (STRAIN KRA1) (TTV1)//P19305
 F-MAMMA1002744//HYPOTHETICAL 13.4 KD PROTEIN IN ACT5-YCK1 INTERGENIC REGION//1.0:52:34//
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38834
 F-MAMMA1002746//HYPOTHETICAL 5.6 KD PROTEIN (ORF A-45)//1.0:22:40//SULFOLOBUS VIRUS-LIKE
 15 PARTICLE SSV1//P20198
 F-MAMMA1002748
 F-MAMMA1002754//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/5.1e-21:56:64//HOMO SAPIENS (HUMAN)//
 P39188
 F-MAMMA1002758//MALE SPECIFIC SPERM PROTEIN MST84DD//0.37:14:64//DROSOPHILA MELA-
 20 NOGASTER (FRUIT FLY)//Q01645
 F-MAMMA1002764//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/4.7e-32:79:60//HOMO SAPIENS (HU-
 MAN)//P39194
 F-MAMMA1002765//PARATHYMOSIN//0.79:63:28//BOS TAURUS (BOVINE)//P08814
 F-MAMMA1002769//GAR2 PROTEIN//0.00037:192:27//SCHIZOSACCHAROMYCES POMBE (FISSION
 25 YEAST)//P41891
 F-MAMMA1002775//HYPOTHETICAL 36.7 KD PROTEIN C2F7.14C IN CHROMOSOME I//5.4e-54:240:49//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09704
 F-MAMMA1002780
 F-MAMMA1002782//MARGATOXIN (MGTX)//1.0:31:38//CENTRUROIDES MARGARITATUS (SCORPION)//
 30 P40755
 F-MAMMA1002796//ICE NUCLEATION PROTEIN//0.0018:100:41//PSEUDOMONAS FLUORESCENS//
 P09815
 F-MAMMA1002807//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/9.3e-23:100:59//HOMO SAPIENS (HUMAN)//
 P39188
 35 F-MAMMA1002820//NEUROTOXIN IV (LQX IV)//1.0:18:50//LEIURUS QUINQUESTRIATUS QUINQUESTRIA-
 TUS (EGYPTIAN SCORPION)//P01489
 F-MAMMA1002830//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/4.7e-24:55:74//HOMO SAPIENS (HU-
 MAN)//P39195
 F-MAMMA1002833//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/2.6e-31:95:73//HOMO SAPIENS (HU-
 40 MAN)//P39189
 F-MAMMA1002835//HYPOTHETICAL 42.1 KD PROTEIN F13G3.3 IN CHROMOSOME I//1.0:54:37//
 CAENORHABDITIS ELEGANS//Q19417
 F-MAMMA1002838//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/2.5e-27:99:70//HOMO SAPIENS (HU-
 MAN)//P39193
 45 F-MAMMA1002842//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.3e-13:65:63//HOMO SAPIENS (HU-
 MAN)//P39195
 F-MAMMA1002843//METALLOTHIONEIN-II (MT-II)//0.97:19:47//MUS MUSCULUS (MOUSE)//P02798
 F-MAMMA1002844//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION//4.9e-08:119:36//
 AUTOGRAPHAL CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV)//P41479
 50 F-MAMMA1002858//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//0.98:37:37//PAN TROGLODYTES
 (CHIMPANZEE)//Q35647
 F-MAMMA1002868//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.8e-10:51:62//HOMO SAPIENS (HUMAN)//
 P39188
 F-MAMMA1002869//PINCH PROTEIN (PARTICULARLY INTERESTING NEW CYS-HIS PROTEIN)//1.8e-95:194:
 55 78//HOMO SAPIENS (HUMAN)//P48059
 F-MAMMA1002880//HYPOTHETICAL 10.0 KD PROTEIN//1.0:25:44//THERMOPROTEUS TENAX VIRUS 1
 (STRAIN MAASTRICHT) (TTV1)//P19305
 F-MAMMA1002880

F-MAMMA1002881//GLIOMA PATHOGENESIS-RELATED PROTEIN (RTVP-1 PROTEIN)//3.3e-22:180:35//HOMO SAPIENS (HUMAN)//P48060
 F-MAMMA1002886//MYOSIN HEAVY CHAIN IB (MYOSIN HEAVY CHAIN IL)//0.00011:148:39//ACANTHAMOEBA CASTELLANII (AMOEBA)//P19706
 5 F-MAMMA1002887
 F-MAMMA1002890//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR//0.030:142:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32323
 F-MAMMA1002892
 10 F-MAMMA1002895//HYPOTHETICAL PROTEIN UL61//0.00099:143:35//HUMAN CYTOMEGALOVIRUS (STRAIN AD169)//P16818
 F-MAMMA1002908//T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11)//0.12:44:43//ORYCTOLAGUS CUNICULUS (RABBIT)//P06333
 F-MAMMA1002909//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.00011:28:75//HOMO SAPIENS (HUMAN)//P39188
 15 F-MAMMA1002930//BOMBYXIN A-7 PRECURSOR (BBX-A7) (4K-PROTHORACICOTROPIC HORMONE) (4K-PTTH)//0.99:45:46//BOMBYX MORI (SILK MOTH)//P26730
 F-MAMMA1002937//ZINC FINGER PROTEIN 42 (MYELOID ZINC FINGER 1) (MZF-1)//6.5e-24:147:34//HOMO SAPIENS (HUMAN)//P28698
 20 F-MAMMA1002938//CERULOPLASMIN PRECURSOR (EC 1.16.3.1) (FERROXIDASE)//4.7e-11:44:68//MUS MUSCULUS (MOUSE)//Q61147
 F-MAMMA1002941//PROTEIN Q300//0.0076:21:61//MUS MUSCULUS (MOUSE)//Q02722
 F-MAMMA1002947//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556//1.9e-08:152:38//STREPTOMYCES FRADIAF//P20186
 F-MAMMA1002964
 25 F-MAMMA1002970//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/0.0057:55:43//HOMO SAPIENS (HUMAN)//P39189
 F-MAMMA1002972//BRAIN-SPECIFIC HOMEBOX/POU DOMAIN PROTEIN 3A (BRN-3A) (OCT-T1) (HOMEBOX/POU DOMAIN PROTEIN RDC-1)//0.84:53:41//HOMO SAPIENS (HUMAN)//Q01851
 F-MAMMA1002973//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/4.6e-11:54:68//HOMO SAPIENS (HUMAN)//P39192
 30 F-MAMMA1002982
 F-MAMMA1002987//HYPOTHETICAL 11.9 KD PROTEIN IN RPC8-MFA2 INTERGENIC REGION//0.17:47:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53906
 F-MAMMA1003003//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/8.6e-09:30:73//HOMO SAPIENS (HUMAN)//P39195
 35 F-MAMMA1003004//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.0071:41:58//HOMO SAPIENS (HUMAN)//P39195
 F-MAMMA1003007//SPERM PROTAMINE P1//0.0076:51:37//TACHYGLOSSUS ACULEATUS ACULEATUS (AUSTRALIAN ECHIDNA)//P35311
 40 F-MAMMA1003011//HISTONE MACRO-H2A.1//1.8e-60:175:70//RATTUS NORVEGICUS (RAT)//Q02874
 F-MAMMA1003013//ACTIN BINDING PROTEIN//0.097:83:31//SACCHAROMYCES EXIGUUS (YEAST)//P38479
 F-MAMMA1003015
 F-MAMMA1003019//MYOTUBULARIN//0.022:56:37//HOMO SAPIENS (HUMAN)//Q13496
 45 F-MAMMA1003026//HYPOTHETICAL 29.3 KD PROTEIN (ORF92)//0.0014:208:27//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV)//O10341
 F-MAMMA1003031//PROBABLE E4 PROTEIN (E1^E4)//0.14:49:32//HUMAN PAPILLOMAVIRUS TYPE 6B//P06459
 50 F-MAMMA1003035//HYPOTHETICAL 24.4 KD PROTEIN IN LPD 3'REGION (ORF4)//5.1e-12:112:34//ZY-MOMONAS MOBILIS//O66114
 F-MAMMA1003039//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.4e-07:68:54//HOMO SAPIENS (HUMAN)//P39188
 F-MAMMA1003040//!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!!/2.8e-39:90:57//HOMO SAPIENS (HUMAN)//P39190
 55 F-MAMMA1003044
 F-MAMMA1003049//PROBABLE E4 PROTEIN//0.50:67:29//HUMAN PAPILLOMAVIRUS TYPE 6C//P20969

F-MAMMA1003055//WEAK TOXIN CM-2//0.99:23:30//NAJA HAJE HAJE (EGYPTIAN COBRA)//P01415
 F-MAMMA1003056//EXPORTED PROTEIN 7 (FRAGMENT)//1.0:52:32//STREPTOCOCCUS PNEUMONIAE//
 P35597

F-MAMMA1003057//MD6 PROTEIN//1.5e-85:168:95//MUS MUSCULUS (MOUSE)//Q60584

5 F-MAMMA1003066//REGB PROTEIN//1.0:62:27//PSEUDOMONAS AERUGINOSA//Q03381

F-MAMMA1003089//!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!!/5.1e-15:44:77//HOMO SAPIENS (HUMAN)//P39190

F-MAMMA1003099//ENDOTHELIAL ACTIN-BINDING PROTEIN (ABP-280) (NONMUSCLE FILAMIN) (FILAMIN 1)//4.8e-20:80:62//HOMO SAPIENS (HUMAN)//P21333

10 F-MAMMA1003104//PHOTOSYSTEM I REACTION CENTRE SUBUNIT VIII//0.98:22:40//SYNECHOCOCCUS ELONGATUS NAEGELI//P25900

F-MAMMA1003113//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (FRAGMENTS)//0.67:35:45//GALLUS GALLUS (CHICKEN)//P02467

F-MAMMA1003127//MYOSIN I ALPHA (MMI-ALPHA)//5.2e-34:141:56//MUS MUSCULUS (MOUSE)//P46735

15 F-MAMMA1003135//HYPOTHETICAL 182.0 KD PROTEIN IN NMD5-HOM6 INTERGENIC REGION//3.6e-05:91:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P47170

F-MAMMA1003140

F-MAMMA1003146//MALE SPECIFIC SPERM PROTEIN MST87F//1.0:33:36//DROSOPHILA MELANOGASTER (FRUIT FLY)//P08175

20 F-MAMMA1003150//HYPOTHETICAL 84.3 KD PROTEIN ZK945.10 IN CHROMOSOME II//4.4e-10:254:30//CAENORHABDITIS ELEGANS//Q09625

F-MAMMA1003166//BRAIN PROTEIN H5//4.0e-42:182:48//HOMO SAPIENS (HUMAN)//O43236

F-NT2RM1000001//HYPOTHETICAL 8.7 KD PROTEIN IN RPL22-RPL23 INTERGENIC REGION (ORF70)//0.15:38:34//ASTASIA LONGA (EUGLENOPHYCEAN ALGA)//P34779

25 F-NT2RM1000018

F-NT2RM1000032//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//0.51:17:41//CYPRINUS CARPIO (COMMON CARP)//P24948

F-NT2RM1000035//3-HYDROXY-3-METHYLGLUTARYL-COENZYME A REDUCTASE (EC 1.1.1.34) (HMG-COA REDUCTASE)//0.00011:114:27//BLATTELLA GERMANICA (GERMAN COCKROACH)//P54960

30 F-NT2RM1000037//METALLOTHIONEIN-II (MT-II)//0.025:19:47//SCYLLA SERRATA (MUD CRAB)//P02806

F-NT2RM1000039//VITELLINE MEMBRANE VM34CA PROTEIN PRECURSOR//0.00083:84:33//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q06521

F-NT2RM1000055//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR//1.1e-07:34:55//PLASMODIUM LOPHURAE//P04929

35 F-NT2RM1000059//MYOCYTE-SPECIFIC ENHANCER FACTOR 2B (SERUM RESPONSE FACTOR-LIKE PROTEIN 2) (XMEF2) (RSRFR2)//0.18:83:36//HOMO SAPIENS (HUMAN)//Q02080

F-NT2RM1000062//PROLINE-RICH PEPTIDE P-B//0.54:34:44//HOMO SAPIENS (HUMAN)//P02814

F-NT2RM1000080//HYPOTHETICAL 35.7 KD PROTEIN SLR1128//2.1e-20:119:40//SYNECHOCYSTIS SP. (STRAIN PCC 6803)//P72655

40 F-NT2RM1000086//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT)//0.20:56:35//HOMO SAPIENS (HUMAN)//P10162

F-NT2RM1000092//COLLAGEN-LIKE PROTEIN//0.0017:44:45//HERPESVIRUS SAIMIRI (SUBGROUP C / STRAIN 488)//P22576

F-NT2RM1000118//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT)//5.7e-07:109:28//NEUROSPORA CRASSA//P87072

45 F-NT2RM1000119//TRANSCRIPTIONAL REGULATOR IE63 (VMW63) (ICP27)//0.0050:135:32//HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52)//P28276

F-NT2RM1000127//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN)//0.032:68:32//SORGHUM VULGARE (SORGHUM)//P24152

50 F-NT2RM1000131//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF)//0.82:33:39//BOS TAURUS (BOVINE)//P37359

F-NT2RM1000132//NADH-UBIQUINONE OXIDOREDUCTASE 13 KD-A SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-13KD-A) (CI-13KD-A)//2.7e-59:124:91//HOMO SAPIENS (HUMAN)//O75380

F-NT2RM1000153//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5)//2.5e-08:148:29//HOMO SAPIENS (HUMAN)//P49902

55 F-NT2RM1000186

NEURIN REGULATORY SUBUNIT 1//5.7e-109:27//NEUROSPORA CRASSA//P87072

F-NT2RM1000187//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE

SPAC10F6.02C//1.0e-12:94:46//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//O42643
 F-NT2RM1000199//CUTICLE COLLAGEN 12 PRECURSOR//0.46:130:33//CAENORHABDITIS ELEGANS//
 P20630
 F-NT2RM1000242//PUTATIVE ATP SYNTHASE J CHAIN, MITOCHONDRIAL (EC 3.6.1.34)//0.85:38:36//
 5 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//O13931
 F-NT2RM1000244//HYPOTHETICAL 131.5 KD PROTEIN C02F12.7 IN CHROMOSOME X//0.0055:98:36//
 CAENORHABDITIS ELEGANS//Q11102
 F-NT2RM1000252//TRICHOHYALIN//2.9e-06:88:36//OVIS ARIES (SHEEP)//P22793
 F-NT2RM1000256//GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE [ISOMERIZING]
 10 (EC 2.6.1.16) (HEXOSEPHOSPHATE AMINOTRANSFERASE) (D-FRUCTOSE-6- PHOSPHATE AMIDOTRANS-
 FERASE) (GFAT)//2.9e-54:153:67//MUS MUSCULUS (MOUSE)//P47856
 F-NT2RM1000257//MAGO NASHI PROTEIN//5.9e-64:136:89//DROSOPHILA MELANOGASTER (FRUIT FLY)//
 P49028
 F-NT2RM1000260
 15 F-NT2RM1000271//GALACTOKINASE (EC 2.7.1.6)//0.99:41:39//BACILLUS SUBTILIS//P39574
 F-NT2RM1000272//HYPOTHETICAL 55.5 KD PROTEIN ZK1128.2 IN CHROMOSOME III//8.8e-25:131:45//
 CAENORHABDITIS ELEGANS//Q09357
 F-NT2RM1000280//VACUOLAR ATP SYNTHASE SUBUNIT D (EC 3.6.1.34) (V-ATPASE D SUBUNIT) (V- AT-
 PASE 28 KD ACCESSORY PROTEIN)//2.5e-63:121:94//BOS TAURUS (BOVINE)//P39942
 20 F-NT2RM1000300//TREACLE PROTEIN (TREACHER COLLINS SYNDROME PROTEIN)//0.51:145:26//HOMO
 SAPIENS (HUMAN)//Q13428
 F-NT2RM1000314
 F-NT2RM1000318//50S RIBOSOMAL PROTEIN L23//0.83:28:35//AQUIFEX AEOLICUS//O66433
 F-NT2RM1000341
 25 F-NT2RM1000354//HYPOTHETICAL 5.8 KD PROTEIN IN PUHA 5'REGION (ORF55)//0.95:43:37//RHODO-
 BACTER CAPSULATUS (RHODOPSEUDOMONAS CAPSULATA)//P26159
 F-NT2RM1000355//SPERM-SPECIFIC PROTEIN PHI-1//0.0016:73:43//MYTILUS EDULIS (BLUE MUSSEL)//
 Q04621
 F-NT2RM1000365//HYPOTHETICAL PROTEIN KIAA0140//3.5e-10:83:49//HOMO SAPIENS (HUMAN)//
 30 Q14153
 F-NT2RM1000377//DUAL SPECIFICITY PROTEIN PHOSPHATASE 9 (EC 3.1.3.48) (EC 3.1.3.16) (MITOGEN-
 ACTIVATED PROTEIN KINASE PHOSPHATASE 4) (MAP KINASE PHOSPHATASE 4) (MKP-4)//4.9e-18:113:
 38//HOMO SAPIENS (HUMAN)//Q99956
 F-NT2RM1000388//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION//0.00023:67:
 35 31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53915
 F-NT2RM1000394//HISTONE H3.3 (H3.B) (H3.3Q)//4.7e-52:71:91//HOMO SAPIENS (HUMAN), MUS MUSCU-
 LUS (MOUSE), RATTUS NORVEGICUS (RAT), ORYCTOLAGUS CUNICULUS (RABBIT), GALLUS GALLUS
 (CHICKEN), SPISULA SOLIDISSIMA (ATLANTIC SURF-CLAM), DROSOPHILA MELANOGASTER (FRUIT FLY),
 AND DROSOPHILA HYDEI (FRUIT FLY)//P06351
 40 F-NT2RM1000399//ENDOTHELIN-2 PRECURSOR (ET-2) (FRAGMENT)//0.92:24:45//CANIS FAMILIARIS
 (DOG)//P12064
 F-NT2RM1000421//CUTICLE COLLAGEN 2C (FRAGMENT)//0.12:93:33//HAEMONCHUS CONTORTUS//
 P16252
 F-NT2RM1000430//PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN PRECURSOR (PELP)//0.13:86:31//NICO-
 45 TIANA TABACUM (COMMON TOBACCO)//Q03211
 F-NT2RM1000499//HYPOTHETICAL PROTEIN KIAA0041 (FRAGMENT)//2.9e-17:75:49//HOMO SAPIENS
 (HUMAN)//Q15057
 F-NT2RM1000539//HYPOTHETICAL 10.4 KD PROTEIN IN FTR1-SPT15 INTERGENIC REGION//2.9e-16:82:
 51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40089
 50 F-NT2RM1000553//GLYCOLIPID TRANSFER PROTEIN (GLTP)//6.4e-06:103:33//SUS SCROFA (PIG)//
 P17403
 F-NT2RM1000555//UNR PROTEIN//8.7e-77:105:95//RATTUS NORVEGICUS (RAT)//P18395
 F-NT2RM1000563//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)//0.15:20:50//HO-
 MO SAPIENS (HUMAN)//P30808
 55 F-NT2RM1000623//CLARA CELL PHOSPHOLIPID-BINDING PROTEIN PRECURSOR (CCBP)/CLARA CELLS
 OF RAT OVARY//P17403
 F-NT2RM1000648//GLYCOSYLTRANSFERASE//2.9e-22:133:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P43636

F-NT2RM1000661//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF) (GIFB)//0.0060:24:33//HOMO SAPIENS (HUMAN)//P25713
F-NT2RM1000666//COLD SHOCK PROTEIN SCOF//9.1e-07:67:41//STREPTOMYCES COELICOLOR//P48859
F-NT2RM1000669//CHLOROPLAST 50S RIBOSOMAL PROTEIN L31//0.071:69:31//PORPHYRA PURPUREA//P51290
F-NT2RM1000672//SIGNAL RECOGNITION PARTICLE SEC65 SUBUNIT (FRAGMENT)//0.27:42:42//KLUYVEROMYCES LACTIS (YEAST)//O13475
F-NT2RM1000691//RETINOBLASTOMA BINDING PROTEIN 2 (RBBP-2)//4.3e-42:241:42//HOMO SAPIENS (HUMAN)//P29375
F-NT2RM1000699//N2,N2-DIMETHYLGUANOSINE TRNA METHYLTRANSFERASE PRECURSOR (EC 2.1.1.32)//0.94:48:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P15565
F-NT2RM1000702//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 1//0.0013:139:25//DROSOPHILA MELANOGASTER (FRUIT FLY)//P26308
F-NT2RM1000725//BASIC PROLINE-RICH PEPTIDE P-E (IB-9)//1.0:15:60//HOMO SAPIENS (HUMAN)//P02811
F-NT2RM1000741//STATHMIN (CLONE XO20) (FRAGMENT)//1.0:53:32//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//Q09005
F-NT2RM1000742//HYPOTHETICAL 24.1 KD PROTEIN IN DHFR 3'REGION (ORF2)//1.0:54:42//HERPESVIRUS SAIMIRI (STRAIN 484-77)//P25049
F-NT2RM1000746//HYPOTHETICAL 16.8 KD PROTEIN C29E6.04 IN CHROMOSOME I//0.11:87:21//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09858
F-NT2RM1000770//DXS6673F PROTEIN//2.0e-38:190:48//HOMO SAPIENS (HUMAN)//Q14202
F-NT2RM1000772//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1//4.3e-12:141:30//PODOSPORA ANSERINA//Q00808
F-NT2RM1000780//MALE SPECIFIC SPERM PROTEIN MST87F//0.98:34:38//DROSOPHILA MELANOGASTER (FRUIT FLY)//P08175
F-NT2RM1000781
F-NT2RM1000800//24.1 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION//7.9e-11:135:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P28707
F-NT2RM1000802//ALPHA-AMYLASE INHIBITOR PAIM I (PIG PANCREATIC ALPHA-AMYLASE INHIBITOR OF MICROBES I)//0.43:62:35//STREPTOMYCES OLIVACEOVIRIDIS (STREPTOMYCES CORCHORUSII)//P09921
F-NT2RM1000811
F-NT2RM1000826//UNR PROTEIN//1.1e-110:144:83//RATTUS NORVEGICUS (RAT)//P18395
F-NT2RM1000829//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//1.0:38:34//DROSOPHILA SIMULANS (FRUIT FLY)//P50270
F-NT2RM1000833//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT//1.4e-62:145:841//CANIS FAMILIARIS (DOG)//P38377
F-NT2RM1000850//TESTIS-SPECIFIC PROTEIN KINASE 1 (EC 2.7.1.-)//6.1e-08:136:33//RATTUS NORVEGICUS (RAT)//Q63572
F-NT2RM1000852//ATP-DEPENDENT RNA HELICASE ROK1//1.6e-34:212:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P45818
F-NT2RM1000857//HISTONE H1.M6.1//0.76:31:48//TRYPANOSOMA CRUZI//P40273
F-NT2RM1000867//MICROSOMAL SIGNAL PEPTIDASE 10.8 KD SUBUNIT (EC 3.4.-.-)//0.0082:76:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P46965
F-NT2RM1000874//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)//0.38:12:58//HOMO SAPIENS (HUMAN)//P30808
F-NT2RM1000882//CYTOCHROME B5//9.0e-13:92:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40312
F-NT2RM1000883//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)//0.79:22:59//HOMO SAPIENS (HUMAN)//P30808
F-NT2RM1000885//HYPOTHETICAL 5.8 KD PROTEIN//0.76:18:38//CLOVER YELLOW MOSAIC VIRUS (CYMV)//P16485
F-NT2RM1000894//DNA-DIRECTED RNA POLYMERASE 1135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE 1) (RPO1) (RPO1A) (RPO1B) (RPO1C) (RPO1D) (RPO1E) (RPO1F) (RPO1G) (RPO1H) (RPO1I) (RPO1J) (RPO1K) (RPO1L) (RPO1M) (RPO1N) (RPO1O) (RPO1P) (RPO1Q) (RPO1R) (RPO1S) (RPO1T) (RPO1U) (RPO1V) (RPO1W) (RPO1X) (RPO1Y) (RPO1Z) (RPO1AA) (RPO1AB) (RPO1AC) (RPO1AD) (RPO1AE) (RPO1AF) (RPO1AG) (RPO1AH) (RPO1AI) (RPO1AJ) (RPO1AK) (RPO1AL) (RPO1AM) (RPO1AN) (RPO1AO) (RPO1AP) (RPO1AQ) (RPO1AR) (RPO1AS) (RPO1AT) (RPO1AU) (RPO1AV) (RPO1AW) (RPO1AX) (RPO1AY) (RPO1AZ) (RPO1BA) (RPO1BB) (RPO1BC) (RPO1BD) (RPO1BE) (RPO1BF) (RPO1BG) (RPO1BH) (RPO1BI) (RPO1BJ) (RPO1BK) (RPO1BL) (RPO1BM) (RPO1BN) (RPO1BO) (RPO1BP) (RPO1BQ) (RPO1BR) (RPO1BS) (RPO1BT) (RPO1BU) (RPO1BV) (RPO1BW) (RPO1BX) (RPO1BY) (RPO1BZ) (RPO1CA) (RPO1CB) (RPO1CC) (RPO1CD) (RPO1CE) (RPO1CF) (RPO1CG) (RPO1CH) (RPO1CI) (RPO1CJ) (RPO1CK) (RPO1CL) (RPO1CM) (RPO1CN) (RPO1CO) (RPO1CP) (RPO1CQ) (RPO1CR) (RPO1CS) (RPO1CT) (RPO1CU) (RPO1CV) (RPO1CW) (RPO1CX) (RPO1CY) (RPO1CZ) (RPO1DA) (RPO1DB) (RPO1DC) (RPO1DD) (RPO1DE) (RPO1DF) (RPO1DG) (RPO1DH) (RPO1DI) (RPO1DJ) (RPO1DK) (RPO1DL) (RPO1DM) (RPO1DN) (RPO1DO) (RPO1DP) (RPO1DQ) (RPO1DR) (RPO1DS) (RPO1DT) (RPO1DU) (RPO1DV) (RPO1DW) (RPO1DX) (RPO1DY) (RPO1DZ) (RPO1EA) (RPO1EB) (RPO1EC) (RPO1ED) (RPO1EE) (RPO1EF) (RPO1EG) (RPO1EH) (RPO1EI) (RPO1EJ) (RPO1EK) (RPO1EL) (RPO1EM) (RPO1EN) (RPO1EO) (RPO1EP) (RPO1EQ) (RPO1ER) (RPO1ES) (RPO1ET) (RPO1EU) (RPO1EV) (RPO1EW) (RPO1EX) (RPO1EY) (RPO1EZ) (RPO1FA) (RPO1FB) (RPO1FC) (RPO1FD) (RPO1FE) (RPO1FF) (RPO1FG) (RPO1FH) (RPO1FI) (RPO1FJ) (RPO1FK) (RPO1FL) (RPO1FM) (RPO1FN) (RPO1FO) (RPO1FP) (RPO1FQ) (RPO1FR) (RPO1FS) (RPO1FT) (RPO1FU) (RPO1FV) (RPO1FW) (RPO1FX) (RPO1FY) (RPO1FZ) (RPO1GA) (RPO1GB) (RPO1GC) (RPO1GD) (RPO1GE) (RPO1GF) (RPO1GG) (RPO1GH) (RPO1GI) (RPO1GJ) (RPO1GK) (RPO1GL) (RPO1GM) (RPO1GN) (RPO1GO) (RPO1GP) (RPO1GQ) (RPO1GR) (RPO1GS) (RPO1GT) (RPO1GU) (RPO1GV) (RPO1GW) (RPO1GX) (RPO1GY) (RPO1GZ) (RPO1HA) (RPO1HB) (RPO1HC) (RPO1HD) (RPO1HE) (RPO1HF) (RPO1HG) (RPO1HH) (RPO1HI) (RPO1HJ) (RPO1HK) (RPO1HL) (RPO1HM) (RPO1HN) (RPO1HO) (RPO1HP) (RPO1HQ) (RPO1HR) (RPO1HS) (RPO1HT) (RPO1HU) (RPO1HV) (RPO1HW) (RPO1HX) (RPO1HY) (RPO1HZ) (RPO1IA) (RPO1IB) (RPO1IC) (RPO1ID) (RPO1IE) (RPO1IF) (RPO1IG) (RPO1IH) (RPO1II) (RPO1IJ) (RPO1IK) (RPO1IL) (RPO1IM) (RPO1IN) (RPO1IO) (RPO1IP) (RPO1IQ) (RPO1IR) (RPO1IS) (RPO1IT) (RPO1IU) (RPO1IV) (RPO1IW) (RPO1IX) (RPO1IY) (RPO1IZ) (RPO1JA) (RPO1JB) (RPO1JC) (RPO1JD) (RPO1JE) (RPO1JF) (RPO1JG) (RPO1JH) (RPO1JI) (RPO1JJ) (RPO1JK) (RPO1JL) (RPO1JM) (RPO1JN) (RPO1JO) (RPO1JP) (RPO1JQ) (RPO1JR) (RPO1JS) (RPO1JT) (RPO1JU) (RPO1JV) (RPO1JW) (RPO1JX) (RPO1JY) (RPO1JZ) (RPO1KA) (RPO1KB) (RPO1KC) (RPO1KD) (RPO1KE) (RPO1KF) (RPO1KG) (RPO1KH) (RPO1KI) (RPO1KJ) (RPO1KK) (RPO1KL) (RPO1KM) (RPO1KN) (RPO1KO) (RPO1KP) (RPO1KQ) (RPO1KR) (RPO1KS) (RPO1KT) (RPO1KU) (RPO1KV) (RPO1KW) (RPO1KX) (RPO1KY) (RPO1KZ) (RPO1LA) (RPO1LB) (RPO1LC) (RPO1LD) (RPO1LE) (RPO1LF) (RPO1LG) (RPO1LH) (RPO1LI) (RPO1LJ) (RPO1LK) (RPO1LL) (RPO1LM) (RPO1LN) (RPO1LO) (RPO1LP) (RPO1LQ) (RPO1LR) (RPO1LS) (RPO1LT) (RPO1LU) (RPO1LV) (RPO1LW) (RPO1LX) (RPO1LY) (RPO1LZ) (RPO1MA) (RPO1MB) (RPO1MC) (RPO1MD) (RPO1ME) (RPO1MF) (RPO1MG) (RPO1MH) (RPO1MI) (RPO1MJ) (RPO1MK) (RPO1ML) (RPO1MN) (RPO1MO) (RPO1MP) (RPO1MQ) (RPO1MR) (RPO1MS) (RPO1MT) (RPO1MU) (RPO1MV) (RPO1MW) (RPO1MX) (R

LAX//P02583

F-NT2RM1000905//GLUTATHIONE S-TRANSFERASE 1-1 (EC 2.5.1.18) (CLASS-THETA)//0.98:39:35//LUCILIA CUPRINA (GREENBOTTLE FLY) (AUSTRALIAN SHEEP BLOWFLY)//P42860

F-NT2RM1000924//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III//1.3e-11:169:28//CAENORHABDITIS ELEGANS//P46577

F-NT2RM1000927//CUTICLE COLLAGEN 1//0.00048:141:31//CAENORHABDITIS ELEGANS//P08124

F-NT2RM1000962//HYPOTHETICAL 35.8 KD PROTEIN C4F8.04 IN CHROMOSOME I//7.1e-13:169:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//O14180

F-NT2RM1000978//HYPOTHETICAL 20.2 KD PROTEIN IN MNN4-PTK1 INTERGENIC REGION//0.61:82:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P36045

F-NT2RM1001003//ALPHA-2 CATENIN (ALPHA N-CATENIN) (NEURAL ALPHA-CATENIN)//1.6e-21:211:31//GALLUS GALLUS (CHICKEN)//P30997

F-NT2RM1001008//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I//3.2e-15:119:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09701

F-NT2RM1001043//ENDOTHELIN-1 (ET-1) (FRAGMENT)//0.78:32:34//MACACA FASCICULARIS (CRAB EATING MACAQUE) (CYNOMOLGUS MONKEY)//Q28469

F-NT2RM1001044

F-NT2RM1001059//LORICRIN//8.6e-08:108:39//HOMO SAPIENS (HUMAN)//P23490

F-NT2RM1001066//METALLOTHIONEIN-LIKE PROTEIN TYPE 2//0.99:24:50//LYCOPERSICON ESCULENTUM (TOMATO)//Q43513

F-NT2RM1001072//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE GAMMA 1 (EC 3.1.4.11) (PLC-GAMMA-1) (PHOSPHOLIPASE C-GAMMA-1) (PLC-II) (PLC-148)//4.7e-15:148:33//HOMO SAPIENS (HUMAN)//P19174

F-NT2RM1001074//HYPOTHETICAL PROTEIN F-215//8.6e-05:126:30//HUMAN ADENOVIRUS TYPE 2//P03291

F-NT2RM1001082//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/6.5e-19:75:54//HOMO SAPIENS (HUMAN)//P39195

F-NT2RM1001085//MALE SPECIFIC SPERM PROTEIN MST84DB//0.49:29:41//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q01643

F-NT2RM1001092//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1)//2.8e-42:200:38//HOMO SAPIENS (HUMAN)//P51522

F-NT2RM1001102//HYPOTHETICAL 62.8 KD PROTEIN IN TAF145-YOR1 INTERGENIC REGION//1.7e-18:161:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53331

F-NT2RM1001105//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556//4.0e-05:157:35//STREPTOMYCES FRADIAE//P20186

F-NT2RM1001112//NONHISTONE CHROMOSOMAL PROTEIN HMG-17//0.18:20:55//BOS TAURUS (BOVINE)//P02313

F-NT2RM1001115

F-NT2RM1001139//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1.8 PRECURSOR (GRP 1.8)//2.0e-25:156:46//PHASEOLUS VULGARIS (KIDNEY BEAN) (FRENCH BEAN)//P10496

F-NT2RM2000006//MITOCHONDRIAL RIBOSOMAL PROTEIN S12//0.76:45:35//LEISHMANIA TARENTOLAE (SAUROLEISHMANIA TARENTOLAE)//Q34940

F-NT2RM2000013//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2)//3.9e-87:238:65//DROSOPHILA MELANOGASTER (FRUIT FLY)//P25167

F-NT2RM2000030//TOXINS 1 AND 2//0.98:21:42//TRIMERESURUS WAGLERI (WAGLER'S PIT VIPER) (TROPIDOLAEMUS WAGLERI)//P24335

F-NT2RM2000032//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.00059:53:49//HOMO SAPIENS (HUMAN)//P39188

F-NT2RM2000042//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N)//1.0:68:26//HOMO SAPIENS (HUMAN)//P22532

F-NT2RM2000092//HYPOTHETICAL 67.5 KD PROTEIN IN PRPS4-STE20 INTERGENIC REGION//7.0e-11:80:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38748

F-NT2RM2000093//OVARY MATURATING PARSIN (OMP)//1.0:26:38//LOCUSTA MIGRATORIA (MIGRATORY LOCUST)//P80045

F-NT2RM2000101//HYPOTHETICAL 39.3 KD PROTEIN C02B8.6 IN CHROMOSOME X//2.2e-06:55:35//CAENORHABDITIS ELEGANS

F-NT2RM2000124//CAMP-DEPENDENT PROTEIN KINASE A (PKA) (CAMP-DEPENDENT PROTEIN KINASE A-ALPHA)//3.1e-35:77:96//MUS MUSCULUS (MOUSE)//P05132

F-NT2RM2000191//3',5'-CYCLIC-NUCLEOTIDE PHOSPHODIESTERASE REGA (EC 3.1.4.17) (PDEASE REGA) //3.3e-05:181:27//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD) //Q23917

F-NT2RM2000192//REPLICATION PROTEIN E1 (FRAGMENTS) //0.019:148:25//COTTONTAIL RABBIT (SHOPE) PAPILLOMAVIRUS (STRAIN WASHINGTON B) (CRPV) //P51894

5 F-NT2RM2000239//PROLINE-RICH PROTEIN MP-3 (FRAGMENT) //0.00032:111:32//MUS MUSCULUS (MOUSE) //P05143

F-ntntntntntntntntntnt//METALLOTHIONEIN-LIKE PROTEIN TYPE 2 //0.046:59:33//LYCOPERSICON ESCULENTUM (TOMATO) //Q43512

10 F-NT2RM2000250//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) //0.054:46:34//RATTUS NORVEGICUS (RAT) //P08699

F-NT2RM2000259//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6) //0.27:112:33//BOVINE HERPES VIRUS TYPE 1 (STRAIN JURA) //P29128

15 F-NT2RM2000260//PROLINE-RICH PROTEIN MP-3 (FRAGMENT) //4.7e-22:191:35//MUS MUSCULUS (MOUSE) //P05143

F-NT2RM2000287//HYPOTHETICAL 11.8 KD PROTEIN C1B3.02C IN CHROMOSOME I //5.0e-19:83:53//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST) //O13868

F-NT2RM2000322//DIAMINOPIMELATE DECARBOXYLASE (EC 4.1.1.20) (DAP DECARBOXYLASE) //0.47:117:29//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI) //P56129

20 F-NT2RM2000359//SPORE GERMINATION PROTEIN 270-11 //0.12:83:36//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD) //P22698

F-NT2RM2000363//BREAKPOINT CLUSTER REGION PROTEIN //1.3e-16:203:30//HOMO SAPIENS (HUMAN) //P11274

F-NT2RM2000368//DEK PROTEIN //0.00027:100:32//HOMO SAPIENS (HUMAN) //P35659

25 F-NT2RM2000371//POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8) (POLYNUCLEOTIDE PHOSPHORYLASE) (PNPASE) //6.8e-36:170:47//ESCHERICHIA COLI //P05055

F-NT2RM2000374//NODAL PRECURSOR //1.1e-32:64:95//MUS MUSCULUS (MOUSE) //P43021

F-NT2RM2000395//IMMEDIATE-EARLY PROTEIN IE180 //0.31:41:43//PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV) //P11675

30 F-NT2RM2000402//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT) //1.2e-30:228:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P32802

F-NT2RM2000407//TRANSMEMBRANE PROTEIN SEX PRECURSOR //0.032:105:30//HOMO SAPIENS (HUMAN) //P51805

35 F-NT2RM2000420//METALLOTHIONEIN (MT) //0.88:42:38//PLEURONECTES PLATESSA (PLAICE) //P07216

F-NT2RM2000422//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73 //2.0e-117:237:87//RATTUS NORVEGICUS (RAT) //Q08469

F-NT2RM2000452//HYPOTHETICAL 63.6 KD PROTEIN IN YPT52-GCN3 INTERGENIC REGION //1.1e-08:157:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P36113

40 F-NT2RM2000469//70 KD ANTIGEN //0.050:207:23//SHIGELLA FLEXNERI //P18010

F-NT2RM2000490//BASIC PROLINE-RICH PEPTIDE P-E (IB-9) //0.022:25:44//HOMO SAPIENS (HUMAN) //P02811

F-NT2RM2000502//MALE SPECIFIC SPERM PROTEIN MST84DD //0.0037:17:58//DROSOPHILA MELANOGASTER (FRUIT FLY) //Q01645

45 F-NT2RM2000504//HYPOTHETICAL 99.0 KD PROTEIN SPBC119.17 //1.7e-22:195:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST) //O42908

F-NT2RM2000522//RAS-RELATED PROTEIN RABA (FRAGMENT) //3.6e-05:67:29//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD) //P34141

50 F-NT2RM2000540//HYPOTHETICAL 83.8 KD PROTEIN C27F2.7 IN CHROMOSOME III //8.4e-33:214:38//CAENORHABDITIS ELEGANS //Q18262

F-NT2RM2000556//HYPOTHETICAL PROTEIN KIAA0288 (HA6116) //1.7e-09:133:36//HOMO SAPIENS (HUMAN) //P56524

F-NT2RM2000566//INTEGRIN ALPHA-6 PRECURSOR (VLA-6) (CD49F) //2.2e-60:244:51//HOMO SAPIENS (HUMAN) //P23229

55 F-NT2RM2000567//PROLINE-RICH PROTEIN MP-3 (FRAGMENT) //2.3e-09:192:34//MUS MUSCULUS (MOUSE) //P05143

F-NT2RM2000569//HYPOTHETICAL PROTEIN C27F2.7 IN CHROMOSOME III //8.4e-33:214:38//CAENORHABDITIS ELEGANS //Q18262

F-NT2RM2000577//SOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS)//
 9.1e-54:225:45//SYNECHOCYSTIS SP. (STRAIN PCC 6803)//P73505
 F-NT2RM2000581//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53)//0.079:111:34//HOMO SA-
 PIENS (HUMAN)//Q15427
 5 F-NT2RM2000588//HYPOTHETICAL PROTEIN KIAA0288 (HA6116)//2.3e-09:193:32//HOMO SAPIENS (HU-
 MAN)//P56524
 F-NT2RM2000594//BASIC PROLINE-RICH PEPTIDE P-E (IB-9)//0.18:33:42//HOMO SAPIENS (HUMAN)//
 P02811
 10 F-NT2RM2000599//DNA (CYTOSINE-5)-METHYLTRANSFERASE (EC 2.1.1.37) (DNA METHYLTRANS-
 FERASE) (DNA METASE) (MCMT) (M.MMU1)//1.5e-09:68:45//MUS MUSCULUS (MOUSE)//P13864
 F-NT2RM2000609//GRANULIN 2//0.83:42:35//CYPRINUS CARPIO (COMMON CARP)//P81014
 F-NT2RM2000612//ZINC FINGER PROTEIN GCS1//7.2e-05:155:29//SACCHAROMYCES CEREVISIAE (BAK-
 ER'S YEAST)//P35197
 15 F-NT2RM2000623//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR//1.8e-09:196:33//SACCHAROMY-
 CES CEREVISIAE (BAKER'S YEAST)//P32323
 F-NT2RM2000624//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR//0.070:113:27//DROSOPHILA ERECTA
 (FRUIT FLY)//P13730
 F-NT2RM2000635//SPERM PROTAMINE P1//0.54:47:38//ANTECHINUS STUARTII//P42129
 F-NT2RM2000636//OUTER MEMBRANE PROTEIN H.8 PRECURSOR//0.096:62:35//NEISSERIA GONOR-
 RHOEAE//P11910
 20 F-NT2RM2000639//HYPOTHETICAL PROTEIN MJ0243//0.99:32:34//METHANOCOCCUS JANNASCHII//
 Q57694
 F-NT2RM2000649//NEURONAL CALCIUM SENSOR 1 (NCS-1)//0.00049:70:35//RATTUS NORVEGICUS
 (RAT), AND GALLUS GALLUS (CHICKEN)//P36610
 25 F-NT2RM2000669//50S RIBOSOMAL PROTEIN L34//1.0:34:44//BACILLUS SUBTILIS//P05647
 F-NT2RM2000691//ACTIN-LIKE PROTEIN 3 (ACTIN-2)//7.0e-116:243:87//HOMO SAPIENS (HUMAN), AND
 BOS TAURUS (BOVINE)//P32391
 F-NT2RM2000714//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-I)//3.8e-21:174:35//HO-
 MO SAPIENS (HUMAN)//Q15404
 30 F-NT2RM2000718//HYPOTHETICAL 52.9 KD SERINE-RICH PROTEIN C11G7.01 IN CHROMOSOME I//0.0022:
 174:29//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//O13695
 F-NT2RM2000735//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6)//1.6e-102:246:74//HOMO SAPIENS
 (HUMAN)//P28160
 F-NT2RM2000740//HYPOTHETICAL 131.1 KD HELICASE IN ALG7-ENP1 INTERGENIC REGION//8.5e-51:212:
 35 49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38144
 F-NT2RM2000795//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//9.0e-41:125:53//HOMO SAPIENS (HU-
 MAN)//P39189
 F-NT2RM2000821//COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP)//1.1e-128:291:89//
 RATTUS NORVEGICUS (RAT)//P23514
 40 F-NT2RM2000837//CYCLIN-DEPENDENT KINASE INHIBITOR 1C (CYCLIN-DEPENDENT KINASE INHIBITOR
 P57) (P57KIP2)//3.9e-05:113:36//HOMO SAPIENS (HUMAN)//P49918
 F-NT2RM2000951//HYPOTHETICAL 60.3 KD PROTEIN R08D7.7 IN CHROMOSOME III//2.5e-49:273:39//
 CAENORHABDITIS ELEGANS//P30646
 F-NT2RM2000952//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H)
 45 (FRAGMENT)//0.037:234:23//RATTUS NORVEGICUS (RAT)//P16884
 F-NT2RM2000984//HYPOTHETICAL 54.7 KD PROTEIN F37A4.1 IN CHROMOSOME III//6.3e-44:216:43//
 CAENORHABDITIS ELEGANS//P41879
 F-NT2RM2001004//SYNAPSINS IA AND IB//0.15:178:32//RATTUS NORVEGICUS (RAT)//P09951
 F-NT2RM2001035//CCR4-ASSOCIATED FACTOR 1 (CAF1)//1.4e-87:188:90//MUS MUSCULUS (MOUSE)//
 50 Q60809
 F-NT2RM2001065//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6)//0.53:122:31//TRYPANOSOMA BRU-
 CEI BRUCEI//P24499
 F-NT2RM2001100//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III//3.4e-13:171:30//
 CAENORHABDITIS ELEGANS//P46577
 55 F-NT2RM2001105//SPORE COAT PROTEIN SP96//7.8e-06:141:34//DICTYOSTELIUM DISCOIDEUM (SLIME
 MOLD)//P14111
 F-NT2RM2001131//PROBABLE EUKARYOTIC NUCLEAR FACTOR FOR TRANSCRIPTION//2.4e-049:111:11//SCHIZOSA-
 CHAROMYCES POMBE (FISSION YEAST)//Q10475

F-NT2RM2001141//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME III.//0.050:134:26//CAENORHABDITIS ELEGANS //P34681
F-NT2RM2001152
F-NT2RM2001177//COLLAGEN ALPHA 1(XIV) CHAIN PRECURSOR (UNDULIN)//0.86:42:40//GALLUS GAL-
LUS (CHICKEN).//P32018
F-NT2RM2001194//SMOOTHELIN.//4.7e-05:77:32//HOMO SAPIENS (HUMAN).//P53814
F-NT2RM2001196//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.7e-18:218:35//MUS MUSCULUS
(MOUSE).//P05143
F-NT2RM2001201//CYSTEINE STRING PROTEIN (CCCS1).//0.041:22:59//TORPEDO CALIFORNICA (PACIFIC
ELECTRIC RAY).//P56101
F-NT2RM2001221//KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (P-CIP10).//1.3e-13:183:32//
RATTUS NORVEGICUS (RAT).//P97924
F-NT2RM2001238//GLUTAMINASE, KIDNEY ISOFORM PRECURSOR (EC 3.5.1.2) (GLS) (L-GLUTAMINE AMI-
DOHYDROLASE).//6.5e-121:218:98//RATTUS NORVEGICUS (RAT).//P13264
F-NT2RM2001243//HYPOTHETICAL 200.0 KD PROTEIN IN GZF3-IME2 INTERGENIC REGION//0.00019:177:
27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P42945
F-NT2RM2001247//LEGUMIN B (FRAGMENT).//0.22:54:35//PISUM SATIVUM (GARDEN PEA).//P14594
F-NT2RM2001256//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//1.8e-109:207:98//MUS MUS-
CULUS (MOUSE).//P53995
F-NT2RM2001291//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.016:22:40//HOMO SAPIENS
(HUMAN).//P22531
F-NT2RM2001306//REF(2)P PROTEIN.//0.61:51:33//DROSOPHILA MELANOGASTER (FRUIT FLY).//P14199
F-NT2RM2001312/////ALU SUBFAMILY SX WARNING ENTRY !!!!!//7.2e-11:33:72//HOMO SAPIENS (HUMAN).//
P39195
F-NT2RM2001319
F-NT2RM2001324//ZYXIN.//5.1e-22:91:38//GALLUS GALLUS (CHICKEN).//Q04584
F-NT2RM2001345//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//7.4e-10:159:27//PODOSPORA AN-
SERINA.//Q00808
F-NT2RM2001360//ACCESSORY GLAND PEPTIDE PRECURSOR (PARAGONIAL PEPTIDE B).//1.0:27:48//
DROSOPHILA MELANOGASTER (FRUIT FLY).//P05623
F-NT2RM2001370//NAPE PROTEIN.//0.98:44:31//PARACOCCUS DENITRIFICANS (SUBSP. THIOSPHAERA
PANTOTROPHA).//Q56348
F-NT2RM2001393//VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LIPOVITELLIN LV-1N; LIPOVITELLIN
LV-1C; LIPOVITELLIN LV-2].//0.0024:163:31//ICHTHYOMYZON UNICUSPUS (SILVER LAMPREY).//Q91062
F-NT2RM2001420
F-NT2RM2001424//HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U).//2.4e-41:140:59//
HOMO SAPIENS (HUMAN).//Q00839
F-NT2RM2001499//HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1) (CAT1) (SYSTEM Y+
BASIC AMINO ACID TRANSPORTER) (ECOTROPIC RETROVIRAL LEUKEMIA RECEPTOR HOMOLOG) (ERR)
(ECOTROPIC RETROVIRUS RECEPTOR HOMOLOG).//3.7e-71:201:68//HOMO SAPIENS (HUMAN).//P30825
F-NT2RM2001504//CUTICLE COLLAGEN 2.//0.028:41:39//CAENORHABDITIS ELEGANS.//P17656
F-NT2RM2001524//HYPOTHETICAL 61.3 KD PROTEIN F25B5.5 IN CHROMOSOME III.//6.7e-47:190:42//
CAENORHABDITIS ELEGANS.//Q09316
F-NT2RM2001544//TELOMERE-BINDING PROTEIN 51 KD SUBUNIT.//0.0027:136:33//EUPLOTES
CRASSUS.//Q06184
F-NT2RM2001547//HYPOTHETICAL 48.6 KD PROTEIN IN BET1-PAN1 INTERGENIC REGION.//8.5e-18:91:50//
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40564
F-NT2RM2001575//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//3.9e-
35:212:41//HOMO SAPIENS (HUMAN).//P19474
F-NT2RM2001582//RESA PROTEIN.//0.0033:72:27//BACILLUS SUBTILIS.//P35160
F-NT2RM2001588//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//1.0e-06:115:32//ZEA MAYS
(MAIZE).//P14918
F-NT2RM2001592//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//0.033:156:23//HO-
MO SAPIENS (HUMAN).//P26371
F-NT2RM2001605//RETINOBLASTOMA BINDING PROTEIN 2 (RBBP 2).//1.1e-116:249:82//HOMO SAPIENS
(HUMAN).//P34711
F-NT2RM2001613//PROTEIN TRANSFERIN PRECURSOR (TRANSFERIN).//1.0e-10:100:100//RATTUS NOR-
VEGICUS (RAT).//P38378

✓12RM2001771/71N/4488841/100% 150-80,24-60/HOMO/SAPIENS/HUMAN/19574,
✓12RM2001782/MANNOSE-6-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP-MANNOSE-1-

PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE).//7.0e-06:61:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P41940
 F-NT2RM2001784//HYPOTHETICAL PROTEIN UL61//0.00070:145:33//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16818
 5 F-NT2RM2001785//LINOLEOYL-COA DESATURASE (EC 1.14.99.25) (DELTA(6)-DESATURASE).//1.5e-08:127:32//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//Q08871
 F-NT2RM2001797//ZINC FINGER PROTEIN 135.//1.6e-73:267:49//HOMO SAPIENS (HUMAN).//P52742
 F-NT2RM2001800//HYPOTHETICAL HELICASE MG018/MG017/MG016 HOMOLOG.//3.9e-12:171:33//MYCOPLASMA PNEUMONIAE.//P75093
 10 F-NT2RM2001803//IKI3 PROTEIN.//1.6e-38:283:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q06706
 F-NT2RM2001805//COLD SHOCK-LIKE PROTEIN CSPH.//0.51:46:32//SALMONELLA TYPHIMURIUM.//O33793
 F-NT2RM2001813//HYPOTHETICAL 40.4 KD TRP-ASP REPEATS CONTAINING PROTEIN C14B1.4 IN CHROMOSOME III.//5.0e-05:82:32//CAENORHABDITIS ELEGANS.//Q17963
 15 F-NT2RM2001823//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2).//3.6e-49:233:45//HOMO SAPIENS (HUMAN).//O14647
 F-NT2RM2001839//RETICULOCALBIN 1 PRECURSOR.//5.2e-65:222:56//HOMO SAPIENS (HUMAN).//Q15293
 F-NT2RM2001840//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//9.6e-33:102:68//HOMO SAPIENS (HUMAN).//P39194
 20 F-NT2RM2001855//BASP1 PROTEIN.//0.054:120:30//HOMO SAPIENS (HUMAN).//P80723
 F-NT2RM2001867//HYPOTHETICAL 56.6 KD PROTEIN IN URE2-SSU72 INTERGENIC REGION.//4.1e-19:88:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53867
 F-NT2RM2001879//HYPOTHETICAL 47.3 KD PROTEIN C22G7.07C IN CHROMOSOME I.//5.9e-15:76:38//
 25 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09800
 F-NT2RM2001886//HYPOTHETICAL 126.9 KD PROTEIN C22G7.04 IN CHROMOSOME I.//1.4e-41:249:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09798
 F-NT2RM2001896//HYPOTHETICAL 83.2 KD PROTEIN IN KAR4-PBN1 INTERGENIC REGION.//2.1e-59:197:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25582
 30 F-NT2RM2001903//HYPOTHETICAL PROTEIN MJ0263.//0.070:132:31//METHANOCOCCUS JANNASCHII.//O06917
 F-NT2RM2001930//THROMBOSPONDIN 2 PRECURSOR.//7.1e-05:53:47//MUS MUSCULUS (MOUSE).//Q03350
 F-NT2RM2001935//PUTATIVE CUTICLE COLLAGEN F55C10.3.//0.00046:116:35//CAENORHABDITIS ELEGANS.//Q21184
 35 F-NT2RM2001936//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION.//4.5e-27:216:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P28320
 F-NT2RM2001950//HIRUDIN HV1 (BUFRUDIN).//0.59:43:34//HIRUDINARIA MANILLENSIS (BUFFALO LEECH).//P81492
 40 F-NT2RM2001982//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-8 SUBUNIT (G GAMMA-C).//0.72:35:42//BOS TAURUS (BOVINE).//P50154
 F-NT2RM2001983//PROLINE-RICH PEPTIDE P-B.//0.00035:23:52//HOMO SAPIENS (HUMAN).//P02814
 F-NT2RM2001989//NUCLEOLAR PROTEIN NOP4 (NUCLEOLAR PROTEIN NOP77).//8.6e-24:197:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P37838
 45 F-NT2RM2001997
 F-NT2RM2001998//IMMEDIATE-EARLY PROTEIN IE180.//0.076:92:27//PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675
 F-NT2RM2002004//SLF1 PROTEIN.//3.5e-06:235:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12034
 50 F-NT2RM2002014//HYPOTHETICAL PROTEIN HI0568.//2.1e-17:235:29//HAEMOPHILUS INFLUENZAE.//P71353
 F-NT2RM2002030//GLUCOSAMINE-FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE [ISOMERIZING] (EC 2.6.1.16) (HEXOSEPHOSPHATE AMINOTRANSFERASE) (D-FRUCTOSE-6-PHOSPHATE AMIDOTRANSFERASE) (GFAT).//9.5e-105:271:76//MUS MUSCULUS (MOUSE).//P47856
 55 F-NT2RM2002049//SMALL PROLINE-RICH PROTEIN 2-1.//0.099:41:41//HOMO SAPIENS (HUMAN).//P35326
 F-NT2RM2002055//YAC114AD PROTEIN.//2.5e-07:100:100//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q07875
 F-NT2RM2002088//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP).

1.1e-09:65:53//MUS MUSCULUS (MOUSE)//Q61990

F-NT2RM2002091//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION//0.072:74:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53214

F-NT2RM2002100//ATP-DEPENDENT RNA HELICASE ROK1//4.5e-50:289:41//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P45818

F-NT2RM2002109//NT-3 GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKC TYROSINE KINASE) (GP145-TRKC) (TRK-C)//1.4e-14:203:32//RATTUS NORVEGICUS (RAT)//Q03351

F-NT2RM2002128//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)//0.0025:139:31//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P17437

F-NT2RM2002142//GASTRULATION SPECIFIC PROTEIN G12//9.2e-20:42:73//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO)//P47805

F-NT2RM2002145//GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT 12 PRECURSOR//0.0085:200:26//TRITICUM AESTIVUM (WHEAT)//P08488

F-NT2RM2002178//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS)//5.8e-05:56:39//BOS TAURUS (BOVINE)//P25508

F-NT2RM2002580//CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B)//2.9e-14:96:37//PETROMYZON MARINUS (SEA LAMPREY)//P25210

F-NT2RM4000024//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2)//8.6e-95:271:67//DROSOPHILA MELANOGASTER (FRUIT FLY)//P25167

F-NT2RM4000027//INTERFERON-ACTIVATABLE PROTEIN 202 (IFI-202)//0.99:72:31//MUS MUSCULUS (MOUSE)//P15091

F-NT2RM4000030//LAS1 PROTEIN//1.4e-14:184:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P36146

F-NT2RM4000046//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENT)//0.99:120:28//RATTUS NORVEGICUS (RAT)//P13941

F-NT2RM4000061

F-NT2RM4000085//ATP-DEPENDENT RNA HELICASE A (NUCLEAR DNA HELICASE II) (NDH II) (DEAD BOX PROTEIN 9) (MHEL-5)//8.5e-40:263:38//MUS MUSCULUS (MOUSE)//O70133

F-NT2RM4000086//HYPOTHETICAL PROTEIN HI1497//1.0:27:37//HAEMOPHILUS INFLUENZAE//P44221

F-NT2RM4000104//ZINC FINGER PROTEIN 134//1.0e-26:64:56//HOMO SAPIENS (HUMAN)//P52741

F-NT2RM4000139//PREPROTEIN TRANSLOCASE SECE SUBUNIT//0.99:38:42//THERMOTOGA MARITIMA//P35874

F-NT2RM4000155//THREONYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.3) (THREONINE--TRNA LIGASE) (THRRS)//6.3e-34:181:40//HOMO SAPIENS (HUMAN)//P26639

F-NT2RM4000156//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)//4.6e-12:142:33//NICOTIANA TABACUM (COMMON TOBACCO)//P13983

F-NT2RM4000167//KINESIN-LIKE PROTEIN KIF4//3.4e-123:269:91//MUS MUSCULUS (MOUSE)//P33174

F-NT2RM4000169//M PROTEIN, SEROTYPE 2.2 PRECURSOR//9.7e-10:229:26//STREPTOCOCCUS PYOGENES//P50469

F-NT2RM4000191//P68-LIKE PROTEIN//2.1e-11:104:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P24783

F-NT2RM4000197//CUTICLE PROTEIN CP463 (CPCP463)//0.84:29:37//CANCER PAGURUS (ROCK CRAB)//P81587

F-NT2RM4000199//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT)//1.8e-06:187:34//HOMO SAPIENS (HUMAN)//P10162

F-NT2RM4000200//HYPOTHETICAL 9.4 KD PROTEIN IN FLAL 3'REGION (ORF3)//0.52:42:40//BACILLUS LICHENIFORMIS//P22754

F-NT2RM4000202//COLLAGEN ALPHA 1(VIII) CHAIN PRECURSOR (ENDOTHELIAL COLLAGEN)//0.00044:168:32//ORYCTOLAGUS CUNICULUS (RABBIT)//P14282

F-NT2RM4000210//EXTENSIN PRECURSOR//0.27:129:27//DAUCUS CAROTA (CARROT)//P06599

F-NT2RM4000215//MAK16 PROTEIN//2.0e-65:234:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P10962

F-NT2RM4000229//GAR2 PROTEIN//0.13:217:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//P41891

F-NT2RM4000244

AA1//P5180

F-NT2RM4000244//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//0.67:59:27//BALAENOPTERA

PHYSALUS (FINBACK WHALE) (COMMON RORQUAL)//P24947

F-NT2RM4000251//PROLINE-RICH PROTEIN MP-3 (FRAGMENT)//0.0059:108:35//MUS MUSCULUS (MOUSE)//P05143

F-NT2RM4000265//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/8.1e-38:70:70//HOMO SAPIENS (HUMAN)//P39188

F-NT2RM4000290//TRANSDUCIN-LIKE ENHANCER PROTEIN 3 (ESG3)//1.6e-115:209:94//HOMO SAPIENS (HUMAN)//Q04726

F-NT2RM4000324//PRESPORE PROTEIN DP87 PRECURSOR//0.14:136:30//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD)//Q04503

F-NT2RM4000327//HYPOTHETICAL 8.9 KD PROTEIN IN IE0-IE1 INTERGENIC REGION//0.91:73:28//AUTOGRAPHAL CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV)//P41703

F-NT2RM4000344//YME1 PROTEIN HOMOLOG (EC 3.4.24.-)//9.4e-78:241:55//CAENORHABDITIS ELE-GANS//P54813

F-NT2RM4000349//CYSTEINE STRING PROTEIN (CCCS1)//0.055:22:59//TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY)//P56101

F-NT2RM4000354//LETHAL(2) DENTICLELESS PROTEIN (DTL83 PROTEIN)//4.6e-26:208:35//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q24371

F-NT2RM4000356//COAT PROTEIN//0.11:105:36//SATELLITE TOBACCO MOSAIC VIRUS (STMV)//P17574

F-NT2RM4000366//IMMEDIATE-EARLY PROTEIN//1.2e-05:215:24//HERPES VIRUS SAIMIRI (STRAIN 11)//Q01042

F-NT2RM4000368//HYPOTHETICAL 7.3 KD PROTEIN IN RPBA-GP46 INTERGENIC REGION//0.54:46:36//BACTERIOPHAGE RB69//O64300

F-NT2RM4000386//RHSC PROTEIN PRECURSOR//0.0096:162:29//ESCHERICHIA COLI//P16918

F-NT2RM4000395//HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION//4.5e-66:256:53//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P43616

F-NT2RM4000414//HYPOTHETICAL 6.0 KD PROTEIN IN THI12 5'REGION//0.13:33:48//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53820

F-NT2RM4000421//MRNA TRANSPORT REGULATOR MTR10//5.0e-13:171:29//SACCHAROMYCES CEREVI-SIAE (BAKER'S YEAST)//Q99189

F-NT2RM4000425//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/2.1e-25:46:80//HOMO SAPIENS (HUMAN)//P39193

F-NT2RM4000433//CUTICLE COLLAGEN 3A3//2.5e-06:77:38//HAEMONCHUS CONTORTUS//P16253

F-NT2RM4000457//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I//4.3e-09:215:22//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10297

F-NT2RM4000471//TRNA SPLICING PROTEIN SPL1//6.7e-73:163:65//CANDIDA ALBICANS (YEAST)//P87185

F-NT2RM4000486//COLLAGEN ALPHA 2(VI) CHAIN PRECURSOR//0.0012:121:34//GALLUS GALLUS (CHICKEN)//P15988

F-NT2RM4000496//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RNA POLYMER-ASE II SUBUNIT 1)//5.9e-09:175:35//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//P36594

F-NT2RM4000511//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR//0.020:122:31//DROSOPHILA SIMU-LANS (FRUIT FLY)//P13729

F-NT2RM4000514//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6)//0.46:68:32//ARTEMIA SANFRAN-CISCANA (BRINE SHRIMP) (ARTEMIA FRANCISCANA)//Q37708

F-NT2RM4000515//GAR2 PROTEIN//3.2e-05:198:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//P41891

F-NT2RM4000520//HYPOTHETICAL 7.5 KD PROTEIN (ORF 63)//0.011:55:38//SPINACIA OLERACEA (SPIN-ACH)//P08974

F-NT2RM4000531//ZINC FINGER PROTEIN 169 (FRAGMENT)//3.6e-44:244:42//HOMO SAPIENS (HUMAN)//Q14929

F-NT2RM4000532//PUTATIVE MEMBRANE PROTEIN 53//1.0:47:34//HERPES VIRUS SAIMIRI (STRAIN 11)//Q01049

F-NT2RM4000534//HYPOTHETICAL 5.9 KD PROTEIN IN WRBA-PUTA INTERGENIC REGION//0.75:26:46//ESCHERICHIA COLI//P56614

F-NT2RM4000585//GAG POLYPROTEIN [CONTAINS CORE PROTEIN P16 CORE PROTEIN P26]//0.019:86:10//HOMO SAPIENS (HUMAN)//P56614

F-NT2RM4000590//RING-LIKE PROTEIN//1.0:47:34//HERPES VIRUS SAIMIRI (STRAIN 11)//Q01049

F-NT2RM4000590//RING-LIKE PROTEIN//1.0:47:34//HERPES VIRUS SAIMIRI (STRAIN 11)//Q01049

F-NT2RM4000595//HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III.//3.8e-62:226:50//CAENORHABDITIS ELEGANS.//P34284

F-NT2RM4000603//SRC SUBSTRATE CORTACTIN (AMPLAXIN) (EMS1 ONCOGENE).//0.077:132:22//HOMO SAPIENS (HUMAN).//Q14247

5 F-NT2RM4000611//HYPOTHETICAL 40.4 KD TRP-ASP REPEATS CONTAINING PROTEIN C14B1.4 IN CHROMOSOME III.//1.9e-06:82:32//CAENORHABDITIS ELEGANS.//Q17963

F-NT2RM4000616//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//5.3e-79:213:62//ESCHERICHIA COLI.//P27550

10 F-NT2RM4000674//HYPOTHETICAL SYMPORTER SLL1374.//1.3e-11:147:32//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//P74168

F-NT2RM4000689

F-NT2RM4000698//CHORION CLASS HIGH-CYSTEINE HCA PROTEIN 12 PRECURSOR (HC-A.12).//0.26:45:33//BOMBYX MORI (SILK MOTH).//P05687

15 F-NT2RM4000700//THIOPHENE AND FURAN OXIDATION PROTEIN THDF.//0.95:165:25//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE).//P53364

F-NT2RM4000712//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME).//2.2e-82:152:63//CAENORHABDITIS ELEGANS.//P34547

20 F-NT2RM4000717//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.80:54:40//DROSOPHILA SIMULANS (FRUIT FLY).//P13729

F-NT2RM4000733//OCTAPEPTIDE-REPEAT PROTEIN T2.//1.5e-08:139:28//MUS MUSCULUS (MOUSE).//Q06666

F-NT2RM4000734//GASTRULA ZINC FINGER PROTEIN XLCGF26.1 (FRAGMENT).//7.2e-20:205:26//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P18715

25 F-NT2RM4000741//SPERM PROTAMINE P1.//0.89:52:38//ISOODON MACRORURUS (SHORT-NOSED BANDICOOT).//P42136

F-NT2RM4000751//ZINC FINGER PROTEIN 26 (ZFP-26) (MKR3 PROTEIN) (FRAGMENT).//5.2e-77:246:52//MUS MUSCULUS (MOUSE).//P10076

30 F-NT2RM4000764//KERATIN, GLYCINE/TYROSINE-RICH OF HAIR.//0.062:33:42//OVIS ARIES (SHEEP).//Q02958

F-NT2RM4000778

F-NT2RM4000779//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).//0.014:53:45//VOLVOX CARTERI.//P21997

35 F-NT2RM4000787//BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BMP-1).//0.00011:73:39//MUS MUSCULUS (MOUSE).//P98063

F-NT2RM4000790//SPORE COAT PROTEIN SP96.//0.00083:157:29//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P14328

F-NT2RM4000795//CHOLINESTERASE PRECURSOR (EC 3.1.1.8) (ACYLCHOLINE ACYLHYDROLASE) (CHOLINE ESTERASE II) (BUTYRYLCHOLINE ESTERASE) (PSEUDOCHOLINESTERASE).//7.4e-41:271:36//HOMO SAPIENS (HUMAN).//P06276

40 F-NT2RM4000796//5-METHYLCYTOSINE-SPECIFIC RESTRICTION ENZYME B (EC 3.1.21.-).//0.28:82:30//ESCHERICHIA COLI.//P15005

F-NT2RM4000798//PROTEIN TRANSPORT PROTEIN SEC7.//4.7e-38:165:48//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P11075

45 F-NT2RM4000813//METALLOTHIONEIN-IB.//0.0025:25:44//OVIS ARIES (SHEEP).//P09577

F-NT2RM4000820

F-NT2RM4000833//HYPOTHETICAL PROTEIN MJ1136.//6.5e-42:206:41//METHANOCOCCUS JANNASCHII.//Q58536

50 F-NT2RM4000848//BRAIN-SPECIFIC HOMEBOX/POU DOMAIN PROTEIN 3A (BRN-3A) (BRN-3.0).//0.00060:159:33//MUS MUSCULUS (MOUSE).//P17208

F-NT2RM4000852//SMALL PROLINE-RICH PROTEIN 2B (SPR-2B).//0.0076:13:69//HOMO SAPIENS (HUMAN).//P35325

F-NT2RM4000855/////ALU SUBFAMILY SQ WARNING ENTRY !!!!!//0.0060:68:44//HOMO SAPIENS (HUMAN).//P39194

55 F-NT2RM4000887//RTS1 PROTEIN (SCS1 PROTEIN).//0.23:153:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P11075

F-NT2RM4000895//HYPOTHETICAL 12.4 KD PROTEIN A PRECURSOR (INTERGEN. PROTEIN).//0.00011:73:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43123

F-NT2RM4000950//HYPOTHETICAL PROTEIN MJ0572//0.090:68:29//METHANOCOCCUS JANNASCHII//
 Q57992
 F-NT2RM4000971//KINESIN LIGHT CHAIN (KLC)//0.79:201:24//LOLIGO PEALEII (LONGFIN SQUID)//P46825
 F-NT2RM4000979//MYOSIN REGULATORY LIGHT CHAIN 2, NONSARCOMERIC (MYOSIN RLC)//1.2e-07:25:
 5 96//HOMO SAPIENS (HUMAN)//P19105
 F-NT2RM4000996//ZINC FINGER PROTEIN 37 (ZFP-37) (MALE GERM CELL SPECIFIC ZINC FINGER PRO-
 TEIN)//1.4e-56:253:46//MUS MUSCULUS (MOUSE)//P17141
 F-NT2RM4001002
 F-NT2RM4001016//GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12;
 10 CORE SHELL PROTEIN P30]//0.25:101:31//FBR MURINE OSTEOSARCOMA VIRUS//P29175
 F-NT2RM4001032//CUTICLE COLLAGEN 2//2.6e-07:130:39//CAENORHABDITIS ELEGANS//P17656
 F-NT2RM4001047//MO25 PROTEIN//5.6e-107:252:80//MUS MUSCULUS (MOUSE)//Q06138
 F-NT2RM4001054//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT//9.0e-109:209:94//CANIS FA-
 MILIARIS (DOG)//P38377
 15 F-NT2RM4001084//HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN UXUR-IADA INTERGENIC RE-
 GION//0.57:95:30//ESCHERICHIA COLI//P39376
 F-NT2RM4001092//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III//2.5e-47:231:47//
 CAENORHABDITIS ELEGANS//Q09531
 F-NT2RM4001116//HYPOTHETICAL 216.3 KD PROTEIN R06F6.8 IN CHROMOSOME II//1.3e-08:243:23//
 20 CAENORHABDITIS ELEGANS//Q09417
 F-NT2RM4001140//HOMEBOX PROTEIN MSH-D//7.1e-13:103:38//BRACHYDANIO RERIO (ZEBRAFISH)
 (ZEBRA DANIO)//Q01704
 F-NT2RM4001151//SYNAPSINS IA AND IB (BRAIN PROTEIN 4.1)//0.26:96:34//HOMO SAPIENS (HUMAN)//
 P17600
 25 F-NT2RM4001155//ADRENAL MEDULLA 50 KD PROTEIN//3.6e-103:201:91//BOS TAURUS (BOVINE)//
 Q27969
 F-NT2RM4001160//GLUTATHIONE S-TRANSFERASE (EC 2.5.1.18) (CLASS-PHI) (FRAGMENTS)//1.0:33:36//
 BRASSICA OLERACEA (CAULIFLOWER)//P48438 F-NT2RM4001187//PREPROTEIN TRANSLOCASE SECA
 SUBUNIT//0.44:158:27//MYCOPLASMA GENITALIUM//P47318
 30 F-NT2RM4001191//LONG NEUROTOXIN 2 (TOXIN C)//0.99:44:43//ASTROTIA STOKESI (STOKES'S SEA
 SNAKE) (DSTEIRA STOKESI)//P01381
 F-NT2RM4001200//ZINC FINGER PROTEIN 135//2.2e-82:245:59//HOMO SAPIENS (HUMAN)//P52742
 F-NT2RM4001203//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION//0.028:94:
 40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53214
 35 F-NT2RM4001204//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66)//0.0096:182:34//HOMO
 SAPIENS (HUMAN)//Q15428
 F-NT2RM4001217//RING CANAL PROTEIN (KELCH PROTEIN)//2.1e-21:221:29//DROSOPHILA MELA-
 NOGASTER (FRUIT FLY)//Q04652
 F-NT2RM4001256//CBP3 PROTEIN PRECURSOR//0.30:55:32//SACCHAROMYCES CEREVISIAE (BAKER'S
 40 YEAST)//P21560
 F-NT2RM4001258//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556//0.00031:132:39//STREP-
 TOMYCES FRADIAE//P20186
 F-NT2RM4001309//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CONTAINS: BASIC
 PEPTIDE P-F] (FRAGMENT)//0.048:132:28//HOMO SAPIENS (HUMAN)//P02812
 45 F-NT2RM4001313//PHOSPHATIDYLINOSITOL 3-KINASE VPS34-LIKE (EC 2.7.1.137) (PI3-KINASE) (PTDINS-
 3-KINASE) (PI3K)//2.6e-37:124:65//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD)//P54676
 F-NT2RM4001316//ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.3)
 (MCAD)//1.7e-10:185:30//RATTUS NORVEGICUS (RAT)//P08503
 F-NT2RM4001320//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-
 50 CIOGENITAL DYSPLASIA PROTEIN HOMOLOG)//1.5e-08:197:26//MUS MUSCULUS (MOUSE)//P52734
 F-NT2RM4001340//UTR4 PROTEIN (UNKNOWN TRANSCRIPT 4 PROTEIN)//7.7e-14:82:36//SACCHAROMY-
 CES CEREVISIAE (BAKER'S YEAST)//P32626
 F-NT2RM4001344//HYPOTHETICAL GTP-BINDING PROTEIN IN POP2-HOL1 INTERGENIC REGION//3.3e-
 16:128:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53742
 55 F-NT2RM4001347//HYPOTHETICAL 76.9 KD PROTEIN IN RPM2-TUB1 INTERGENIC REGION//0.067:111:30
 F-NT2RM4001351//HYPOTHETICAL 100.5 KD PROTEIN IN RPM2-TUB1 INTERGENIC REGION//0.067:111:30
 F-NT2RM4001382//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR//1.0e-08:82:39//PLASMODIUM FALCIPARUM

RAE//P04929

F-NT2RM4001384

F-NT2RM4001410//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR//2.1e-08:185:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32323

5 F-NT2RM4001411//EARLY NODULIN 20 PRECURSOR (N-20)//5.3e-05:105:38//MEDICAGO TRUNCATULA (BARREL MEDIC)//P93329

F-NT2RM4001412//GTPASE-ACTIVATING PROTEIN (GAP) (RAS P21 PROTEIN ACTIVATOR) (P120GAP) (RASGAP)//6.2e-17:109:41//RATTUS NORVEGICUS (RAT)//P50904

F-NT2RM4001414//ZINC FINGER PROTEIN 177//8.3e-06:54:50//HOMO SAPIENS (HUMAN)//Q13360

10 F-NT2RM4001437/////ALU SUBFAMILY SC WARNING ENTRY /////2.1e-24:87:65//HOMO SAPIENS (HUMAN)//P39192

F-NT2RM4001444//PROBABLE ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS) (FRAGMENT)//2.6e-45:197:47//CIONA INTESTINALIS//Q94425

15 F-NT2RM4001454//HYPOTHETICAL PROTEIN KIAA0041 (FRAGMENT)//0.0060:95:29//HOMO SAPIENS (HUMAN)//Q15057

F-NT2RM4001455//PROBABLE E5B PROTEIN//0.41:44:36//HUMAN PAPILLOMAVIRUS TYPE 6B//P06461

F-NT2RM4001483//ZINC FINGER PROTEIN 136//1.7e-28:85:64//HOMO SAPIENS (HUMAN)//P52737

F-NT2RM4001489//PTB-ASSOCIATED SPLICING FACTOR (PSF)//0.086:111:34//HOMO SAPIENS (HUMAN)//P23246

20 F-NT2RM4001519//ACID UREASE ALPHA SUBUNIT (EC 3.5.1.5) (UREA AMIDOHYDROLASE)//0.82:51:47//LACTOBACILLUS FERMENTUM//P26929

F-NT2RM4001522//TROPOMYOSIN//0.030:117:23//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q02088

F-NT2RM4001557

25 F-NT2RM4001565//HYPOTHETICAL 44.3 KD PROTEIN C1F7.07C IN CHROMOSOME I//0.99:42:40//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09919

F-NT2RM4001566//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)//0.054:190:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P08640

30 F-NT2RM4001569//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (ACTIVATED PROTEIN KINASE C RECEPTOR HOMOLOG)//0.72:64:31//TRYPANOSOMA BRUCEI BRUCEI//Q94775

F-NT2RM4001582

F-NT2RM4001592//DNA REPAIR PROTEIN RAD9//0.00037:198:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P14737

35 F-NT2RM4001594//IMMEDIATE-EARLY PROTEIN IE180//1.9e-05:147:34//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV)//P33479

F-NT2RM4001597//THIOL:DISULFIDE INTERCHANGE PROTEIN TLPA (CYTOCHROME C BIOGENESIS PROTEIN TLPA)//5.7e-06:122:29//BRADYRHIZOBIUM JAPONICUM//P43221

F-NT2RM4001605//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155) (155 KD NUCLEOPORIN) (P140)//1.7e-128:249:96//RATTUS NORVEGICUS (RAT)//P37199

40 F-NT2RM4001611//SIS2 PROTEIN (HALOTOLERANCE PROTEIN HAL3)//1.5e-35:128:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P36024

F-NT2RM4001629//MAGUK P55 SUBFAMILY MEMBER 3 (MPP3 PROTEIN) (DISCS, LARGE HOMOLOG 3)//5.8e-42:254:37//HOMO SAPIENS (HUMAN)//Q13368

45 F-NT2RM4001650//HOMEBOX PROTEIN HOX-A4 (CHOX-1.4)//0.62:19:57//GALLUS GALLUS (CHICKEN)//P17277

F-NT2RM4001662//PROTEIN KINASE C, ALPHA TYPE (EC 2.7.1.-) (PKC-ALPHA)//0.29:90:32//HOMO SAPIENS (HUMAN)//P17252

F-NT2RM4001666//HYPOTHETICAL 48.6 KD PROTEIN IN ALPA-GABP INTERGENIC REGION//1.1e-31:137:44//ESCHERICHIA COLI//P37339

50 F-NT2RM4001682//PROBABLE 60S RIBOSOMAL PROTEIN L22//0.98:55:29//CAENORHABDITIS ELEGANS//P52819

F-NT2RM4001710//HYPOTHETICAL PROTEIN KIAA0039 (FRAGMENT)//0.56:113:28//HOMO SAPIENS (HUMAN)//Q15054

55 F-NT2RM4001714//SEPTIN 2 HOMOLOG (FRAGMENT)//1.4e-108:255:77//HOMO SAPIENS (HUMAN)

F-NT2RM4001715//HYPOTHETICAL PROTEIN IN CHROMOSOME I//0.99:42:40//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09919

F-NT2RM4001716//HYPOTHETICAL PROTEIN IN CHROMOSOME I//0.99:42:40//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10342

F-NT2RM4001731//HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III.//1.1e-05:90:33//
 CAENORHABDITIS ELEGANS //P34284
 F-NT2RM4001741//TALIN.//1.1e-106:208:99//MUS MUSCULUS (MOUSE).//P26039
 F-NT2RM4001746//EBNA-1 NUCLEAR PROTEIN.//1.6e-09:155:38//EPSTEIN-BARR VIRUS (STRAIN B95-8)
 5 (HUMAN HERPESVIRUS 4).//P03211
 F-NT2RM4001754//COLLAGEN ALPHA 5(IV) CHAIN PRECURSOR.//0.93:158:33//HOMO SAPIENS (HUMAN).//
 P29400
 F-NT2RM4001758//PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).//5.1e-113:277:79//
 HOMO SAPIENS (HUMAN).//P27448
 10 F-NT2RM4001776//MYOSIN I ALPHA (MMI-ALPHA).//2.2e-73:262:54//MUS MUSCULUS (MOUSE).//P46735
 F-NT2RM4001783//ZINC FINGER PROTEIN HRX (ALL-1) (FRAGMENT).//5.3e-26:169:39//MUS MUSCULUS
 (MOUSE).//P55200
 F-NT2RM4001810//MALE SPECIFIC SPERM PROTEIN MST84DB.//2.3e-05:68:42//DROSOPHILA MELA-
 NOGASTER (FRUIT FLY).//Q01643
 15 F-NT2RM4001813//RHODOCETIN ALPHA SUBUNIT.//2.3e-05:115:34//AGKISTRODON RHODOSTOMA (MA-
 LAYAN PIT VIPER) (CALLOSELASMA RHODOSTOMA).//P81397
 F-NT2RM4001819//CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE RECEPTOR)
 (CELL SURFACE GLYCOPROTEIN F4/80).//1.7e-06:159:25//MUS MUSCULUS (MOUSE).//Q61549
 F-NT2RM4001823//ZINC FINGER PROTEIN ZIC1 (ZINC FINGER PROTEIN OF THE CEREBELLUM 1).//2.6e-
 20 18:114:40//MUS MUSCULUS (MOUSE).//P46684
 F-NT2RM4001828//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//4.0e-81:253:59//HOMO SA-
 PIENS (HUMAN).//P51523
 F-NT2RM4001836//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//0.21:176:30//NEPHILA CLA-
 VIPES (ORB SPIDER).//P46804
 25 F-NT2RM4001841//PROLINE-RICH PEPTIDE P-B.//0.046:27:40//HOMO SAPIENS (HUMAN).//P02814
 F-NT2RM4001842//HYPOTHETICAL 7.0 KD PROTEIN B03B8.1 IN CHROMOSOME III.//0.98:35:42//
 CAENORHABDITIS ELEGANS //Q11104
 F-NT2RM4001856//HYPOTHETICAL 75.2 KD PROTEIN IN ACS1-GCV3 INTERGENIC REGION.//2.3e-37:242:
 37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39722
 30 F-NT2RM4001858//T-BOX PROTEIN VEGT (T-BOX PROTEIN BRAT) (T-BOX PROTEIN ANTIPODEAN).//1.8e-
 23:78:64//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P87377
 F-NT2RM4001865//NEURONAL CALCIUM SENSOR 2 (NCS-2).//0.012:83:28//CAENORHABDITIS ELEGANS //
 P36609
 F-NT2RM4001876//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECUR-
 35 SOR.//3.8e-10:242:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47179
 F-NT2RM4001880//EC PROTEIN HOMOLOG.//0.22:59:32//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//
 P93746
 F-NT2RM4001905//60S RIBOSOMAL PROTEIN L40 (CEP52).//0.57:20:60//HOMO SAPIENS (HUMAN), RAT-
 TUS NORVEGICUS (RAT), AND GALLUS GALLUS (CHICKEN).//P14793
 40 F-NT2RM4001922
 F-NT2RM4001930//PUTATIVE GLUCOSYLTRANSFERASE C08B11.8 (EC 2.4.1.-).//5.5e-45:167:53//
 CAENORHABDITIS ELEGANS //Q09226
 F-NT2RM4001938//RTOA PROTEIN (RATIO-A).//0.0036:120:32//DICTYOSTELIUM DISCOIDEUM (SLIME
 MOLD).//P54681
 45 F-NT2RM4001940//IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-1 (FRAGMENT).//0.32:31:48//HOMO
 SAPIENS (HUMAN).//P78415
 F-NT2RM4001953//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//2.2e-43:56:85//HOMO SAPIENS (HUMAN).//
 P39192
 F-NT2RM4001965//IG ALPHA-1 CHAIN C REGION.//0.56:73:34//GORILLA GORILLA GORILLA (LOWLAND GO-
 50 RILLA).//P20758
 F-NT2RM4001969//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CON-
 TAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H].//0.0016:140:27//HOMO SAPIENS (HUMAN).//P04280
 F-NT2RM4001979//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.9e-21:103:51//HOMO SA-
 PIENS (HUMAN).//P51523
 55 F-NT2RM4001984//HYPOTHETICAL PROTEIN LAMBDA-SP5 //0 0034:50:40//MUS MUSCULUS (MOUSE) "
 F074
 F-NT2RM4001987//IRREGULAR PHASMID HIGHEST PROTEIN PRECURSOR - PRECURSOR PROTEIN -
 DROSOPHILA MELANOGASTER (FRUIT FLY).//Q08180

F-NT2RM4002301//GENERAL STRESS PROTEIN CTC (FRAGMENT)//0.56:43:39//BACILLUS CALDOLYTICUS./P42832
F-NT2RM4002323//NONHISTONE CHROMOSOMAL PROTEIN HMG-17//0.0080:73:35//BOS TAURUS (BOVINE)./P02313
F-NT2RM4002339//METALLOTHIONEIN 10-III (MT-10-III)//0.67:34:38//MYTILUS EDULIS (BLUE MUSSEL)./
P80248
F-NT2RM4002344//METALLOTHIONEIN-I (MT-I)//0.84:41:31//MUS MUSCULUS (MOUSE)/P02802
F-NT2RM4002373//GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT DY10 PRECURSOR//0.0019:190:28//
TRITICUM AESTIVUM (WHEAT)/P10387
F-NT2RM4002374//5E5 ANTIGEN//0.0059:170:32//RATTUS NORVEGICUS (RAT)/Q63003
F-NT2RM4002383/////ALU SUBFAMILY SP WARNING ENTRY !!!!!/0.13:17:88//HOMO SAPIENS (HUMAN)./
P39193
F-NT2RM4002390
F-NT2RM4002398//HNRP ARGinine N-METHYLTRANSFERASE (EC 2.1.1.-) (ODP1 PROTEIN)//0.034:110:
27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)/P38074
F-NT2RM4002409//ACETYL-COENZYM E A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- AC-
TIVATING ENZYME)//4.0e-20:179:31//METHANOTRIX SOEHNGENII/P27095
F-NT2RM4002438/////ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.7e-15:41:95//HOMO SAPIENS (HUMAN)./
P39194
F-NT2RM4002446//CRYPTIDIN-RELATED PROTEIN 4C-1 PRECURSOR (CRS4C)//0.0058:24:50//MUS MUS-
CULUS (MOUSE)/P17534
F-NT2RM4002452//METALLOTHIONEIN 10-II (MT-10-II)//0.83:48:37//MYTILUS EDULIS (BLUE MUSSEL)./
P80247
F-NT2RM4002457/////ALU SUBFAMILY SC WARNING ENTRY !!!!!/4.9e-07:52:63//HOMO SAPIENS (HUMAN)./
P39192
F-NT2RM4002460//C-HORDEIN (CLONE PC-919) (FRAGMENT)//0.92:43:30//HORDEUM VULGARE (BAR-
LEY)/P17992
F-NT2RM4002479//RNA HELICASE-LIKE PROTEIN DB10//1.7e-28:200:41//NICOTIANA SYLVESTRI (WOOD
TOBACCO)/P46942
F-NT2RM4002482//HYPOTHETICAL 65.9 KD PROTEIN YPR065W//8.8e-26:123:49//SACCHAROMYCES CER-
EVISIAE (BAKER'S YEAST)/Q12514 F-NT2RM4002493//LARVAL CUTICLE PROTEIN I PRECURSOR//0.17:
126:27//DROSOPHILA MIRANDA (FRUIT FL Y)/P91627
F-NT2RM4002499/////ALU SUBFAMILY SQ WARNING ENTRY !!!!!/9.4e-34:92:80//HOMO SAPIENS (HUMAN)./
P39194
F-NT2RM4002504/////ALU SUBFAMILY SB WARNING ENTRY !!!!!/3.4e-19:55:83//HOMO SAPIENS (HUMAN)./
P39189
F-NT2RM4002527//WD-40 REPEAT PROTEIN MSI2//3.0e-07:193:27//ARABIDOPSIS THALIANA (MOUSE-
EAR CRESS)/O22468
F-NT2RM4002532//AEROLYSIN REGULATORY PROTEIN//0.97:19:47//AEROMONAS SOBRIA/P09165
F-NT2RM4002534//MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L32 PRECURSOR (YML32)//0.76:86:22//
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)/P25348
F-NT2RM4002558//LONG-CHAIN FATTY ACID TRANSPORT PROTEIN (FATP)//4.2e-55:204:50//MUS MUSCU-
LUS (MOUSE)/Q60714
F-NT2RM4002565//CHYMOTRYPSIN/ELASTASE ISOINHIBITORS 2 TO 5//1.0:16:62//ASCARIS SUUM (PIG
ROUND WORM) (ASCARIS LUMBROIDES)/P07852
F-NT2RM4002567//HYPOTHETICAL 74.0 K D PROTEIN IN CAJ1-HOM3 INTERGENIC REGION//2.7e-10:184:
29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)/P40032
F-NT2RM4002571//POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-
UDP ACETYLGALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYLGALACTOS-
AMINYLTRANSFERASE) (GALNAC-T1)//2.4e-25:124:47//HOMO SAPIENS (HUMAN)/Q10472
F-NT2RM4002593//HYPOTHETICAL 9.1 K D PROTEIN IN TETB-EXOA INTERGENIC REGION//0.95:36:38//BA-
CILLUS SUBTILIS/P37509
F-NT2RM4002594//MSP1 PROTEIN HOMOLOG//9.0e-68:227:60//CAENORHABDITIS ELEGANS/P54815
F-NT2RM4002623//ASPARYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE) (ASPRS)//
3.3e-54:243:47//SYNECHOCYSTIS SP. (STRAIN PCC 6803) /P73851
F-NT2RM1000008 //SLIPDIKIN LIKE PROTEIN FROM DROSOPHILA MELANOGASTER.
FROM YEAST..P32583
F-NT2RM1000035//RING CANAL PROTEIN (KELCH PROTEIN)//1.0e-06:63:34//DROSOPHILA MFLA

NOGASTER (FRUIT FLY)//Q04652

F-NT2RP1000040//LETHAL NEUROTOXIN TX1//0.69:21:47//PHONEUTRIA NIGRIVENTER (BRAZILIAN ARMED SPIDER)//P17727

F-NT2RP1000063//HYPOTHETICAL 25.1 KD PROTEIN IN SMC3-MRPL8 INTERGENIC REGION//3.8e-14:130:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40359

F-NT2RP1000086//HYPOTHETICAL 9.4 KD PROTEIN IN RNPA-THDF INTERGENIC REGION//0.16:44:40//ESCHERICHIA COLI//P22847

F-NT2RP1000101//45.8 KD PROTEIN IN SHM1-MRPL37 INTERGENIC REGION//1.9e-06:74:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38344

F-NT2RP1000111//COP1 REGULATORY PROTEIN (FUSCA PROTEIN FUS1)//2.7e-19:135:36//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)//P43254

F-NT2RP1000112//DUAL SPECIFICITY PROTEIN KINASE TTK (EC 2.7.1.-) (PYT)//1.2e-39:91:62//HOMO SAPIENS (HUMAN)//P33981

F-NT2RP1000124//ATP-DEPENDENT PROTEASE LA 2 (EC 3.4.21.53)//0.074:131:24//MYXOCOCCUS XANTHUS//P36774

F-NT2RP1000130//HEPATOMA-DERIVED GROWTH FACTOR (HDGF)//1.5e-49:186:56//MUS MUSCULUS (MOUSE)//P51859

F-NT2RP1000163//METALLOTHIONEIN (MT)//0.98:41:34//PLEURONECTES PLATESSA (PLAICE)//P07216

F-NT2RP1000170//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT)//0.85:64:35//HOMO SAPIENS (HUMAN)//P10162

F-NT2RP1000174//IMMEDIATE-EARLY PROTEIN IE180//0.00056:89:37//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV)//P33479

F-NT2RP1000191//NIFU PROTEIN//0.53:78:35//FRANKIA ALNI//P40045

F-NT2RP1000202//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT)//9.1e-21:148:39//HOMO SAPIENS (HUMAN)//Q01485

F-NT2RP1000243//HYPOTHETICAL PROTEIN MJ1136//1.4e-37:219:36//METHANOCOCCUS JANNASCHII//Q58536

F-NT2RP1000259//HYPOTHETICAL PROTEIN TP0318//0.18:25:44//TREPONEMA PALLIDUM//O83338

F-NT2RP1000272//SPLICING FACTOR, ARGININE/SERINE-RICH 3 (PRE-MRNA SPLICING FACTOR SRP20) (X16 PROTEIN)//1.6e-18:133:36//HOMO SAPIENS (HUMAN), AND MUS MUSCULUS (MOUSE)//P23152

F-NT2RP1000324

F-NT2RP1000326//HYPOTHETICAL 29.8 KD PROTEIN ZC97.1 IN CHROMOSOME III//1.0e-23:129:36//CAENORHABDITIS ELEGANS//P34599

F-NT2RP1000333//ANTI-SILENCING PROTEIN 1//2.5e-45:147:57//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32447

F-NT2RP1000348//REDUCED VIABILITY UPON STARVATION PROTEIN 161//4.8e-14:119:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P25343

F-NT2RP1000357//TRYPOMASTIGOTE DECAY-ACCELERATING FACTOR (T-DAF) (FRAGMENT)//1.0:43:32//TRYPANOSOMA CRUZI//Q26327

F-NT2RP1000358//HYPOTHETICAL 84.4 KD PROTEIN IN RPC2/RET1 3'REGION//7.9e-28:244:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P39744

F-NT2RP1000363//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)//2.2e-07:178:30//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P17437

F-NT2RP1000376//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN)//1.5e-20:254:31//HOMO SAPIENS (HUMAN)//P16157

F-NT2RP1000409//CYTOCHROME C3 (CYTOCHROME C7) (C551.5)//1.0:34:26//DESULFUROMONAS ACETOXIDANS (CHLOROPSEUDOMONAS ETHYLICA)//P00137

F-NT2RP1000413//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (NAP1 PROTEIN)//3.7e-131:230:97//RATTUS NORVEGICUS (RAT)//P55161

F-NT2RP1000416//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR//0.83:54:40//DROSOPHILA SIMULANS (FRUIT FLY)//P13729

F-NT2RP1000418//HYPOTHETICAL 9.9 KD PROTEIN IN GCVT-SPOIIIAA INTERGENIC REGION//0.24:91:35//BACILLUS SUBTILIS//P49779

F-NT2RP1000439//HYPOTHETICAL 100.5 KD PROTEIN C1B9.04 IN CHROMOSOME I//0.13:172:22//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10429

F-NT2RP1000443//CRYSTALLIN 1//1.9e-08:167:24//HOMO SAPIENS (HUMAN)//Q08251

F-NT2RP1000460//NUCLEAR MOVEMENT PROTEIN NUDC//1.0e-18:149:34//EMERICELLA NIDULANS (AS

PERGILLUS NIDULANS).//P17624

F-NT2RP1000470//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III//1.3e-43:180:47//CAENORHABDITIS ELEGANS//P34580

F-NT2RP1000478//TUBULIN BETA-6 CHAIN (CLASS-VI).//1.5e-45:85:63//GALLUS GALLUS (CHICKEN).//P09207

F-NT2RP1000481//HYPOTHETICAL 5.8 KD PROTEIN IN PUHA 5'REGION (ORF55).//0.083:21:47//RHODOBACTER CAPSULATUS (RHODOPSEUDOMONAS CAPSULATA).//P26159

F-NT2RP1000493//POSSIBLE DNA-REPAIR PROTEIN XP-E (POSSIBLE XERODERMA PIGMENTOSUM GROUP E PROTEIN) (UV-DAMAGED DNA-BINDING PROTEIN) (UV-DDB).//6.6e-11:139:31//CERCOPITHECUS AETHIOPS (GREEN MONKEY) (GRIVET).//P33194

F-NT2RP1000513//60S RIBOSOMAL PROTEIN L22.//0.017:92:30//DROSOPHILA MELANOGASTER (FRUIT FLY).//P50887

F-NT2RP1000522//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1).//0.0055:86:36//MUS MUSCULUS (MOUSE).//Q61068

F-NT2RP1000547//COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).//1.2e-09:69:36//CRICETULUS GRISEUS (CHINESE HAMSTER).//P49020

F-NT2RP1000574//HOMEBOX PROTEIN MEIS2 (MEIS1-RELATED PROTEIN 1).//6.0e-39:141:65//MUS MUSCULUS (MOUSE).//P97367

F-NT2RP1000577//PUTATIVE ATP-DEPENDENT RNA HELICASE YDL031W.//0.00016:48:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12389

F-NT2RP1000581//VON WILLEBRAND FACTOR PRECURSOR.//0.00017:61:50//HOMO SAPIENS (HUMAN).//P04275

F-NT2RP1000609//LINOLEOYL-COA DESATURASE (EC 1.14.99.25) (DELTA(6)-DESATURASE).//4.4e-07:128:31//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//Q08871

F-NT2RP1000629//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN).//4.2e-70:167:86//MUS MUSCULUS (MOUSE).//P35585

F-NT2RP1000630//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR.//0.0011:238:21//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47179

F-NT2RP1000677//COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR.//0.99:71:33//HOMO SAPIENS (HUMAN).//Q07092

F-NT2RP1000688//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//0.0024:19:94//HOMO SAPIENS (HUMAN).//P39193

F-NT2RP1000695//HYPOTHETICAL 83.8 KD PROTEIN C27F2.7 IN CHROMOSOME III.//2.2e-30:185:37//CAENORHABDITIS ELEGANS.//Q18262

F-NT2RP1000701//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP).//3.2e-65:128:93//RATTUS NORVEGICUS (RAT).//P54319

F-NT2RP1000721//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).//2.3e-06:139:34//HOMO SAPIENS (HUMAN).//O00268

F-NT2RP1000730//MYOSIN LIGHT CHAIN 1, SLOW-TWITCH MUSCLE B/VENTRICULAR ISOFORM (FRAGMENT).//0.89:40:40//MUS MUSCULUS (MOUSE).//P09542

F-NT2RP1000733//METALLOTHIONEIN-LIKE PROTEIN CRS5.//0.024:24:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P41902

F-NT2RP1000738//SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1 / PRP-3) (PRP-2 / PRP-4) (PIF-F / PIF-S) (PROTEIN A / PROTEIN C) [CONTAINS: PEPTIDE P-C].//0.040:82:36//HOMO SAPIENS (HUMAN).//P02810

F-NT2RP1000746//HYPOTHETICAL 27.1 KD PROTEIN UFD4-CAP1 INTERGENIC REGION.//2.0e-30:170:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33201

F-NT2RP1000767//PSEUDOMONAS PEPSIN PRECURSOR (EC 3.4.23.37) (PEPSTATIN-INSENSITIVE CARBOXYL PROTEINASE).//0.99:75:34//PSEUDOMONAS SP. (STRAIN 101).//P42790

F-NT2RP1000782//CELL SURFACE GLYCOPROTEIN A15 (T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA ASSOCIATED ANTIGEN 1) (TALLA-1) (MEMBRANE COMPONENT, X CHROMOSOME, SURFACE MARKER 1).//2.3e-23:159:35//HOMO SAPIENS (HUMAN).//P41732

F-NT2RP1000796//CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUAMOUS CELL MARKER, SPRP).//3.1e-37:89:64//HOMO SAPIENS (HUMAN).//P04275

F-NT2RP1000825//GTPASE-ACTIVATING PROTEIN RHOGAP (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR, RHO42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//3.1e-37:89:64//HOMO SAPIENS (HUMAN).//P04275

MAN)//Q07960

F-NT2RP1000833//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930)//0.32:29:48//HOMO SAPIENS (HUMAN)//P22531

F-NT2RP1000834//2-ARYLPROPIONYL-COA EPIMERASE (EC 5.-.-.-)//6.4e-67:202:68//RATTUS NORVEGICUS (RAT)//P70473

F-NT2RP1000836//HYPOTHETICAL 7.3 KD PROTEIN IN 100 KD PROTEIN REGION//1.0:35:54//HUMAN ADENOVIRUS TYPE 41//P23691

F-NT2RP1000846//SMALL PROLINE-RICH PROTEIN 2-1//0.013:35:48//HOMO SAPIENS (HUMAN)//P35326

F-NT2RP1000851//PERIOD CLOCK PROTEIN (FRAGMENT)//0.082:28:57//DROSOPHILA SALTANS (FRUIT FLY)//Q04536

F-NT2RP1000856//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN)//2.5e-26:190:30//MUS MUSCULUS (MOUSE)//O35566

F-NT2RP1000860//POTENTIAL TRANSCRIPTIONAL ADAPTOR//0.13:86:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q02336

F-NT2RP1000902//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III//7.6e-11:200:35//CAENORHABDITIS ELEGANS//Q09531

F-NT2RP1000915//HYPOTHETICAL GTP-BINDING PROTEIN IN PMI40-PAC2 INTERGENIC REGION//1.4e-06:88:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40010

F-NT2RP1000916//SUPPRESSOR PROTEIN SRP40//0.40:90:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32583

F-NT2RP1000943//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)//0.099:75:34//HOMO SAPIENS (HUMAN)//Q02817

F-NT2RP1000944//HYPOTHETICAL 29.3 KD PROTEIN (ORF92) //7.6e-06:65:41//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV)//O10341

F-NT2RP1000947//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2)//3.6e-12:27:77//HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), RATTUS NORVEGICUS (RAT), AND XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P51669

F-NT2RP1000954//RING CANAL PROTEIN (KELCH PROTEIN)//2.8e-15:169:28//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q04652

F-NT2RP1000958//HYPOTHETICAL GTP-BINDING PROTEIN IN PMI40-PAC2 INTERGENIC REGION//4.2e-16:162:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40010

F-NT2RP1000959//CORNIFIN A (SMALL PROLINE-RICH PROTEIN IA) (SPR-IA) (SPRK)//0.0031:34:44//HOMO SAPIENS (HUMAN)//P35321

F-NT2RP1000966//NUCLEOLIN (PROTEIN C23)//1.5e-52:110:95//HOMO SAPIENS (HUMAN)//P19338

F-NT2RP1000980//LIGHT-HARVESTING PROTEIN B-1015, ALPHA CHAIN PRECURSOR (ANTENNA PIGMENT PROTEIN, ALPHA CHAIN)//0.87:37:45//RHODOPSEUDOMONAS VIRIDIS//P04123

F-NT2RP1000988

F-NT2RP1001011//PROTEIN P19//0.96:30:50//BACTERIOPHAGE PRD1//P17638

F-NT2RP1001013//DNA-BINDING PROTEIN 65 (PROTEIN GP65)//1.0:20:45//BACTERIOPHAGE T4//P16012

F-NT2RP1001014

F-NT2RP1001033//TUBULIN GAMMA CHAIN//2.5e-16:112:42//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//P25295

F-NT2RP1001073//HYPOTHETICAL 10.4 KD PROTEIN IN FTR1-SPT15 INTERGENIC REGION//7.6e-16:82:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40089

F-NT2RP1001079//SARCOSINE OXIDASE (EC 1.5.3.1)//4.8e-15:95:40//ARTHROBACTER SP. (STRAIN TE1826)//P40873

F-NT2RP1001080//PROBABLE ATP-DEPENDENT RNA HELICASE DBP9//2.4e-29:126:46//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q06218

F-NT2RP1001113//SMALL PROLINE-RICH PROTEIN 2-1//0.49:38:39//HOMO SAPIENS (HUMAN)//P35326

F-NT2RP1001173//RHOMBOTIN-1 (CYSTEINE RICH PROTEIN TTG-1) (T-CELL TRANSLOCATION PROTEIN 1) (LIM-ONLY PROTEIN 1)//0.99:54:37//HOMO SAPIENS (HUMAN)//P25800

F-NT2RP1001177//HISTONE MACRO-H2A.1//1.6e-29:85:76//RATTUS NORVEGICUS (RAT)//Q02874

F-NT2RP1001185

F-NT2RP1001199//NEUROTOXIN 1//1.0:23:47//CENTRUROIDES SCULPTURATUS (BARK SCORPION)

F-NT2RP1001247//TRANSFORMING GROWTH FACTOR BETA 4 PRECURSOR (TGF-BETA 4) (TGF-BETA 4 BLEEDING-ASSOCIATED FACTOR)//3.3e-08:28:89//HOMO SAPIENS (HUMAN)//O00292

F-NT2RP1001248//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN)//0.33:49:28//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE) (HIV-1)//P18804

F-NT2RP1001253//GLUCOSAMINE-6-PHOSPHATE ISOMERASE (EC 5.3.1.10) (GLUCOSAMINE-6-PHOSPHATE DEAMINASE) (GNPDA) (OSCILLIN) (KIAA0060)//3.8e-46:115:81//HOMO SAPIENS (HUMAN)//P46926

5 F-NT2RP1001286//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-34 GALACTOSIDE-BINDING LECTIN)//0.16:48:37//MUS MUSCULUS (MOUSE)//P16110

F-NT2RP1001294//MICROTUBULE-ASSOCIATED PROTEIN YTM1//6.1e-05:92:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q12024

10 F-NT2RP1001302//MICROTUBULE-ASSOCIATED PROTEIN YTM1//1.2e-05:92:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q12024

F-NT2RP1001310//PROBABLE E4 PROTEIN//0.99:109:26//HUMAN PAPILLOMAVIRUS TYPE 5//P06924

F-NT2RP1001311//SODIUM/HYDROGEN EXCHANGER 5 (NA(+)/H(+) EXCHANGER 5) (NHE-5) (FRAGMENT)//0.99:94:31//HOMO SAPIENS (HUMAN)//Q14940

15 F-NT2RP1001313//CYTOCHROME B5//9.0e-13:92:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40312

F-NT2RP1001361//NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-B14.5B) (CI-B14.5B)//1.2e-47:117:74//BOS TAURUS (BOVINE)//Q02827

F-NT2RP1001385//CELL DIVISION PROTEIN FTSN//0.64:107:28//ESCHERICHIA COLI//P29131

20 F-NT2RP1001395//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (FRAGMENTS)//0.25:35:45//GALLUS GALLUS (CHICKEN)//P02467

F-NT2RP1001410//PUTATIVE GTP-BINDING PROTEIN W08E3.3//2.2e-41:129:67//CAENORHABDITIS ELEGANS//P91917

F-NT2RP1001424//UREASE ACCESSORY PROTEIN UREF (FRAGMENT)//0.87:24:45//ESCHERICHIA COLI//Q03286

25 F-NT2RP1001432//CYSTEINE PROTEINASE INHIBITOR B (CYSTATIN B) (SCB)//1.0:35:42//HELIANTHUS ANNUUS (COMMON SUNFLOWER)//Q10993

F-NT2RP1001449//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN)//0.053:37:37//OVIS ARIES (SHEEP)//P26372

30 F-NT2RP1001457//HYPOTHETICAL 57.0 KD TRP-ASP REPEATS CONTAINING PROTEIN IN CPR4-SSK22 INTERGENIC REGION//2.9e-16:159:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P25382

F-NT2RP1001466//HYPOTHETICAL PROTEIN MJ0284//5.3e-15:162:35//METHANOCOCCUS JANNASCHII//Q57732

F-NT2RP1001475//HYPOTHETICAL 195.1 KD PROTEIN IN DNA43-UBI1 INTERGENIC REGION//0.69:119:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40457

35 F-NT2RP1001482//PROTEASOME COMPONENT C9 (EC 3.4.99.46) (MACROPAIN SUBUNIT C9) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C9)//1.0:58:32//HOMO SAPIENS (HUMAN)//P25789

F-NT2RP1001494//MALE STERILITY PROTEIN 2//2.4e-12:84:42//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)//Q08891

40 F-NT2RP1001543//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS)//6.3e-37:94:52//SPIRODELA POLYRRHIZA//P42803

F-NT2RP1001546//LEUKOCYTE SURFACE ANTIGEN CD53 (CELL SURFACE GLYCOPROTEIN CD53)//9.3e-11:98:29//HOMO SAPIENS (HUMAN)//P19397

F-NT2RP1001569//SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BETA)//2.2e-64:159:84//MUS MUSCULUS (MOUSE)//P47758

45 F-NT2RP1001616//HYPOTHETICAL 13.5 KD PROTEIN C45G9.7 IN CHROMOSOME III//9.2e-05:49:42//CAENORHABDITIS ELEGANS//Q09506

F-NT2RP1001665//REGB PROTEIN//0.99:29:37//PSEUDOMONAS AERUGINOSA//Q03381

F-NT2RP2000001//SMALL PROLINE-RICH PROTEIN 2-1//0.64:36:41//HOMO SAPIENS (HUMAN)//P35326

50 F-NT2RP2000006//DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HEAT SHOCK PROTEIN 40) (HSP40)//1.7e-19:74:52//HOMO SAPIENS (HUMAN)//P25685

F-NT2RP2000007//TROPOMYOSIN, FIBROBLAST AND EPITHELIAL MUSCLE-TYPE (TM36) (TME1) (TM1)//0.93:126:23//HOMO SAPIENS (HUMAN)//P06468

F-NT2RP2000008//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065) (HA0946) (FRAGMENT)//4.2e-35:156:54//HOMO SAPIENS (HUMAN)//Q06730

55 F-NT2RP2000031//MACACA FASCIOCLARIS (FRUG-EATING MACAQUE) (CYNOMOLGUS MONKEY)//P50665

F-NT2RP2000032//BAX PROTEIN (CYTOPLASMIC ISOFORM GAMMA)//1.0:35:34//HOMO SAPIENS (HUMAN)//P40312

MAN)//Q07815

F-NT2RP2000040//BASIC PROLINE-RICH PEPTIDE IB-1//0.0024:58:36//HOMO SAPIENS (HUMAN)//P04281

F-NT2RP2000045//DNAJ PROTEIN//1.1e-12:42:66//THERMUS AQUATICUS (SUBSP. THERMOPHILUS)//Q56237

5 F-NT2RP2000054//GONADOLIBERIN III PRECURSOR (GONADOTROPIN-RELEASING HORMONE III) (GN-RH-III) (LH-RH III) (LULIBERIN III)//0.20:46:36//ONCORHYNCHUS MASOU (CHERRY SALMON) (MASU SALMON)//P30973

F-NT2RP2000056//PROTEIN-TYROSINE PHOSPHATASE EPSILON PRECURSOR (EC 3.1.3.48) (R-PTP- EP-SILON)//1.3e-18:45:100//MUS MUSCULUS (MOUSE)//P49446

10 F-NT2RP2000067//HOMEBOX PROTEIN HOX-A5 (S12-B) (FRAGMENT)//0.71:44:40//SALMO SALAR (ATLANTIC SALMON)//P09637

F-NT2RP2000070//INSULIN//0.94:30:43//HYSTRIX CRISTATA (CRESTED PORCUPINE)//P01328

F-NT2RP2000076//ETS-LIKE PROTEIN POINTED P1 (D-ETS-2)//0.0013:76:40//DROSOPHILA MELANOGASTER (FRUIT FLY)//P51022

15 F-NT2RP2000077//U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C (U1-C)//0.24:49:40//HOMO SAPIENS (HUMAN)//P09234

F-NT2RP2000079//PLATELET FACTOR 4 (PF-4)//0.15:52:30//SUS SCROFA (PIG)//P30034

F-NT2RP2000088//HYPOTHETICAL 13.6 KD PROTEIN IN SPT4-ROM1 INTERGENIC REGION//1.0:36:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53245

20 F-NT2RP2000091//HYPOTHETICAL PROTEIN HI0149 PRECURSOR//0.22:38:47//HAEMOPHILUS INFLUENZAE//P43953

F-NT2RP2000097//VIRUS ATTACHMENT PROTEIN (O61R)//0.75:33:36//AFRICAN SWINE FEVER VIRUS (STRAIN BA71V) (ASFV)//P32510

F-NT2RP2000098

25 F-NT2RP2000108//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.4e-09:50:70//HOMO SAPIENS (HUMAN)//P39195

F-NT2RP2000114//WISKOTT-ALDRICH SYNDROME PROTEIN (WASP)//0.024:52:44//HOMO SAPIENS (HUMAN)//P42768

F-NT2RP2000120//5.8 KD PROTEIN IN HMC OPERON (ORF 4)//0.67:37:32//DESULFOVIBRIO VULGARIS (STRAIN HILDENBOROUGH)//P33391

30 F-NT2RP2000126//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1)//1.5e-23:94:47//HOMO SAPIENS (HUMAN)//O14646

F-NT2RP2000133//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53)//5.6e-10:82:39//HOMO SAPIENS (HUMAN)//Q15427

35 F-NT2RP2000147//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN)//6.7e-89:96:98//MUS MUSCULUS (MOUSE)//P35585

F-NT2RP2000153//PEPTIDYLPROLYL ISOMERASE CYP-1 (EC 5.2.1.8) (PEPTIDYLPROLYL CIS-TRANS ISOMERASE) (CYCLOPHILIN) (PPIASE)//1.7e-05:136:33//BRUGIA MALAYI//Q27450

40 F-NT2RP2000157//MLO2 PROTEIN//2.7e-06:62:40//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09329

F-NT2RP2000161//DIS3 PROTEIN HOMOLOG//2.7e-33:173:45//CAENORHABDITIS ELEGANS//Q17632

F-NT2RP2000173//HYPOTHETICAL 10.5 KD PROTEIN IN SODA-COMGA INTERGENIC REGION//0.99:62:25//BACILLUS SUBTILIS//P54499

45 F-NT2RP2000175//MALE SPECIFIC SPERM PROTEIN MST84DB//0.19:41:43//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q01643

F-NT2RP2000183//DIHYDROPYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (NEURAL SPECIFIC PROTEIN NSP60)//4.1e-19:114:44//BOS TAURUS (BOVINE)//O02675

F-NT2RP2000195//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//0.99:30:33//MICROTUS PENNSYLVANICUS (MEADOW VOLE)//P24949

50 F-NT2RP2000205//MERCURIC TRANSPORT PROTEIN PERIPLASMIC COMPONENT PRECURSOR (PERIPLASMIC MERCURY ION BINDING PROTEIN) (MERCURY SCAVENGER PROTEIN)//0.098:88:25//SHEWANELLA PUTREFACIENS (PSEUDOMONAS PUTREFACIENS)//Q54463

F-NT2RP2000208//MALE SPECIFIC SPERM PROTEIN MST84DD//0.020:19:57//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q01645

55 F-NT2RP2000224//HYPOTHETICAL PROTEIN IN SPT4-ROM1 INTERGENIC REGION//1.0:36:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53245

F-NT2RP2000232//P55-C-FOS PROTO-ONCOGENE PROTEIN (FRAGMENT)//1.0:44:38//OVIS ARIES

(SHEEP)//O02761

F-NT2RP2000233//GASTRIN/CHOLECYSTOKININ TYPE B RECEPTOR (CCK-B RECEPTOR) (CCK-BR)//0.34:53:43//CANIS FAMILIARIS (DOG)//P30552

F-NT2RP2000239//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT)//0.019:69:33//RATTUS NORVEGICUS (RAT)//P10164

F-NT2RP2000248//OVOMUCOID (FRAGMENT)//0.88:18:55//POLYPLECTRON EMPHANUM (PALAWAN PEACOCK-PHEASANT)//P52250

F-NT2RP2000257//PUTATIVE MITOCHONDRIAL CARRIER YIL006W//6.4e-09:83:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40556

F-NT2RP2000258//MYOSIN II HEAVY CHAIN, NON MUSCLE//0.081:217:28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD)//P08799

F-NT2RP2000270//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.4e-17:80:57//HOMO SAPIENS (HUMAN)//P39188

F-NT2RP2000274//HYPOTHETICAL 5.8 KD PROTEIN//0.082:22:45//CLOVER YELLOW MOSAIC VIRUS (CYMV)//P16485

F-NT2RP2000283//HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III//0.39:38:34//CAENORHABDITIS ELEGANS//P34535

F-NT2RP2000288

F-NT2RP2000289//HYPOTHETICAL 9.4 KD PROTEIN IN RNPA-THDF INTERGENIC REGION//0.40:38:42//ESCHERICHIA COLI//P22847

F-NT2RP2000297//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1)//2.3e-62:206:47//HOMO SAPIENS (HUMAN)//Q03923

F-NT2RP2000298//CUTICLE COLLAGEN 12 PRECURSOR//0.55:81:40//CAENORHABDITIS ELEGANS//P20630

F-NT2RP2000310//RUBREDOXIN (RD)//0.13:43:41//TREPONEMA PALLIDUM//O83956

F-NT2RP2000327//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//1.0:46:30//GADUS MORHUA (ATLANTIC COD)//P15996

F-NT2RP2000328//HYPOTHETICAL 86.6 KD PROTEIN IN PFK1-TDS4 INTERGENIC REGION//2.0e-21:198:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53313

F-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3)//1.8e-91:155:92//BOS TAURUS (BOVINE)//P08760

F-NT2RP2000337//PROTEIN A54//0.75:48:35//VACCINIA VIRUS (STRAIN WR), AND VACCINIA VIRUS (STRAIN COPENHAGEN)//P21072

F-NT2RP2000346//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116//9.7e-13:114:42//MUS MUSCULUS (MOUSE)//P17564

F-NT2RP2000369//CALTRIN (CALCIUM TRANSPORT INHIBITOR)//0.98:47:34//MUS MUSCULUS (MOUSE)//Q09098

F-NT2RP2000412//SHORT NEUROTOXIN D PRECURSOR//0.66:57:36//AIPYSURUS LAEVIS (OLIVE SEA SNAKE)//P19960

F-NT2RP2000414//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN F (HNRNP F)//1.0e-27:96:67//HOMO SAPIENS (HUMAN)//P52597

F-NT2RP2000420//ZINC FINGER PROTEIN 191//0.16:47:38//HOMO SAPIENS (HUMAN)//O14754

F-NT2RP2000422//PUTATIVE PHOSPHOACETYLGLUCOSAMINE MUTASE (EC 5.4.2.3) (ACETYLGLUCOSAMINE PHOSPHOMUTASE) (N-ACETYLGLUCOSAMINE-PHOSPHATE MUTASE)//3.6e-19:148:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09687

F-NT2RP2000438//TUBULIN GAMMA CHAIN//0.86:190:27//RETICULOMYXA FILOSA//P54405

F-NT2RP2000448//OXYSTEROL-BINDING PROTEIN//3.7e-13:140:42//HOMO SAPIENS (HUMAN)//P22059

F-NT2RP2000459//NEURONAL PROTEIN 3.1 (P311 PROTEIN)//1.0:45:35//HOMO SAPIENS (HUMAN)//Q16612

F-NT2RP2000498//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/0.062:25:68//HOMO SAPIENS (HUMAN)//P39194

F-NT2RP2000503

F-NT2RP2000510//TOXIN IV-5//1.0:51:33//TITYUS BAHIIENSIS (BRAZILIAN SCORPION)//P56608

F-NT2RP2000516//SLYX PROTEIN//1.0:52:32//ESCHERICHIA COLI//P30857

F-NT2RP2000523//PHORBOLIN I (FRAGMENTS)//1.4e-06:36:47//HOMO-SAPIENS (HUMAN) //P31941

F-NT2RP2000603//ALPHA-BLUBERIN//1.0:52:32//ESCHERICHIA COLI//P30857

F-NT2RP2000604//WHEAT//P0447

F-NT2RP2000617//SPERM-PROTAMINE//1.0:56:16:62//OVIS ARIES

(SHEEP), AND CAPRA HIRCUS (GOAT).//P04102

F-NT2RP2000634//NEDD-4 PROTEIN (EC 6.3.2.-) (KIAA0093) (FRAGMENT).//1.8e-05:128:28//HOMO SAPIENS (HUMAN).//P46934

F-NT2RP2000644//HYPOTHETICAL PROTEIN HI1566 PRECURSOR.//0.85:48:39//HAEMOPHILUS INFLUENZAE.//P44257

F-NT2RP2000656//EARLY GROWTH RESPONSE PROTEIN 1 (EGR-1) (NERVE GROWTH FACTOR-INDUCED PROTEIN A) (NGFI-A).//1.0:111:24//RATTUS NORVEGICUS (RAT).//P08154

F-NT2RP2000658//URONATE ISOMERASE (EC 5.3.1.12) (GLUCURONATE ISOMERASE) (URONIC ISOMERASE).//0.49:79:31//ESCHERICHIA COLI.//P42607

F-NT2RP2000668//MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2) (45 KD MEROZOITE SURFACE ANTIGEN).//0.020:115:30//PLASMODIUM FALCIPARUM (ISOLATE 3D7).//P50498

F-NT2RP2000678//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.00085:38:68//HOMO SAPIENS (HUMAN).//P39188

F-NT2RP2000704//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.2e-17:55:74//HOMO SAPIENS (HUMAN).//P39188

F-NT2RP2000710//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE) (ASPRS).//8.9e-47:106:59//TREPONEMA PALLIDUM.//O83950

F-NT2RP2000715

F-NT2RP2000731//CONIDIATION-SPECIFIC PROTEIN 10.//0.094:31:41//NEUROSPORA CRASSA.//P10713

F-NT2RP2000758//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.00027:31:74//HOMO SAPIENS (HUMAN).//P39188

F-NT2RP2000764//NIFS PROTEIN.//2.7e-27:175:47//ANABAENA SP. (STRAIN PCC 7120).//P12623

F-NT2RP2000809//HYPOTHETICAL PROTEIN MG381 HOMOLOG.//0.91:85:25//MYCOPLASMA PNEUMONIAE.//P75219

F-NT2RP2000812//DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN 5A).//2.8e-07:133:31//MUS MUSCULUS (MOUSE).//Q99104

F-NT2RP2000814//40S RIBOSOMAL PROTEIN S27A.//0.93:44:38//LYCOPERSICON ESCULENTUM (TOMATO), AND SOLANUM TUBEROSUM (POTATO).//P27083

F-NT2RP2000816//HYPOTHETICAL 88.4 KD PROTEIN B0464.7 IN CHROMOSOME III.//3.3e-21:123:39//CAENORHABDITIS ELEGANS.//Q03565

F-NT2RP2000819//TROPOMYOSIN 5, CYTOSKELETAL TYPE.//1.0:71:30//MUS MUSCULUS (MOUSE).//P21107

F-NT2RP2000841//GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP).//0.0011:133:26//MUS MUSCULUS (MOUSE).//P27671

F-NT2RP2000842//LYSOPHOSPHATIDIC ACID RECEPTOR (EDG-2).//6.4e-13:22:95//HOMO SAPIENS (HUMAN).//Q92633

F-NT2RP2000845//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR (MSTI).//0.92:24:41//MEDICAGO SCUTELLATA (SNAIL MEDIC).//P80321

F-NT2RP2000863//N-MYC PROTO-ONCOGENE PROTEIN.//0.010:148:27//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P24793

F-NT2RP2000880//PROBABLE TRANSLATION INITIATION FACTOR IF-2.//4.0e-100:199:94//HOMO SAPIENS (HUMAN).//O60841

F-NT2RP2000892//PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS: CHONDROCALCIN].//0.43:45:44//MUS MUSCULUS (MOUSE).//P28481

F-NT2RP2000931//MATRIIN 3.//2.8e-46:104:92//RATTUS NORVEGICUS (RAT).//P43244

F-NT2RP2000932//2-5A-DEPENDENT RIBONUCLEASE (EC 3.1.26.-) (2-5A-DEPENDENT RNAASE) (RNASE L) (RIBONUCLEASE 4) (FRAGMENT).//3.9e-07:113:31//MUS MUSCULUS (MOUSE).//Q05921

F-NT2RP2000938//VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID).//0.026:59:45//RATTUS NORVEGICUS (RAT).//Q01956

F-NT2RP2000943//HYPOTHETICAL PROTEIN KIAA0079 (HA3543).//5.9e-18:161:42//HOMO SAPIENS (HUMAN).//P53992

F-NT2RP2000965//INNER CENTROMERE PROTEIN (INCENP).//0.062:156:25//GALLUS GALLUS (CHICKEN).//P53352

F-NT2RP2000970//EC PROTEIN HOMOLOG.//1.0:50:30//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P93746

F-NT2RP2000981

F-NT2RP2000982//HYPOTHETICAL PROTEIN KIAA0079 (HA3543).//5.9e-18:161:42//HOMO SAPIENS (HUMAN).//P53992

F-NT2RP2000983//INSECT TOXIN 4 (INSECT TOXIN AAH (T4)).//1.0:32:34//ANDROCTONUS AUSTRALIS (HONEYBEE).//P53352

- TOR (SAHARA SCORPION)//P21150
F-NT2RP2001036//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.2e-33:65:81//HOMO SAPIENS (HUMAN)//P39193
- 5 F-NT2RP2001044//HIRUSTASIN//0.97:15:66//HIRUDO MEDICINALIS (MEDICINAL LEECH)//P80302
F-NT2RP2001056//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.0e-24:85:65//HOMO SAPIENS (HUMAN)//P39194
F-NT2RP2001065//BOWMAN-BIRK TYPE SEED TRYPSIN AND CHYMOTRYPSIN INHIBITOR (BTCI)//0.41:50:32//VIGNA UNGUICULATA (COWPEA)//P17734
- 10 F-NT2RP2001070//PROBABLE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (EC 1.4.3.5) (PNP/PMP OXIDASE) (FPRA PROTEIN)//6.2e-18:64:48//MYXOCOCCUS XANTHUS//P21159
F-NT2RP2001081//SYNAPTOTAGMIN IV//7.8e-16:94:46//RATTUS NORVEGICUS (RAT)//P50232
F-NT2RP2001094//METALLOTHIONEIN-I (MT-I)//1.0:24:33//RATTUS NORVEGICUS (RAT)//P02803
F-NT2RP2001119//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/7.5e-11:61:63//HOMO SAPIENS (HUMAN)//P39195
- 15 F-NT2RP2001127//XE169 PROTEIN (SMCX PROTEIN) (FRAGMENTS)//1.0e-47:155:58//MUS MUSCULUS (MOUSE)//P41230
F-NT2RP2001137//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS)//0.10:68:39//BOS TAURUS (BOVINE)//P25508
F-NT2RP2001149//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.1e-13:81:59//HOMO SAPIENS (HUMAN)//P39188
- 20 F-NT2RP2001168//PROTEIN KINASE C SUBSTRATE 80 KD PROTEIN (FRAGMENTS)//0.0071:77:33//RATTUS NORVEGICUS (RAT)//P20468
F-NT2RP2001173//CYTOSKELETON-ASSOCIATED PROTEIN CKAPI (TUBULIN FOLDING COFACTOR B)//1.0:36:41//HOMO SAPIENS (HUMAN)//Q99426
- 25 F-NT2RP2001174//ZINC FINGER PROTEIN 137//7.2e-11:65:43//HOMO SAPIENS (HUMAN)//P52743
F-NT2RP2001196//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 (EC 1.6.5.3)//1.0:95:26//CAPRA HIRCUS (GOAT)//Q36346
F-NT2RP2001218//HYPOTHETICAL 59.2 KD PROTEIN IN MOB1-SGA1 INTERGENIC REGION//0.00024:80:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40486
- 30 F-NT2RP2001226//RABPHILIN-3A (FRAGMENT)//4.6e-05:121:39//MUS MUSCULUS (MOUSE)//P47708
F-NT2RP2001233//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT)//3.2e-61:153:56//HOMO SAPIENS (HUMAN)//P16415
F-NT2RP2001245//SYNAPTONEMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN)//4.9e-05:230:21//HOMO SAPIENS (HUMAN)//Q15431
- 35 F-NT2RP2001268//HOMEBOX PROTEIN CEH-32//0.23:159:25//CAENORHABDITIS ELEGANS//Q23175
F-NT2RP2001277
F-NT2RP2001290//BETA-SOLUBLE NSF ATTACHMENT PROTEIN (SNAP-BETA) (SNAP-ALPHA HOMOLOG) (BRAIN PROTEIN I47) (FRAGMENT)//1.0e-86:131:97//MUS MUSCULUS (MOUSE)//P28663
F-NT2RP2001295
- 40 F-NT2RP2001312//N-ACETYLGLUCOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.14) (G6S) (GLUCOSAMINE-6-SULFATASE)//0.64:80:33//CAPRA HIRCUS (GOAT)//P50426
F-NT2RP2001327//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN)//1.0e-36:118:65//HOMO SAPIENS (HUMAN)//Q13829
F-NT2RP2001328//PROBABLE E5 PROTEIN//1.0:46:41//HUMAN PAPILLOMAVIRUS TYPE 33//P06426
- 45 F-NT2RP2001347//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/4.5e-19:66:62//HOMO SAPIENS (HUMAN)//P39193
F-NT2RP2001366//SPERM-SPECIFIC PROTEIN PHI-1//0.66:55:32//MYTILUS EDULIS (BLUE MUSSEL)//Q04621
F-NT2RP2001378//VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID) (FRAGMENT)//0.060:78:33//HOMO SAPIENS (HUMAN)//Q14003
- 50 F-NT2RP2001381//26S PROTEASE REGULATORY SUBUNIT 8 (SUG1 HOMOLOG) (XSUG1)//1.0:167:26//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P46470
F-NT2RP2001392//KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIIA3//0.0080:82:32//OVIS ARIES (SHEEP)//P02441
- 55 F-NT2RP2001394//POLYHOMEOTIC-PROXIMAL CHROMATIN PROTEIN//0.024:39:53//DROSOPHILA MELANOGASTER//P07880

F-NT2RP2001420//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H]//0.00018:113:38//HOMO SAPIENS (HUMAN)//P04280
 F-NT2RP2001423//HYPOTHETICAL 9.4 KD PROTEIN IN GP31-CD INTERGENIC REGION (ORF A)//0.90:23:43//BACTERIOPHAGE T4//P17307
 5 F-NT2RP2001427//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.2e-11:38:68//HOMO SAPIENS (HUMAN)//P39188
 F-NT2RP2001436//DYNEIN LIGHT INTERMEDIATE CHAIN 2, CYTOSOLIC (LIC53/55) (LIC-2)//0.25:124:28//RATTUS NORVEGICUS (RAT)//Q62698
 F-NT2RP2001440//14-3-3 PROTEIN GAMMA (PROTEIN KINASE C INHIBITOR PROTEIN-1) (KCIP-1)//4.8e-62:145:90//RATTUS NORVEGICUS (RAT)//P35214
 10 F-NT2RP2001445
 F-NT2RP2001449//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT)//9.5e-118:226:95//BOS TAURUS (BOVINE)//Q10568
 F-NT2RP2001450
 15 F-NT2RP2001467//SHORT NEUROTOXIN 1 (TOXIN V-II-1)//1.0:25:40//BUNGARUS FASCIATUS (BANDED KRAIT)//P10808
 F-NT2RP2001506
 F-NT2RP2001511//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME III//0.49:124:29//CAENORHABDITIS ELEGANS//P34681
 20 F-NT2RP2001520//VITAMIN D-DEPENDENT CALCIUM-BINDING PROTEIN, INTESTINAL (CABP) (CALBINDIN D9K)//0.035:71:33//HOMO SAPIENS (HUMAN)//P29377
 F-NT2RP2001526
 F-NT2RP2001536//METALLOTHIONEIN-I (MT-1)//1.0:19:42//COLUMBA LIVIA (DOMESTIC PIGEON)//P15786
 F-NT2RP2001560//CUTICLE COLLAGEN 12 PRECURSOR//0.0018:144:35//CAENORHABDITIS ELEGANS//P20630
 25 F-NT2RP2001569//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.7e-31:102:67//HOMO SAPIENS (HUMAN)//P39194
 F-NT2RP2001576//SMP3 PROTEIN//0.00016:75:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q04174
 30 F-NT2RP2001581//TRANSMEMBRANE PROTEIN SEX PRECURSOR//0.040:46:36//HOMO SAPIENS (HUMAN)//P51805
 F-NT2RP2001597//PROBABLE E4 PROTEIN//0.00042:113:34//HUMAN PAPILLOMAVIRUS TYPE 5//P06924
 F-NT2RP2001601
 F-NT2RP2001613//HOMEBOX PROTEIN SAX-1 (CHOX-3) (FRAGMENT)//0.14:59:32//GALLUS GALLUS (CHICKEN)//P19601
 35 F-NT2RP2001628//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR//0.056:140:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32323
 F-NT2RP2001634//ALPHA-CATENIN//7.1e-12:152:35//DROSOPHILA MELANOGASTER (FRUIT FLY)//P35220
 40 F-NT2RP2001660//HYPOTHETICAL 80.4 KD PROTEIN IN SMC3-MRPL8 INTERGENIC REGION//0.43:119:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40358
 F-NT2RP2001663//ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (NON-NEURAL ENOLASE) (NNE) (PHOSPHOPYRUVATE HYDRATASE)//1.2e-26:126:56//HOMO SAPIENS (HUMAN)//P06733
 45 F-NT2RP2001675//HYPOTHETICAL 107.7 KD PROTEIN IN RPSO 5'REGION (ORF1)//0.25:148:25//CAMPYLOBACTER JEJUNI//Q46089
 F-NT2RP2001677//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT)//0.010:101:31//RATTUS NORVEGICUS (RAT)//P10164
 50 F-NT2RP2001678//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.6e-18:83:61//HOMO SAPIENS (HUMAN)//P39188
 F-NT2RP2001699//PROTEIN C14//0.98:51:31//VACCINIA VIRUS (STRAIN COPENHAGEN)//P21045
 F-NT2RP2001720//MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2) (ALLELIC FORM 1)//0.16:145:30//PLASMODIUM FALCIPARUM (ISOLATE CAMP / MALAYSIA)//Q99317
 55 F-NT2RP2001721//MALE-SPECIFIC LETHAL 2 PROTEIN//0.00090:48:39//DROSOPHILA MELANOGASTER
 F-NT2RP2001740//ANNEXIN V-ANNEXIN A FRAGMENT//0.143:25//BOS TAURUS (BOVINE)//P20011
 F-NT2RP2001748//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAG

MENT) //0.77:111:28//HOMO SAPIENS (HUMAN) //P10162

F-NT2RP2001762

F-NT2RP2001813//PHOTOSYSTEM I REACTION CENTRE SUBUNIT VIII (PSI-I) //1.0:22:40//PICEA ABIES (NORWAY SPRUCE) (PICEA EXCELSA) //O47040

5 F-NT2RP2001839//SCY1 PROTEIN //6.8e-17:204:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P53009

F-NT2RP2001861//D15KZ1 PROTEIN (FRAGMENT) //0.31:56:39//MUS MUSCULUS (MOUSE) //Q61466

F-NT2RP2001869//CORNEODESMOSIN (S PROTEIN) (FRAGMENT) //0.97:78:30//SUS SCROFA (PIG) //O19084

10 F-NT2RP2001876//ALLOGRAFT INFLAMMATORY FACTOR-1 (AIF-1) (IONIZED CALCIUM BINDING ADAPTER MOLECULE 1) //3.5e-36:106:66//HOMO SAPIENS (HUMAN) //P55008

F-NT2RP2001883//CATHEPSIN L (EC 3.4.22.15) //0.95:29:41//OVIS ARIES (SHEEP) //Q10991

F-NT2RP2001898//TYPE II INOSITOL-1,4,5-TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR (EC 3.1.3.56) (5PTASE) (FRAGMENT) //1.6e-84:185:88//HOMO SAPIENS (HUMAN) //P32019

15 F-NT2RP2001900//ACTIN-LIKE PROTEIN ARP5 //1.1e-17:180:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P53946

F-NT2RP2001907//HYPHAL WALL PROTEIN 1 (CELL ELONGATION PROTEIN 2) //0.13:108:27//CANDIDA ALBICANS (YEAST) //P46593

20 F-NT2RP2001926//HYPOTHETICAL 7.6 KD PROTEIN YCF33 //0.55:57:26//CYANOPHORA PARADOXA //P48273

F-NT2RP2001936

F-NT2RP2001943//HYPOTHETICAL 57.7 KD PROTEIN IN AIP1-CTF13 INTERGENIC REGION //1.8e-13:208:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //Q04305

25 F-NT2RP2001946//HYPOTHETICAL 13.0 KD PROTEIN IN ALGR3 3'REGION //0.59:76:28//PSEUDOMONAS AERUGINOSA //P21485

F-NT2RP2001947//ZINC FINGER PROTEIN DAN (N03) //0.53:68:29//RATTUS NORVEGICUS (RAT) //Q06880

F-NT2RP2001969//CHLOROPLAST 30S RIBOSOMAL PROTEIN S18 //0.0015:52:34//CHLORELLA VULGARIS //P56353

30 F-NT2RP2001976//DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN 5A) //9.5e-07:201:22//MUS MUSCULUS (MOUSE) //Q99104

F-NT2RP2001985//PROLINE-RICH PROTEIN MP-2 PRECURSOR //0.016:90:32//MUS MUSCULUS (MOUSE) //P05142

F-NT2RP2001991//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73 //8.0e-14:47:76//RATTUS NORVEGICUS (RAT) //Q08469

35 F-NT2RP2002025//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO) //2.9e-30:211:42//GALLUS GALLUS (CHICKEN) //P35331

F-NT2RP2002032//FLOCCULANT-ACTIVE PROTEINS MO2.1 AND MO2.2 //0.23:20:40//MORINGA OLEIFERA (HORSERADISH TREE) (MORINGA PTERYGOSPERMA) //P24303

40 F-NT2RP2002033//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!! //0.88:27:62//HOMO SAPIENS (HUMAN) //P39193

F-NT2RP2002041

F-NT2RP2002046//MATING PROCESS PROTEIN MID2 (SERINE-RICH PROTEIN SMS1) (PROTEIN KINASE A INTERFERENCE PROTEIN) //1.0:85:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P36027

F-NT2RP2002047

45 F-NT2RP2002058//DOM34 INTERACTING PROTEIN 2 //9.4e-25:165:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //Q12220

F-NT2RP2002066//TIGHT JUNCTION PROTEIN ZO-1 (TIGHT JUNCTION PROTEIN 1) //5.7e-12:108:41//HOMO SAPIENS (HUMAN) //Q07157

F-NT2RP2002070//CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1) (FRAGMENT) //0.88:28:50//ASTERINA PECTINIFERA (STARFISH) //P11958

50 F-NT2RP2002076//TRP-ASP REPEATS CONTAINING PROTEIN RBA-2 //0.0031:124:27//CAENORHABDITIS ELEGANS //P90916

F-NT2RP2002078//KERATIN, GLYCINE/TYROSINE-RICH OF HAIR //0.82:30:40//OVIS ARIES (SHEEP) //Q02958

55 F-NT2RP2002079//OUTER DENSE FIBER PROTEIN //0.34:41:39//HOMO SAPIENS (HUMAN) //Q14990

F-NT2RP2002080//HYPOTHETICAL 1.5 KD PROTEIN

F-NT2RP2002081//HYPOTHETICAL 1.5 KD PROTEIN

F-NT2RP2002082//HYPOTHETICAL 1.5 KD PROTEIN

F-NT2RP2002105//COLLAGEN (X) CHAIN PRECURSOR //0.0012:100:34//BOS TAURUS (BOVINE) //P23206

F-NT2RP2002124//EARLY GROWTH RESPONSE PROTEIN 1 (EGR-1) (KROX24) (TRANSCRIPTION FACTOR ETR103) (ZINC FINGER PROTEIN 225) (AT225)//0.74:72:31//HOMO SAPIENS (HUMAN)//P18146
F-NT2RP2002137//NEUROTOXIN B-II//1.0:27:44//CEREBRATULUS LACTEUS (MILKY RIBBON WORM)//P01526
F-NT2RP2002154//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-34 GALACTOSIDE-BINDING LECTIN)//0.0029:112:34//MUS MUSCULUS (MOUSE)//P16110
F-NT2RP2002172
F-NT2RP2002185//UBIQUITIN-LIKE PROTEIN DSK2//1.8e-07:87:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P48510
F-NT2RP2002192
F-NT2RP2002193//CUTICLE COLLAGEN 40//0.0062:70:37//CAENORHABDITIS ELEGANS//P34804
F-NT2RP2002208//PEROXISOME ASSEMBLY PROTEIN PEX10 (PEROXIN-10)//0.00011:45:40//HOMO SAPIENS (HUMAN)//060683
F-NT2RP2002219
F-NT2RP2002231//V-TYPE SODIUM ATP SYNTHASE SUBUNIT E (EC 3.6.1.34) (NA(+)-TRANSLOCATING ATPASE SUBUNIT E)//1.0:68:32//ENTEROCOCCUS HIRAE//P43436
F-NT2RP2002235//INFECTED CELL PROTEIN ICP34.5 (NEUROVIRULENCE FACTOR ICP34.5)//0.0022:66:45//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN CVG-2)//P37318
F-NT2RP2002252//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT)//0.071:110:31//CRICETULUS GRISEUS (CHINESE HAMSTER)//P11414
F-NT2RP2002256//CYTOCHROME P450 26 (EC 1.14.-.-) (RETINOIC ACID-METABOLIZING CYTOCHROME) (P450RA1) (RETINOIC ACID 4-HYDROXYLASE)//3.1e-31:75:84//MUS MUSCULUS (MOUSE)//O55127
F-NT2RP2002259//L-MYC-1 PROTO-ONCOGENE PROTEIN//1.9e-17:41:90//HOMO SAPIENS (HUMAN)//P12524
F-NT2RP2002270//HYPOTHETICAL 26.0 KD PROTEIN IN CYB5-LEU4 INTERGENIC REGION//2.1e-27:164:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53930
F-NT2RP2002292//IMMEDIATE-EARLY PROTEIN RSP40//0.018:107:23//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV)//P24827
F-NT2RP2002312//PHOSPHATIDATE CYTIDYLYLTRANSFERASE (EC 2.7.7.41) (CDP-DIGLYCERIDE SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE) (CDP-DIACYLGLYCEROL SYNTHASE) (CDS) (CTP:PHOSPHATIDATE CYTIDYLYLTRANSFERASE) (CDP-DAG SYNTHASE)//1.4e-52:174:55//HOMO SAPIENS (HUMAN)//Q92903
F-NT2RP2002316//HISTONE H1.C6/H1.C9//1.0:40:40//TRYPANOSOMA CRUZI//P40269
F-NT2RP2002325//PEROXISOMAL MEMBRANE PROTEIN PMP30A (PMP31) (PEROXIN 11A)//2.2e-06:145:26//CANDIDA BOIDINII (YEAST)//Q00316
F-NT2RP2002333//HYPOTHETICAL 39.1 KD PROTEIN IN RNPB-SOHA INTERGENIC REGION (ORF 3)//0.30:86:32//ESCHERICHIA COLI//P23524
F-NT2RP2002373//SYNAPSINS IA AND IB//0.080:145:31//BOS TAURUS (BOVINE)//P17599
F-NT2RP2002385//ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN) [CONTAINS: KNOB PROTEIN GP70; SPIKE PROTEIN P15E; R PROTEIN]//0.021:66:28//MINK CELL FOCUS-FORMING MURINE LEUKEMIA VIRUS (ISOLATE CI-3)//P03388
F-NT2RP2002394
F-NT2RP2002408//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS)//0.00030:107:37//BOS TAURUS (BOVINE)//P02453
F-NT2RP2002426
F-NT2RP2002439//CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)//0.00032:79:32//PLASMODIUM BERGHEI (STRAIN ANKA)//P23093
F-NT2RP2002442//HESA PROTEIN//6.0e-16:163:30//PLECTONEMA BORYANUM//P46037
F-NT2RP2002457
F-NT2RP2002464//HYPOTHETICAL 60.7 KD PROTEIN C56F8.17C IN CHROMOSOME I//9.3e-18:165:32//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10264
F-NT2RP2002475//CYSTEINE-RICH HEART PROTEIN (HCRHP)//0.91:45:35//HOMO SAPIENS (HUMAN)//P50238
F-NT2RP2002479//ATP BINDING CASSETTE TRANSPORTER 3 PRECURSOR (ABCT3 PRECURSOR)
F-NT2RP2002498//HYPOTHETICAL 10.0 KD PROTEIN IN RNPB-SOHA INTERGENIC REGION (ORF 3)
MONAS AERUGINOSA//P04139

- F-NT2RP2002503//ZINC FINGER PROTEIN 45 (BRC1744)//1.3e-31:124:59//HOMO SAPIENS (HUMAN)//Q02386
- F-NT2RP2002504//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155) (155 KD NUCLEOPORIN) (P140)//1.2e-123:240:92//RATTUS NORVEGICUS (RAT)//P37199
- 5 F-NT2RP2002520//ACIDIC PROLINE-RICH PROTEIN HP43A PRECURSOR//0.94:83:28//MESOCRICETUS AURATUS (GOLDEN HAMSTER)//P06680
- F-NT2RP2002537//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X//4.0e-10:194:23//CAENORHABDITIS ELEGANS//Q11073
- F-NT2RP2002546
- 10 F-NT2RP2002549//G2/MITOTIC-SPECIFIC CYCLIN C13-1 (A-LIKE CYCLIN) (FRAGMENT)//0.98:65:30//DAUCUS CAROTA (CARROT)//P25010
- F-NT2RP2002591//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)//2.6e-19:60:61//HOMO SAPIENS (HUMAN)//P51523
- 15 F-NT2RP2002595//ANNEXIN VII (SYNEXIN)//1.2e-15:121:49//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//Q92125
- F-NT2RP2002606//PROTEIN TRANSPORT PROTEIN SEC2//0.00034:98:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P17065
- F-NT2RP2002609//HYPOTHETICAL 52.0 KD PROTEIN IN CLB6-SPT6 INTERGENIC REGION//0.00022:79:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53264
- 20 F-NT2RP2002618//PROTEIN ARGININE N-METHYLTRANSFERASE 1 (EC 2.1.1.-)//6.2e-37:180:44//RATTUS NORVEGICUS (RAT)//Q63009
- F-NT2RP2002621//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT)//0.98:37:35//LEMUR CATTAL (RING-TAILED LEMUR)//Q34879
- F-NT2RP2002643//INFECTED CELL PROTEIN ICP34.5 (NEUROVIRULENCE FACTOR ICP34.5)//0.042:77:32//25 HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN MGH-10)//P37319
- F-NT2RP2002672//PROTEIN Q300//0.0018:41:43//MUS MUSCULUS (MOUSE)//Q02722
- F-NT2RP2002701//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I//3.6e-17:100:42//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09701
- 30 F-NT2RP2002706//IMMEDIATE-EARLY PROTEIN IE180//0.00027:139:33//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV)//P33479
- F-NT2RP2002710//SH3-BINDING PROTEIN 3BP-1//6.9e-09:96:40//MUS MUSCULUS (MOUSE)//P55194
- F-NT2RP2002727//TUBERIN (TUBEROUS SCLEROSIS 2 HOMOLOG PROTEIN)//3.6e-20:160:36//RATTUS NORVEGICUS (RAT)//P49816
- F-NT2RP2002736
- 35 F-NT2RP2002740
- F-NT2RP2002741//RHO1 GDP-GTP EXCHANGE PROTEIN 2//2.0e-07:178:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P51862
- F-NT2RP2002750//ALU SUBFAMILY SB2 WARNING ENTRY!!!!//1.6e-09:43:72//HOMO SAPIENS (HUMAN)//P39191
- 40 F-NT2RP2002752//LOW CALCIUM RESPONSE LOCUS PROTEIN T//0.95:33:39//YERSINIA PSEUDOTUBERCULOSIS//Q00932
- F-NT2RP2002753//ENDOGLUCANASE EG-1 PRECURSOR (EC 3.2.1.4) (ENDO-1,4-BETA-GLUCANASE) (CELLULASE)//0.71:78:33//TRICHODERMA LONGIBRACHIATUM//Q12714
- F-NT2RP2002769//50 KD SPICULE MATRIX PROTEIN PRECURSOR//0.44:76:32//STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN)//P11994
- 45 F-NT2RP2002778
- F-NT2RP2002800//CRAMBIN//0.99:20:50//CRAMBE ABYSSINICA (ABYSSINIAN CRAMBE)//P01542
- F-NT2RP2002839//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CONTAINS: BASIC PEPTIDE P-F] (FRAGMENT)//0.010:87:31//HOMO SAPIENS (HUMAN)//P02812
- 50 F-NT2RP2002857//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP33)//0.00018:57:45//RATTUS NORVEGICUS (RAT)//P04474
- F-NT2RP2002862//HYPOTHETICAL 27.1 KD PROTEIN UFD4-CAP1 INTERGENIC REGION//7.2e-27:140:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P33201
- F-NT2RP2002880//DNA REPAIR PROTEIN RAD32//0.83:67:28//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09683
- 55 F-NT2RP2002881//ADRENERGIC RECEPTOR (ALPHA-1)-ADRENOCEPTOR (ALPHA-1A)
- F-NT2RP2002925//ADRENERGIC RECEPTOR (ALPHA-1)-ADRENOCEPTOR (ALPHA-1A)

ADRENERGIC RECEPTOR)//0.31:48:43//HOMO SAPIENS (HUMAN)//P25100

F-NT2RP2002928//CELL DIVISION CONTROL PROTEIN 40//2.8e-26:142:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40968

F-NT2RP2002929//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHROMOSOME II//2.0e-31:186:35//CAENORHABDITIS ELEGANS//Q18964

F-NT2RP2002939//ADENYLATE CYCLASE, TYPE V (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (CA(2+)-INHIBITABLE ADENYLYL CYCLASE)//0.0022:98:39//CANIS FAMILIARIS (DOG)//P30803

F-NT2RP2002954//U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A' (U2 SNRNP-A')//0.0019:107:30//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)//P43333

F-NT2RP2002959//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2)//2.8e-11:33:81//HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), RATTUS NORVEGICUS (RAT), AND XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P51669

F-NT2RP2002979

F-NT2RP2002980//30S RIBOSOMAL PROTEIN S10//1.1e-09:98:36//MYCOPLASMA CAPRICOLUM//P10129

F-NT2RP2002986//RING CANAL PROTEIN (KELCH PROTEIN)//1.1e-19:141:39//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q04652

F-NT2RP2002987//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!1.3e-07:78:47//HOMO SAPIENS (HUMAN)//P39192

F-NT2RP2002993//DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUBUNIT)//8.0e-77:165:85//RATTUS NORVEGICUS (RAT)//O54888

F-NT2RP2003000//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!2.8e-19:62:64//HOMO SAPIENS (HUMAN)//P39194

F-NT2RP2003034//HYPOTHETICAL PROTEIN HI1458//1.0:42:35//HAEMOPHILUS INFLUENZAE//P44204

F-NT2RP2003073//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!0.0051:16:87//HOMO SAPIENS (HUMAN)//P39189

F-NT2RP2003099

F-NT2RP2003108//BASIC PROLINE-RICH PEPTIDE IB-1//0.84:47:34//HOMO SAPIENS (HUMAN)//P04281

F-NT2RP2003117

F-NT2RP2003121//HYPOTHETICAL 96.7 KD PROTEIN IN STE2-FRS2 INTERGENIC REGION//9.0e-08:99:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P43572

F-NT2RP2003125//TRANSCRIPTION REGULATOR PROTEIN BACH2 (BTB AND CNC HOMOLOG 2)//9.2e-08:134:28//MUS MUSCULUS (MOUSE)//P97303

F-NT2RP2003129

F-NT2RP2003137//UBIQUITIN//3.4e-06:70:30//NEUROSPORA CRASSA//P13117

F-NT2RP2003157//HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II//7.8e-13:84:40//CAENORHABDITIS ELEGANS//Q09217

F-NT2RP2003158//26S PROTEASOME REGULATORY SUBUNIT S3 (PROTEASOME SUBUNIT P58)//3.1e-65:155:84//HOMO SAPIENS (HUMAN)//O43242

F-NT2RP2003161//PROLINE-RICH PROTEIN MP-2 PRECURSOR//0.0011:59:42//MUS MUSCULUS (MOUSE)//P05142

F-NT2RP2003164//ZYXIN//0.0037:85:36//MUS MUSCULUS (MOUSE)//Q62523

F-NT2RP2003165//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!1.2e-24:77:64//HOMO SAPIENS (HUMAN)//P39194

F-NT2RP2003177//MALE SPECIFIC SPERM PROTEIN MST84DB//0.55:38:39//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q01643

F-NT2RP2003194//HYPOTHETICAL 12.5 KD PROTEIN ZK637.2 IN CHROMOSOME III//2.3e-14:87:37//CAENORHABDITIS ELEGANS//P30629

F-NT2RP2003206//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6.5.3)//1.0:100:28//DIDELPHIS MARSUPIALIS VIRGINIANA (NORTH AMERICAN OPOSSUM)//P41306

F-NT2RP2003228//DNA REPLICATION LICENSING FACTOR MCM4 (CDC21 HOMOLOG) (P1-CDC21)//9.3e-82:211:81//HOMO SAPIENS (HUMAN)//P33991

F-NT2RP2003230//SEC14 CYTOSOLIC FACTOR (PHOSPHATIDYLINOSITOL/PHOSPHATIDYLCHOLINE TRANSFER PROTEIN) (PI/PC TP) //1.0:51:31//CANDIDA GLABRATA (YEAST) (TORULOPSIS GLABRATA) //P39194

F-NT2RP2003237//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!1.0e-04:55:84//HOMO SAPIENS (HUMAN) //P39194

F-NT2RP2003243//M PROTEIN, SEROTYPE 5 PRECURSOR.//0.027:204:23//STREPTOCOCCUS PYO-
 GENES.//P02977
 F-NT2RP2003265//BP4A PROTEIN.//0.95:35:34//BRASSICA NAPUS (RAPE)//P41505
 F-NT2RP2003272//ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX) (FRAGMENT)//5.5e-
 06:78:35//BRASSICA NAPUS (RAPE)//P40603
 5 F-NT2RP2003277//NAM7 PROTEIN (NONSENSE-MEDIATED MRNA DECAY PROTEIN 1) (UP-FRAMESHIFT
 SUPPRESSOR 1).//1.9e-19:145:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P30771
 F-NT2RP2003280
 F-NT2RP2003286//RNA 3'-TERMINAL PHOSPHATE CYCLASE (EC 6.5.1.4) (RNA-3'-PHOSPHATE CYCLASE)
 10 (RNA CYCLASE).//2.1e-32:137:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q08096
 F-NT2RP2003293//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.7e-12:175:33//HOMO SA-
 PIENS (HUMAN)//P51522
 F-NT2RP2003295//PTB-ASSOCIATED SPLICING FACTOR (PSF).//0.055:44:45//HOMO SAPIENS (HUMAN).//
 P23246
 15 F-NT2RP2003297
 F-NT2RP2003307//KINESIN LIGHT CHAIN (KLC).//2.0e-18:87:49//RATTUS NORVEGICUS (RAT)//P37285
 F-NT2RP2003308//CROOKED NECK PROTEIN.//2.1e-91:244:67//DROSOPHILA MELANOGASTER (FRUIT
 FLY).//P17886
 F-NT2RP2003329//HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III.//5.8e-57:186:55//
 20 CAENORHABDITIS ELEGANS.//P34284
 F-NT2RP2003339//SHORT NEUROTOXIN 1 (NEUROTOXIN ALPHA).//0.98:11:72//DENDROASPIS POLYLEPIS
 POLYLEPIS (BLACK MAMBA).//P01416
 F-NT2RP2003347//60S RIBOSOMAL PROTEIN L38.//0.83:42:33//OSTERTAGIA OSTERTAGI.//O61570
 F-NT2RP2003367//SYNERGISTIC-TYPE VENOM PROTEIN C9S3, CHAIN 1.//1.0:37:35//DENDROASPIS AN-
 25 GUSTICEPS (EASTERN GREEN MAMBA).//P01408
 F-NT2RP2003391//MRNA TRANSPORT REGULATOR MTR10.//3.3e-11:229:24//SACCHAROMYCES CEREVI-
 SIAE (BAKER'S YEAST).//Q99189
 F-NT2RP2003393//PROTOCHLOROPHYLLIDE REDUCTASE CHLB SUBUNIT (EC 1.3.1.33) (NADPH- PROTO-
 CHLOROPHYLLIDE OXIDOREDUCTASE CHLB SUBUNIT) (FRAGMENT).//0.94:29:34//ARAUCARIA HETERO-
 30 PHYLLA.//P37843
 F-NT2RP2003394
 F-NT2RP2003401//60 KD CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN).//0.95:125:28//THERMUS
 AQUATICUS (SUBSP. THERMOPHILUS).//P45746
 F-NT2RP2003433//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//9.8e-78:178:84//RATTUS
 35 NORVEGICUS (RAT).//P38378
 F-NT2RP2003445
 F-NT2RP2003446//HYPOTHETICAL PROTEIN E-115.//0.00030:106:33//HUMAN ADENOVIRUS TYPE 2.//
 P03290
 F-NT2RP2003456//PHOTOSYSTEM II REACTION CENTRE M PROTEIN.//1.0:27:51//MARCHANTIA POLY-
 40 MORPHA (LIVERWORT).//P12168
 F-NT2RP2003466//LINOLEOYL-COA DESATURASE (EC 1.14.99.25) (DELTA(6)-DESATURASE).//6.7e-06:108:
 32//SYNECHOCYSTIS SP. (STRAIN PCC 6803)//Q08871
 F-NT2RP2003480//TRANSCRIPTION FACTOR BF-2 (BRAIN FACTOR 2) (BF2) (CBF-2) (T-14-6).//7.2e-15:38:
 50 50//GALLUS GALLUS (CHICKEN).//Q98937
 F-NT2RP2003499//5E5 ANTIGEN.//0.090:114:32//RATTUS NORVEGICUS (RAT).//Q63003
 F-NT2RP2003506//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//2.0e-11:91:43//SUS
 SCROFA (PIG).//P04175
 F-NT2RP2003511//PARAMYOSIN, SHORT FORM (MIMIPARAMYOSIN).//0.0020:108:25//DROSOPHILA MELA-
 NOGASTER (FRUIT FLY).//P35416
 50 F-NT2RP2003513//PTB-ASSOCIATED SPLICING FACTOR (PSF).//1.2e-05:96:36//HOMO SAPIENS (HU-
 MAN).//P23246
 F-NT2RP2003517//HYPOTHETICAL 12.9 KD PROTEIN CY49.27.//0.0059:22:31//MYCOBACTERIUM TUBER-
 CULOSIS.//Q10696
 F-NT2RP2003522//HYPOTHETICAL 10.0 KD PROTEIN.//1.0:65:30//THERMOPROTEUS TENAX VIRUS 1
 55 (STRAIN KRA1) (TTV1).//P19283
 F-NT2RP2003543//SYNAPSINS IA AND IB.//0.045:101:35//RATTUS NORVEGICUS (RAT).//P09951

- F-NT2RP2003559//ITBA2 PROTEIN (DXS9879E)//0.98:37:37//HOMO SAPIENS (HUMAN)//Q14657
 F-NT2RP2003564//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))//6.4e-35:175:44//HOMO SAPIENS (HUMAN)//P19474
 F-NT2RP2003567//HYPOTHETICAL 11.2 KD PROTEIN T18D3.7 IN CHROMOSOME X//0.72:82:34//
 5 CAENORHABDITIS ELEGANS//Q22544
 F-NT2RP2003581//HOMEBOX PROTEIN OTX1//0.90:61:37//MUS MUSCULUS (MOUSE)//P80205
 F-NT2RP2003596//ELONGATION FACTOR P (EF-P)//0.83:61:32//MYCOPLASMA GENITALIUM//P47272
 F-NT2RP2003604//ALPHA-CATENIN//1.5e-11:152:33//DROSOPHILA MELANOGASTER (FRUIT FLY)//P35220
 10 F-NT2RP2003629//PHOSPHOLIPASE A2 ALPHA (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE)
 //0.97:85:27//CROTALUS ADAMANTEUS (EASTERN DIAMONDBACK RATTLESNAKE)//P00623
 F-NT2RP2003643//ACYLNEURAMINATE CYTIDYLYLTRANSFERASE (EC 2.7.7.43) (CMP-N- ACETYL-
 NEURAMINIC ACID SYNTHETASE) (CMP-NEUNAC SYNTHETASE) (CMP-SIALIC ACID SYNTHETASE)//3.9e-
 12:84:40//NEISSERIA MENINGITIDIS//Q57385
 15 F-NT2RP2003668//!!!! ALU-SUBFAMILY SX WARNING ENTRY !!!!!/5.0e-33:74:81//HOMO SAPIENS (HUMAN)//
 P39195
 F-NT2RP2003687//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/5.7e-05:40:67//HOMO SAPIENS (HUMAN)//
 P39188
 F-NT2RP2003691//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.5e-37:56:67//HOMO SAPIENS (HUMAN)//
 20 P39194
 F-NT2RP2003702//HYPOTHETICAL OXIDOREDUCTASE IN INLA 5'REGION (EC 1.-.-) (ORFA)//1.3e-07:98:
 37//LISTERIA MONOCYTOGENES//P25145
 F-NT2RP2003704//GAMMA-GLUTAMYLTRANSFERASE 5 PRECURSOR (EC 2.3.2.2) (GAMMA-
 GLUTAMYLTRANSFERASE 5) (GGT-REL)//0.66:23:52//HOMO SAPIENS (HUMAN)//P36269
 25 F-NT2RP2003706//GLUTAMYL AMINOPEPTIDASE (EC 3.4.11.7) (EAP) (AMINOPEPTIDASE A) (APA) (DIFFER-
 ENTATION ANTIGEN GP160)//1.2e-22:187:35//HOMO SAPIENS (HUMAN)//Q07075
 F-NT2RP2003713//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 6 (EC 3.1.2.15) (UBIQUITIN THIOLESTE-
 RASE 6) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 6) (DEUBIQUITINATING ENZYME 6) (PROTO-ON-
 COGENE TRE-2)//2.7e-06:119:34//HOMO SAPIENS (HUMAN)//P35125
 30 F-NT2RP2003714//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7)//6.7e-27:68:75//HO-
 MO SAPIENS (HUMAN)//Q05481
 F-NT2RP2003727//HYPOTHETICAL PROTEIN MG007 HOMOLOG//0.64:110:30//MYCOPLASMA PNEUMONI-
 AE//P75105
 F-NT2RP2003737//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN- PROTEIN
 35 LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2)//1.2e-72:147:90//HOMO SAPIENS (HUMAN), MUS
 MUSCULUS (MOUSE), RATTUS NORVEGICUS (RAT), AND XENOPUS LAEVIS (AFRICAN CLAWED FROG)//
 P51669
 F-NT2RP2003751//EXTRACELLULAR GLOBIN PRECURSOR//0.67:68:30//PSEUDOTERRANOVA DECIPI-
 ENS (COD WORM)//P26914
 40 F-NT2RP2003760//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP)//1.0e-98:235:
 82//BOS TAURUS (BOVINE)//P53620
 F-NT2RP2003764//HYPOTHETICAL 29.3 KD PROTEIN (ORF92)//0.011:69:34//ORGYIA PSEUDOTSUGATA
 MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV)//O10341
 F-NT2RP2003769//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//1.0:33:36//EQUUS CABALLUS
 45 (HORSE)//P48663
 F-NT2RP2003770//PHOSPHATE REGULON SENSOR PROTEIN PHOR (EC 2.7.3.-) (FRAGMENT)//0.029:35:
 42//PSEUDOMONAS AERUGINOSA//P23621
 F-NT2RP2003777//HYPOTHETICAL 82 KD AVIRULENCE PROTEIN IN AVRBS3 REGION//0.041:67:34//XAN-
 THOMONAS CAMPESTRIS (PV. VESICATORIA)//P14728
 50 F-NT2RP2003781//HYPOTHETICAL 36.7 KD PROTEIN AH6.2 IN CHROMOSOME II//4.7e-54:204:47//
 CAENORHABDITIS ELEGANS//Q09201
 F-NT2RP2003793//PSEUDO-HEVEIN (MINOR HEVEIN)//0.61:30:36//HEVEA BRASILIENSIS (PARA RUBBER
 TREE)//P80359
 F-NT2RP2003825//ENDOTHELIN-1 PRECURSOR (ET-1) (FRAGMENT)//1.0:35:37//CANIS FAMILIARIS
 55 (DOG)//P13206
 F-NT2RP2003840//HYPOTHETICAL 11.2 KD PROTEIN T18D3.7 IN CHROMOSOME X//0.72:82:34//
 CAENORHABDITIS ELEGANS//Q22544
 F-NT2RP2003857//BACTERIOCIN MICROGIN R17 PRECURSOR (MCB17)//0.54:28:50//ESCHERICHIA CO

LI//P05834

F-NT2RP2003859//DROSOCIN PRECURSOR//1.0:37:35//DROSOPHILA MELANOGASTER (FRUIT FLY)//P36193

F-NT2RP2003871

5 F-NT2RP2003885//CUTICLE PROTEIN 32 (LM-32) (LM-ACP 32) (FRAGMENT)//1.0:28:50//LOCUSTA MIGRATORIA (MIGRATORY LOCUST)//P11736

F-NT2RP2003912//SERINE/THREONINE-PROTEIN KINASE NEK1 (EC 2.7.1.-) (NIMA-RELATED PROTEIN KINASE 1)//4.8e-110:268:80//MUS MUSCULUS (MOUSE)//P51954

10 F-NT2RP2003952//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B)//0.00024:92:31//RATTUS NORVEGICUS (RAT)//O09175

F-NT2RP2003968//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)//9.2e-05:101:36//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P17437

15 F-NT2RP2003976//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.7e-21:62:62//HOMO SAPIENS (HUMAN)//P39188

F-NT2RP2003981//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS8//2.7e-08:165:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P39702

F-NT2RP2003984//UNC-87 PROTEIN//0.75:71:28//CAENORHABDITIS ELEGANS//P37806

20 F-NT2RP2003986//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/5.3e-19:47:70//HOMO SAPIENS (HUMAN)//P39193

F-NT2RP2003988//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.2e-18:80:58//HOMO SAPIENS (HUMAN)//P39195

F-NT2RP2004013//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3) //1.0e-52:141:77//HOMO SAPIENS (HUMAN)//P20290

25 F-NT2RP2004014//MACROPHAGE INFLAMMATORY PROTEIN-2-ALPHA (MIP2-ALPHA) (CINC-2-ALPHA)//0.99:45:26//RATTUS NORVEGICUS (RAT)//Q10746

F-NT2RP2004041//SYNAPSINS IA AND IB//0.0022:51:37//BOS TAURUS (BOVINE)//P17599

F-NT2RP2004042//CRUSTACEAN HYPERGLYCEMIC HORMONE PRECURSOR (CHH) (FRAGMENT)//1.0:49:28//PENAEUS VANNAMEI (PENOEID SHRIMP) (EUROPEAN WHITE SHRIMP)//Q26181

30 F-NT2RP2004066//CALDESMON (CDM)//2.9e-05:175:21//GALLUS GALLUS (CHICKEN)//P12957

F-NT2RP2004081//CADMIUM-METALLOTHIONEIN (CD-MT)//0.93:59:23//HELIX POMATIA (ROMAN SNAIL) (EDIBLE SNAIL)//P33187

F-NT2RP2004098//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1)//4.6e-09:121:30//HOMO SAPIENS (HUMAN)//Q15404

35 F-NT2RP2004124//NONHISTONE CHROMOSOMAL PROTEIN HMG-17//0.068:63:31//GALLUS GALLUS (CHICKEN)//P02314

F-NT2RP2004142//HYPOTHETICAL 59.1 KD PROTEIN IN VPS15-YMC2 INTERGENIC REGION//7.9e-05:94:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38262

F-NT2RP2004152//LAMIN L(I)//0.25:167:19//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P09010

40 F-NT2RP2004165//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION//0.0014:124:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53214

F-NT2RP2004170//PROLINE-RICH PROTEIN MP-3 (FRAGMENT)//0.012:125:30//MUS MUSCULUS (MOUSE)//P05143

F-NT2RP2004172//HYPOTHETICAL 105.7 KD PROTEIN IN TPK3-PIR1 INTERGENIC REGION//4.1e-26:214:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P36051

45 F-NT2RP2004187//ZINC FINGER PROTEIN 174//3.7e-12:76:47//HOMO SAPIENS (HUMAN)//Q15697

F-NT2RP2004194//HYPOTHETICAL 10.5 KD PROTEIN C31A2.13C IN CHROMOSOME I//0.0013:92:23//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09730

50 F-NT2RP2004196//METALLOTHIONEIN 10-II (MT-10-II)//0.92:36:36//MYTILUS EDULIS (BLUE MUSSEL)//P80247

F-NT2RP2004207//MALE ACCESSORY GLAND SECRETORY PROTEIN 355A PRECURSOR//0.92:62:35//DROSOPHILA SIMULANS (FRUIT FLY)//P33737

F-NT2RP2004226//66 KD STRESS PROTEIN (P66)//0.030:113:26//PHYSARUM POLYCEPHALUM (SLIME MOLD)//P90587

55 F-NT2RP2004232//PROTEIN KINASE C, MU TYPE (EC 2.7.1.1) (NPKC-MU) //2.0e-48:211:51//HOMO SAPIENS (HUMAN)

F-NT2RP2004239//GLUTAMINE-INDUCED MITOCHONDRIAL PROTEIN 1 (GIM1) PRECURSOR (GIM1-0035)
50//TRITICUM AESTIVUM (WHEAT)//P08489

- F-NT2RP2004240//METALLOTHIONEIN-II (MT-II) (METALLOTHIONEIN-LIKE PROTEIN) (MT-CE)//1.0:39:28//
CAENORHABDITIS ELEGANS//P17512
- F-NT2RP2004242//RAS-RELATED PROTEIN RGP1 (GTP-BINDING REGULATORY PROTEIN RGP1)//0.0036:
64:28//ORYZA SATIVA (RICE)//P25766
- 5 F-NT2RP2004245//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//1.0:21:42//PONGO PYGMAEUS PYG-
MAEUS (BORNEAN ORANGUTAN)//P92896
- F-NT2RP2004270//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT)//0.00023:118:33//NEPHILA CLA-
VIPES (ORB SPIDER)//P46804
- F-NT2RP2004300//PROBABLE E4 PROTEIN//0.18:77:40//HUMAN PAPILLOMAVIRUS TYPE 8//P06425
- 10 F-NT2RP2004316
F-NT2RP2004321//HYPOTHETICAL 10.8 KD PROTEIN SSR2439//1.0:50:28//SYNECHOCYSTIS SP. (STRAIN
PCC 6803)//Q01904
- F-NT2RP2004339//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/5.0e-33:84:77//HOMO SAPIENS (HUMAN)//
P39195
- 15 F-NT2RP2004347//HYPOTHETICAL 40.9 KD PROTEIN F33H1.3 FROM CHROMOSOME II//0.78:96:30//
CAENORHABDITIS ELEGANS//Q09556
- F-NT2RP2004364//MINOR OUTER CAPSID PROTEIN (NS26) (NONSTRUCTURAL PROTEIN VP9)//0.059:143:
30//BOVINE ROTAVIRUS (STRAIN UK)//P04515
- F-NT2RP2004365//EAMZP30-47 PROTEIN (FRAGMENT)//0.27:38:39//EIMERIA ACERVULINA//P21959
- 20 F-NT2RP2004366//GLYCOPROTEIN L PRECURSOR//0.64:71:28//MAREK'S DISEASE HERPESVIRUS
(STRAIN GA) (MDHV)//P52510
- F-NT2RP2004373//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR (HISTIDINE-PROLINE RICH GLYCO-
PROTEIN) (HPRG) (FRAGMENT)//0.59:50:40//ORYCTOLAGUS CUNICULUS (RABBIT)//Q28640
- F-NT2RP2004389//HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III//4.0e-16:89:43//
25 CAENORHABDITIS ELEGANS//P34388
- F-NT2RP2004392
F-NT2RP2004396//SINGLE-STRANDED NUCLEIC ACID-BINDING PROTEIN//0.42:89:29//SACCHAROMY-
CES CEREVISIAE (BAKER'S YEAST)//P10080
- F-NT2RP2004399//SOMATOTROPIN PRECURSOR (GROWTH HORMONE)//1.0:72:34//MESOCRICETUS AU-
30 RATUS (GOLDEN HAMSTER)//P37886
- F-NT2RP2004400
F-NT2RP2004412//SPERM PROTAMINE P1//0.24:38:31//NOTORYCTES TYPHLOPS (MARSUPIAL MOLE)//
P42143
- F-NT2RP2004425//SUPPRESSOR PROTEIN SRP40//0.0087:197:22//SACCHAROMYCES CEREVISIAE (BAK-
35 ER'S YEAST)//P32583
- F-NT2RP2004463//ALPHA-2A ADRENERGIC RECEPTOR (ALPHA-2A ADRENOCEPTOR) (ALPHA-2AAR)//
1.3e-05:121:37//MUS MUSCULUS (MOUSE)//Q01338
- F-NT2RP2004476//NICKEL-SENSITIVE T-TYPE CALCIUM CHANNEL ALPHA-1 SUBUNIT (RBE-II)//0.20:68:
36//RATTUS NORVEGICUS (RAT)//Q07652
- 40 F-NT2RP2004490//FOS-RELATED ANTIGEN 1//0.94:59:33//HOMO SAPIENS (HUMAN)//P15407
- F-NT2RP2004512//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.3) (FRAGMENTS)//1.0:37:
32//PISASTER OCHRACEUS (SEA STAR)//P24998
- F-NT2RP2004523//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.1e-15:57:71//HOMO SAPIENS (HUMAN)//
P39194
- 45 F-NT2RP2004538//KINESIN-LIKE PROTEIN KIF1A (AXONAL TRANSPORTER OF SYNAPTIC VESICLES)//
1.2e-48:121:60//HOMO SAPIENS (HUMAN)//Q12756
- F-NT2RP2004551//HYPOTHETICAL 7.6 KD PROTEIN (ORF 65)//1.0:20:50//EUGLENA GRACILIS//P32095
- F-NT2RP2004568//PUTATIVE ATP-DEPENDENT RNA HELICASE C30D11.03//5.2e-07:150:30//SCHIZOSAC-
CHAROMYCES POMBE (FISSION YEAST)//Q09903
- 50 F-NT2RP2004580//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/3.7e-37:100:78//HOMO SAPIENS (HU-
MAN)//P39192
- F-NT2RP2004587//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION//8.2e-06:
150:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53214
- F-NT2RP2004594//HYPOTHETICAL 45.3 KD PROTEIN C09F5.7 IN CHROMOSOME II//0.84:105:24//
55 CAENORHABDITIS ELEGANS//Q09458
- F-NT2RP2004602//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.1e-05:50:58//HOMO SAPIENS (HUMAN)

P39188

F-NT2RP2004614//HYPOTHETICAL 11.6 KD PROTEIN.//1.0:68:33/VACCINIA VIRUS (STRAIN COPENHAGEN)//P20561

F-NT2RP2004655//GLYCINE-RICH RNA-BINDING PROTEIN 7.1/7.0e-05:70.42//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)//Q03250

F-NT2RP2004664//HYPOTHETICAL 104.0 KD PROTEIN C32A11.03C IN CHROMOSOME I//0.30:78:38//
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10328

F-NT2RP2004675

F-NT2RP2004681

F-NT2RP2004689//HYPOTHETICAL 78.3 KD PROTEIN IN RAM2-ATP7 INTERGENIC REGION.//0.021:179:24//
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P34243

F-NT2RP2004709//HYPOTHETICAL PROTEIN MJ0647//0.90:39:43//METHANOCOCCUS JANNASCHII//
Q58063

F-NT2RP2004710//GAR2 PROTEIN//0.085:60:30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P41891

F-NT2RP2004736/////ALU SUBFAMILY J WARNING ENTRY !!!!!/4.4e-15:97:49//HOMO SAPIENS (HUMAN).//
P39188

F-NT2RP2004743//MALE SPECIFIC SPERM PROTEIN MST87F.//0.43:24:41//DROSOPHILA MELANOGASTER (FRUIT FLY) //P08175

F-NT2RP2004767//36.4 KD PROLINE-RICH PROTEIN//0.0051:88:27//LYCOPERSICON ESCULENTUM (TOMATO)//Q00451

F-NT2RP2004768//SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RICH KINASE 1)//9.0e-29:166:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38692

F-NT2RP2004775

F-NT2RP2004791//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE) (LEURS)/J7.4e-60:226:53//CAENORHABDITIS ELEGANS./Q09996

F-NT2RP2004799//SUCCINYL-COA LIGASE [GDP-FORMING], BETA-CHAIN PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA)//2.2e-42:133:57//NEOCALLIMASTIX FRONTALIS (RUMEN FUNGUS)//P53587

F-NT2RP2004802//HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3'REGION.//0.018:86:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38898

F-NT2RP2004816//H<BETA>58 PROTEIN.//1.0e-68:145:93//MUS MUSCULUS (MOUSE).//P40336

F-NT2RP2004841//DSRD PROTEIN.//0.83:33:39//ARCHAEOGLOBUS FULGIDUS.//P70742

F-NT2RP2004861//KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIIA3A.//0.0072:41:39//OVIS ARIES (SHEEP)//P02443

F-NT2RP2004897//METALLOTHIONEIN-LIKE PROTEIN 1.//0.99:41:41//CASUARINA GLAUCA (SWAMP OAK)//Q39511

F-NT2RP2004933//DEATH-ASSOCIATED PROTEIN KINASE 1 (EC 2.7.1.-) (DAP KINASE 1)//8.4e-34:102:67//
HOMO SAPIENS (HUMAN)//P53355

F-NT2RP2004936//HIGH POTENTIAL IRON-SULFUR PROTEIN, ISOZYME 2 (HIPIP 2)//0.87:36:33//EC-TOTHIORHODOSPIRA VACUOLATA.//P38524

F-NT2RP2004959//STEM CELL FACTOR PRECURSOR (SCF) (MAST CELL GROWTH FACTOR) (MGF) (C-KIT LIGAND)//1.0:69:28//CANIS FAMILIARIS (DOG)//Q06220

F-NT2RP2004961//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065) (HA0946)
(FRAGMENT)//2.1e-21:73:58//HOMO SAPIENS (HUMAN)//Q06730

F-NT2RP2004962///// ALU SUBFAMILY SB WARNING ENTRY !!!!!0.17:28:57//HOMO SAPIENS (HUMAN).//
P39189

F-NT2RP2004967//HYPOTHETICAL 7.3 KD PROTEIN//0.76:41:31//THERMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1)//P19301

F-NT2RP2004978//SPERMATID-SPECIFIC PROTEIN T2[CONTAINS: SPERM PROTAMINE SP2]//0.44:40:45//
SEPIA OFFICINALIS (COMMON CUTTLEFISH)//P80002

F-NT2RP2004982

F-NT2RP2004985//HYPOTHETICAL PROTEIN KIAA0144//1.2e-51:204:57//HOMO SAPIENS (HUMAN)//Q14157

F-NT2RP2004999//LONG NEUROTOXIN 1 (ALPHA-BUNGAROTOXIN) (BGTX) //0 23 73 26//BUNGARUS MURIEI

UNIPROT: P16965 (BAKERS YEAST) / P16965
 TRYP20050000/ATPASE STABILIZING FACTOR 1 (BAKERS YEAST) / P16965

F-NT2RP2005001//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930)//0.90:54:31//HOMO SAPIENS (HUMAN)//P22531

F-NT2RP2005003//DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR//1.6e-30:78:56//MUS MUSCULUS (MOUSE)//P15533

5 F-NT2RP2005012//NPL1 PROTEIN (SEC63 PROTEIN)//0.00024:94:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P14906

F-NT2RP2005018//GAG POLYPROTEIN (CORE POLYPROTEIN) [CONTAINS: CORE PROTEINS P19, P10] (FRAGMENT)//1.0:91:28//AVIAN ENDOGENOUS ROUS-ASSOCIATED VIRUS-0 (EV-2) (AVIAN RETROVIRUS RAV-0)//P06937

10 F-NT2RP2005020

F-NT2RP2005022//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1//4.9e-11:106:35//PODOSPORA ANSERINA//Q00808

F-NT2RP2005031

15 F-NT2RP2005037//ANTI-SILENCING PROTEIN 1//2.2e-32:117:55//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32447

F-NT2RP2005038//DNA NUCLEOTIDYLEXOTRANSFERASE (EC 2.7.7.31) (TERMINAL ADDITION ENZYME) (TERMINAL DEOXYNUCLEOTIDYLTRANSFERASE) (TERMINAL TRANSFERASE)//9.3e-28:187:40//AMBYSTOMA MEXICANUM (AXOLOTL)//O57486

F-NT2RP2005108//CUTICLE COLLAGEN 2//0.33:62:38//CAENORHABDITIS ELEGANS//P17656

20 F-NT2RP2005116//PUTATIVE EUKARYOTIC TRANSLATION INITIATION FACTOR 3 ALPHA SUBUNIT (EIF-3 ALPHA)//4.0e-54:161:63//CAENORHABDITIS ELEGANS//P34466

F-NT2RP2005126//CHLOROPLAST 50S RIBOSOMAL PROTEIN L27 (FRAGMENT)//0.23:46:39//PLEUROCHYSIS HAPTONEMOFERA//P41552

F-NT2RP2005139//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS)//0.016:43:37//BOS TAURUS (BOVINE)//P25508

25 F-NT2RP2005140//HYPOTHETICAL 7.4 KD PROTEIN YCF33//0.96:51:39//GUILLARDIA THETA (CRYPTOMONAS PHI)//O78517

F-NT2RP2005144//TUBBY PROTEIN//5.6e-08:66:45//MUS MUSCULUS (MOUSE)//P50586

F-NT2RP2005147

30 F-NT2RP2005159//PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECURSOR//0.94:57:29//NICOTIANA TABACUM (COMMON TOBACCO), AND SPINACIA OLERACEA (SPINACH)//P12164

F-NT2RP2005162//HYPOTHETICAL 54.2 KD PROTEIN IN ERP5-ORC6 INTERGENIC REGION//1.2e-33:139:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38821

F-NT2RP2005168//HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U)//2.8e-33:102:61//HOMO SAPIENS (HUMAN)//Q00839

35 F-NT2RP2005204//DNA DAMAGE TOLERANCE PROTEIN RHC31 (RAD31 HOMOLOG)//3.9e-28:141:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q06624

F-NT2RP2005227

F-NT2RP2005239//TRNA SPLICING PROTEIN SPL1//2.0e-38:117:64//CANDIDA ALBICANS (YEAST)//P87185

40 F-NT2RP2005254//OMEGA-AGATOXIN IB (OMEGA-AGA-IB) (FRAGMENT)//0.26:29:48//AGELENOPSIS APERTA (FUNNEL-WEB SPIDER)//P15970

F-NT2RP2005270//HOMEBOX PROTEIN HOX-A4 (CHOX-1.4)//0.037:82:34//GALLUS GALLUS (CHICKEN)//P17277

F-NT2RP2005276//LONG-CHAIN-FATTY-ACID--COA LIGASE 4 (EC 6.2.1.3) (LONG-CHAIN ACYL-COA SYNTHETASE 4) (LACS 4)//2.0e-59:174:61//RATTUS NORVEGICUS (RAT)//O35547

45 F-NT2RP2005287//ZINC FINGER PROTEIN 26 (ZINC FINGER PROTEIN KOX20) (FRAGMENT)//1.5e-05:27:70//HOMO SAPIENS (HUMAN)//P17031

F-NT2RP2005288//PROBABLE RUBREDOXIN HUPI//1.0:42:28//RHIZOBIUM LEGUMINOSARUM (BIOVAR VICIAE)//P28151

50 F-NT2RP2005289//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.1e-21:75:70//HOMO SAPIENS (HUMAN)//P39193

F-NT2RP2005293//TRANSLATION INITIATION FACTOR IF-2//0.58:170:24//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI)//P55972

F-NT2RP2005315//CUTICLE COLLAGEN 7 (FRAGMENT)//0.091:65:38//CAENORHABDITIS ELEGANS//P18832

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CONTAINS PANCREASTATIN-RELATED PEPTIDE//4.9e-09:98:39//HOMO SAPIENS (HUMAN)//P10641

F-NT2RP2005336//HYPOTHETICAL 68.7 KD PROTEIN IN STB1-MCK1 INTERGENIC REGION//0.00011:124:

28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P42846

F-NT2RP2005344//PROBABLE CALCIUM-TRANSPORTING ATPASE 4 (EC 3.6.1.38)//4.7e-21:92:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q12675

F-NT2RP2005354

5 F-NT2RP2005358//MYOSIN IC HEAVY CHAIN//0.012:91:39//ACANTHAMOEBA CASTELLANII (AMOEBA)//P10569

F-NT2RP2005360//ACROSIN PRECURSOR (EC 3.4.21.10)//0.0022:73:36//ORYCTOLAGUS CUNICULUS (RABBIT)//P48038

10 F-NT2RP2005393//HYPOTHETICAL 25.9 KD PROTEIN AH6.3 IN CHROMOSOME II//0.00085:135:28//CAENORHABDITIS ELEGANS //Q09202

F-NT2RP2005407//SQUALENE MONOOXYGENASE (EC 1.14.99.7) (SQUALENE EPOXIDASE) (SE)//0.96:109:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32476

F-NT2RP2005436//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN)//0.0011:54:42//ZEA MAYS (MAIZE)//P14918

15 F-NT2RP2005441//PROLINE-RICH PROTEIN MP-2 PRECURSOR//0.039:182:29//MUS MUSCULUS (MOUSE)//P05142

F-NT2RP2005453

F-NT2RP2005457//NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-B14.5B) (CI-B14.5B)//4.0e-10:124:37//BOS TAURUS (BOVINE)//Q02827

20 F-NT2RP2005464//HYPOTHETICAL 9.5 KD PROTEIN//0.96:42:33//VACCINIA VIRUS (STRAIN COPENHAGEN)//P20553

F-NT2RP2005465//MITOCHONDRIAL CARRIER PROTEIN RIM2//4.6e-09:92:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38127

25 F-NT2RP2005472//HYPOTHETICAL PROTEIN BB0129//0.76:80:32//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE)//O51155

F-NT2RP2005476//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.0e-31:39:89//HOMO SAPIENS (HUMAN)//P39193

F-NT2RP2005490//METALLOTHIONEIN-II (MT-II)//0.14:27:33//SCYLLA SERRATA (MUD CRAB)//P02806

30 F-NT2RP2005491//DNA-DIRECTED RNA POLYMERASE SUBUNIT I (EC 2.7.7.6)//0.95:45:31//METHANOCOCCUS JANNASCHII//Q58785

F-NT2RP2005495//HYPOTHETICAL 10.8 KD PROTEIN IN GP30-RIII INTERGENIC REGION//0.99:68:30//BACTERIOPHAGE T4//Q02407

F-NT2RP2005496//ZINC FINGER PROTEIN 135//1.4e-54:120:59//HOMO SAPIENS (HUMAN)//P52742

35 F-NT2RP2005498//PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, ALPHA ISOFORM (PROTEIN PHOSPHATASE PP2A B SUBUNIT ALPHA ISOFORM) (ALPHA-PR55)//9.5e-76:146:86//RATTUS NORVEGICUS (RAT)//P36876

F-NT2RP2005501//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-31) (GALACTOSIDE-BINDING PROTEIN) (GALBP)//0.025:70:40//HOMO SAPIENS (HUMAN)//P17931

40 F-NT2RP2005509//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR//1.0:166:27//GALLUS GALLUS (CHICKEN)//P02457

F-NT2RP2005520//CHROMOSOME ASSEMBLY PROTEIN XCAP-E//7.9e-45:118:79//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P50533

45 F-NT2RP2005525//50S RIBOSOMAL PROTEIN L11//1.0:47:27//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE)//O51354

F-NT2RP2005531//PROTEIN-TYROSINE PHOSPHATASE MEG1 (EC 3.1.3.48) (PTPASE-MEG1) (MEG)//9.8e-13:84:45//HOMO SAPIENS (HUMAN)//P29074

50 F-NT2RP2005539//RING CANAL PROTEIN (KELCH PROTEIN)//4.9e-10:90:33//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q04652

F-NT2RP2005540//NUCLEOTIDE BINDING PROTEIN EXPZ//0.36:119:21//BACILLUS SUBTILIS//P39115

F-NT2RP2005549//HYPOTHETICAL 32.0 KD PROTEIN C16C10.10 IN CHROMOSOME III//6.0e-39:179:46//CAENORHABDITIS ELEGANS//Q09253

F-NT2RP2005555

55 F-NT2RP2005557//HYPOTHETICAL 23.7 KD PROTEIN C13G6.14 IN CHROMOSOME I//4.9e-06:90:35//CAENORHABDITIS ELEGANS//Q09253

F-NT2RP2005581

F-NT2RP2005600//BASIC PROLINE-RICH PEPTIDE P-R (B-9)//0.014:37:40//HOMO SAPIENS (HUMAN),

P02811

F-NT2RP2005605//GONADOLIBERIN I PRECURSOR (LHRH I) (LUTEINIZING HORMONE RELEASING HORMONE I) (GONADOTROPIN RELEASING HORMONE I) (GNRH I) (LULIBERIN I) (FRAGMENT)//0.64:26:42//MACACA MULATTA (RHESUS MACAQUE)//P55247

5 F-NT2RP2005620//HYPOTHETICAL 45.1 KD PROTEIN IN RPS5-ZMS1 INTERGENIC REGION//8.7e-31:138:49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P47160

F-NT2RP2005622//NEUROTOXIN-LIKE PROTEIN STR1 (ANATOXIN AAH STR1)//0.39:22:40//ANDROCTONUS AUSTRALIS HECTOR (SAHARA SCORPION)//P80950

10 F-NT2RP2005635//HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION//5.8e-43:144:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38795

F-NT2RP2005637//VPU PROTEIN (U ORF PROTEIN)//0.91:33:45//CHIMPANZEE IMMUNODEFICIENCY VIRUS (SIV(CPZ)) (CIV)//P17286

F-NT2RP2005640//METALLOTHIONEIN-LIKE PROTEIN LSC54//0.63:41:31//BRASSICA NAPUS (RAPE)//P43402

15 F-NT2RP2005645

F-NT2RP2005651//OCTAMER-BINDING TRANSCRIPTION FACTOR 3A (OCT-3A) (OCT-4)//0.0023:50:42//HOMO SAPIENS (HUMAN)//Q01860

F-NT2RP2005654//HYPOTHETICAL 48.6 KD PROTEIN IN BET1-PAN1 INTERGENIC REGION//6.1e-16:76:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40564

20 F-NT2RP2005669//METALLOTHIONEIN-II (MT-II)//0.76:16:50//SCYLLA SERRATA (MUD CRAB)//P02806

F-NT2RP2005675//PUTATIVE ORAL CANCER SUPPRESSOR (DELETED IN ORAL CANCER-1)//6.5e-26:116:54//MESOCRICETUS AURATUS (GOLDEN HAMSTER)//P49119

F-NT2RP2005683//HYPOTHETICAL PROTEIN HI0275//0.17:50:40//HAEMOPHILUS INFLUENZAE//P43975

25 F-NT2RP2005690//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE)//1.3e-16:75:30//PISUM SATIVUM (GARDEN PEA)//Q04708

F-NT2RP2005694//HYPOTHETICAL PROTEIN KIAA0032//9.6e-11:135:34//HOMO SAPIENS (HUMAN)//Q15034

F-NT2RP2005701//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) [CONTAINS: PEPTIDE P-D] (FRAGMENT)//0.084:158:32//HOMO SAPIENS (HUMAN)//P10161

30 F-NT2RP2005712//METALLOTHIONEIN-II (MT-II)//0.19:14:50//STENELLA COERULEOALBA (STRIPED DOLPHIN)//P14425

F-NT2RP2005719//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENT)//1.0:36:41//ORYCTOLAGUS CUNICULUS (RABBIT)//P02456

35 F-NT2RP2005722//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT)//7.8e-37:131:62//HOMO SAPIENS (HUMAN)//P16415

F-NT2RP2005723//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/0.98:23:60//HOMO SAPIENS (HUMAN)//P39192

F-NT2RP2005726//HYPOTHETICAL PROTEIN TP0375//0.98:30:43//TREPONEMA PALLIDUM//O83390

40 F-NT2RP2005732//PERIOD CLOCK PROTEIN (FRAGMENT)//0.41:20:55//DROSOPHILA ROBUSTA (FRUIT FLY)//Q03296

F-NT2RP2005741//SMR1 PROTEIN PRECURSOR (VCS-ALPHA 1)//0.38:58:36//RATTUS NORVEGICUS (RAT)//P13432

F-NT2RP2005748//ZINC FINGER PROTEIN KOX23 (FRAGMENT)//0.026:19:68//HOMO SAPIENS (HUMAN)//P17034

45 F-NT2RP2005752//PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR//0.90:101:31//HOMO SAPIENS (HUMAN)//P02461

F-NT2RP2005753//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)//0.50:22:59//HOMO SAPIENS (HUMAN)//P30808

50 F-NT2RP2005763//PUTATIVE ATP-DEPENDENT RNA HELICASE STE13//4.7e-14:108:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09181

F-NT2RP2005767//NONHISTONE CHROMOSOMAL PROTEIN 6B//4.1e-08:65:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P11633

F-NT2RP2005773//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE)//1.2e-14:65:61//HOMO SAPIENS (HUMAN)//P32322

55 F-NT2RP2005775//NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL) (NEUROLYSIN) (RABBIT) (P4267)

F-NT2RP2005781//SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1 / PRP-2) (RABBIT) (P4267)

3) (PRP-2 / PRP-4) (PIF-F / PIF-S) (PROTEIN A / PROTEIN C) [CONTAINS: PEPTIDE P-C]//0.090:73:36//HOMO SAPIENS (HUMAN)//P02810
F-NT2RP2005784//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (ALPHA-0 PROTEIN)//3.5e-06:79:37//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)//P08393
F-NT2RP2005804//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT)//1.8e-07:43:55//OWENIA FUSIFORMIS//P21260
F-NT2RP2005812//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION//6.3e-14:143:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40004
F-NT2RP2005815//FERROCHELATASE (EC 4.99.1.1) (PROTOHEME FERRO-LYASE) (HEME SYNTHETASE)//0.0017:123:37//MYCOBACTERIUM AVIUM//O07401
F-NT2RP2005835//SHP1 PROTEIN//1.2e-08:135:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P34223
F-NT2RP2005841//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N)//0.23:28:53//HOMO SAPIENS (HUMAN)//P22532
F-NT2RP2005853//HYPOTHETICAL 8.5 KD PROTEIN IN ASIA-MOTA INTERGENIC REGION//0.99:33:48//BACTERIOPHAGE T4//P22917
F-NT2RP2005857//CHROMOSOME ASSEMBLY PROTEIN XCAP-C//8.6e-84:235:66//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P50532
F-NT2RP2005859//MALE SPECIFIC SPERM PROTEIN MST84DB//0.017:60:40//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q01643
F-NT2RP2005868//ATP SYNTHASE B' CHAIN PRECURSOR (EC 3.6.1.34) (SUBUNIT II)//0.28:121:28//SPINACIA OLERACEA (SPINACH)//P31853
F-NT2RP2005886//MICRONUCLEAR LINKER HISTONE POLYPROTEIN (MIC LH) [CONTAINS: LINKER HISTONE PROTEINS ALPHA, BETA, DELTA AND GAMMA]//0.80:130:28//TETRAHYMENA THERMOPHILA//P40631
F-NT2RP2005890
F-NT2RP2005901//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//0.35:18:44//DROSOPHILA YAKUBA (FRUIT FLY)//P03933
F-NT2RP2005908//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.0e-28:61:65//HOMO SAPIENS (HUMAN)//P39194
F-NT2RP2005933//PERIOD CLOCK PROTEIN (P230) (FRAGMENT)//1.7e-11:85:49//ACETABULARIA MEDITERRANEA (MERMAID'S WINE GLASS)//P12347
F-NT2RP2005942//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE)//7.2e-59:216:58//BOS TAURUS (BOVINE)//P25500
F-NT2RP2005980//HYPOTHETICAL 11.5 KD PROTEIN IN RSP8A-AST1 INTERGENIC REGION//1.0:49:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38185
F-NT2RP2006023//DNA REPAIR PROTEIN REC N (RECOMBINATION PROTEIN N) (FRAGMENT)//1.0:40:45//VIBRIO CHOLERAЕ//P52118
F-NT2RP2006038//HYPOTHETICAL 30.2 KD PROTEIN C02F5.4 IN CHROMOSOME III//4.0e-11:90:34//CAENORHABDITIS ELEGANS//P34281
F-NT2RP2006043//LAMININ BETA-1 CHAIN VARIANT (LAMININ BETA-1-2 CHAIN) (FRAGMENT)//0.00067:73:38//GALLUS GALLUS (CHICKEN)//Q01636
F-NT2RP2006052//METALLOTHIONEIN-I (MT-I)//0.19:31:38//CERCOPITHECUS AETHIOPS (GREEN MONKEY) (GRIVET)//P02797
F-NT2RP2006069//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENTS)//1.0:66:34//RATTUS NORVEGICUS (RAT)//P02466
F-NT2RP2006071//RESTIN//0.40:156:29//GALLUS GALLUS (CHICKEN)//O42184
F-NT2RP2006098//HYPOTHETICAL 21.7 KD PROTEIN IN TUP1-ABP1 INTERGENIC REGION//0.99:95:20//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P25651
F-NT2RP2006100//LONG NEUROTOXIN 4 (ALPHA-NEUROTOXIN)//0.94:43:34//OPHIOPHAGUS HANNAH (KING COBRA) (NAJA HANNAH)//P80156
F-NT2RP2006103//50S RIBOSOMAL PROTEIN L32//0.40:36:38//SYNECHOCYSTIS SP. (STRAIN PCC 6803)//P73014
F-NT2RP2006106//CUTICLE COLLAGEN 1 //0 28:85:29//CAENORHABDITIS ELEGANS //P08124
F-NT2RP2006107//CUTICLE COLLAGEN 1 //0 28:85:29//CAENORHABDITIS ELEGANS //P08124
F-NT2RP2006108//CUTICLE COLLAGEN 1 //0 28:85:29//CAENORHABDITIS ELEGANS //P08124
F-NT2RP2006109//CUTICLE COLLAGEN 1 //0 28:85:29//CAENORHABDITIS ELEGANS //P08124
F-NT2RP2006110//CUTICLE COLLAGEN 1 //0 28:85:29//CAENORHABDITIS ELEGANS //P08124
F-NT2RP2006111//CUTICLE COLLAGEN 1 //0 28:85:29//CAENORHABDITIS ELEGANS //P08124
F-NT2RP2006112//CUTICLE COLLAGEN 1 //0 28:85:29//CAENORHABDITIS ELEGANS //P08124
F-NT2RP2006113//CUTICLE COLLAGEN 1 //0 28:85:29//CAENORHABDITIS ELEGANS //P08124
F-NT2RP2006114//CUTICLE COLLAGEN 1 //0 28:85:29//CAENORHABDITIS ELEGANS //P08124
F-NT2RP2006115//CUTICLE COLLAGEN 1 //0 28:85:29//CAENORHABDITIS ELEGANS //P08124
F-NT2RP2006116//CUTICLE COLLAGEN 1 //0 28:85:29//CAENORHABDITIS ELEGANS //P08124
F-NT2RP2006117//CUTICLE COLLAGEN 1 //0 28:85:29//CAENORHABDITIS ELEGANS //P08124
F-NT2RP2006118//CUTICLE COLLAGEN 1 //0 28:85:29//CAENORHABDITIS ELEGANS //P08124
F-NT2RP2006119//CUTICLE COLLAGEN 1 //0 28:85:29//CAENORHABDITIS ELEGANS //P08124
F-NT2RP2006120//CUTICLE COLLAGEN 1 //0 28:85:29//CAENORHABDITIS ELEGANS //P08124
F-NT2RP2006121//CUTICLE COLLAGEN 1 //0 28:85:29//CAENORHABDITIS ELEGANS //P08124
F-NT2RP2006122//CUTICLE COLLAGEN 1 //0 28:85:29//CAENORHABDITIS ELEGANS //P08124
F-NT2RP2006123//CUTICLE COLLAGEN 1 //0 28:85:29//CAENORHABDITIS ELEGANS //P08124
F-NT2RP2006124//CUTICLE COLLAGEN 1 //0 28:85:29//CAENORHABDITIS ELEGANS //P08124
F-NT2RP2006125//CUTICLE COLLAGEN 1 //0 28:85:29//CAENORHABDITIS ELEGANS //P08124
F-NT2RP2006126//CUTICLE COLLAGEN 1 //0 28:85:29//CAENORHABDITIS ELEGANS //P08124
F-NT2RP2006127//CUTICLE COLLAGEN 1 //0 28:85:29//CAENORHABDITIS ELEGANS //P08124
F-NT2RP2006128//CUTICLE COLLAGEN 1 //0 28:85:29//CAENORHABDITIS ELEGANS //P08124
F-NT2RP2006129//CUTICLE COLLAGEN 1 //0 28:85:29//CAENORHABDITIS ELEGANS //P08124
F-NT2RP2006130//CUTICLE COLLAGEN 1 //0 28:85:29//CAENORHABDITIS ELEGANS //P08124
F-NT2RP2006131//CUTICLE COLLAGEN 1 //0 28:85:29//CAENORHABDITIS ELEGANS //P08124
F-NT2RP2006132//CUTICLE COLLAGEN 1 //0 28:85:29//CAENORHABDITIS ELEGANS //P08124
F-NT2RP2006133//CUTICLE COLLAGEN 1 //0 28:85:29//CAENORHABDITIS ELEGANS //P08124
F-NT2RP2006134//CUTICLE COLLAGEN 1 //0 28:85:29//CAENORHABDITIS ELEGANS //P08124
F-NT2RP2006135//CUTICLE COLLAGEN 1 //0 28:85:29//CAENORHABDITIS ELEGANS //P08124
F-NT2RP2006136//CUTICLE COLLAGEN 1 //0 28:85:29//CAENORHABDITIS ELEGANS //P08124
F-NT2RP2006137//CUTICLE COLLAGEN 1 //0 28:85:29//CAENORHABDITIS ELEGANS //P08124
F-NT2RP2006138//CUTICLE COLLAGEN 1 //0 28:85:29//CAENORHABDITIS ELEGANS //P08124
F-NT2RP2006139//CUTICLE COLLAGEN 1 //0 28:85:29//CAENORHABDITIS ELEGANS //P08124
F-NT2RP2006140//CUTICLE COLLAGEN 1 //0 28:85:29//CAENORHABDITIS ELEGANS //P08124
F-NT2RP2006141//CUTICLE COLLAGEN 1 //0 28:85:29//CAENORHABDITIS ELEGANS //P08124
F-NT2RP2006142//CUTICLE COLLAGEN 1 //0 28:85:29//CAENORHABDITIS ELEGANS //P08124
F-NT2RP2006143//CUTICLE COLLAGEN 1 //0 28:85:29//CAENORHABDITIS ELEGANS //P08124
F-NT2RP2006144//CUTICLE COLLAGEN 1 //0 28:85:29//CAENORHABDITIS ELEGANS //P08124
F-NT2RP2006145//CUTICLE COLLAGEN 1 //0 28:85:29//CAENORHABDITIS ELEGANS //P08124
F-NT2RP2006146//CUTICLE COLLAGEN 1 //0 28:85:29//CAENORHABDITIS ELEGANS //P08124
F-NT2RP2006147//CUTICLE COLLAGEN 1 //0 28:85:29//CAENORHABDITIS ELEGANS //P08124
F-NT2RP2006148//CUTICLE COLLAGEN 1 //0 28:85:

F-NT2RP2006184//HYPOTHETICAL 11.2 KD PROTEIN IN CSGC-MDOG INTERGENIC REGION PRECURSOR//0.95:87:26//ESCHERICHIA COLI.//P75917

F-NT2RP2006186//MICROTUBULE-ASSOCIATED PROTEIN 2//0.088:124:33//MUS MUSCULUS (MOUSE)//P20357

5 F-NT2RP2006196//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/4.0e-05:49:61//HOMO SAPIENS (HUMAN)//P39193

F-NT2RP2006200//PROCOLLAGEN ALPHA 2(V) CHAIN PRECURSOR//0.0013:205:32//HOMO SAPIENS (HUMAN)//P05997

10 F-NT2RP2006219//GONADAL PROTEIN GDL//3.5e-18:158:37//DROSOPHILA MELANOGASTER (FRUIT FLY)//P22468

F-NT2RP2006237//FIBRINOGEN- AND IG-BINDING PROTEIN PRECURSOR (MRP PROTEIN)//0.79:103:28//STREPTOCOCCUS PYOGENES//P30141

F-NT2RP2006238//PROLINE-RICH PROTEIN MP-3 (FRAGMENT)//4.7e-07:127:39//MUS MUSCULUS (MOUSE)//P05143

15 F-NT2RP2006258//PROBABLE E5 PROTEIN//0.78:47:34//RHESUS PAPILLOMAVIRUS TYPE 1 (RHPV 1)//P24834

F-NT2RP2006261//PENAEIDIN-3A PRECURSOR (P3-A)//0.61:35:40//PENAEUS VANNAMEI (PENOEID SHRIMP) (EUROPEAN WHITE SHRIMP)//P81058

F-NT2RP2006275//ELECTROMOTOR NEURON-ASSOCIATED PROTEIN 2 (FRAGMENT)//1.2e-28:59:57//TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY)//P14401

20 F-NT2RP2006312//HIGH-MOBILITY-GROUP PROTEIN (NONHISTONE CHROMOSOMAL PROTEIN)//1.6e-06:53:35//TETRAHYMENA PYRIFORMIS//P40625

F-NT2RP2006320//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT)//0.90:24:41//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BH5 ISOLATE) (HIV-1)//P04612

25 F-NT2RP2006321//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/0.0051:25:76//HOMO SAPIENS (HUMAN)//P39193

F-NT2RP2006323//WISKOTT-ALDRICH SYNDROME PROTEIN (WASP)//0.84:33:39//HOMO SAPIENS (HUMAN)//P42768

F-NT2RP2006333//MYOTOXIN 3 PRECURSOR (CROTAMINE 3)//0.56:37:40//CROTALUS DURISSUS TERRIFICUS (SOUTH AMERICAN RATTLESNAKE)//P24333

30 F-NT2RP2006334//SUCCINYL-COA LIGASE [GDP-FORMING], ALPHA-CHAIN 3 PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, ALPHA CHAIN 3)//0.00097:46:41//TRICHOMONAS VAGINALIS//P53401

F-NT2RP2006365//NONSPECIFIC LIPID-TRANSFER PROTEIN 4.3 PRECURSOR (LTP 4.3)//0.18:75:29//HORDEUM VULGARE (BARLEY)//Q42842

35 F-NT2RP2006393//OMEGA-CONOTOXIN MVIIC PRECURSOR (FRAGMENT)//0.82:15:66//CONUS MAGUS (MAGUS CONE)//P37300

F-NT2RP2006436//ANTERIOR-RESTRICTED HOMEBOX PROTEIN (RATHKE POUCH HOMEO BOX)//1.4e-08:50:50//MUS MUSCULUS (MOUSE)//Q61658

F-NT2RP2006441//METALLOTHIONEIN-LIKE PROTEIN 1//0.99:22:54//MIMULUS GUTTATUS (SPOTTED MONKEY FLOWER) (YELLOW MONKEY FLOWER)//P20238

40 F-NT2RP2006454//SPERM PROTAMINE P1//0.60:47:36//TACHYGLOSSUS ACULEATUS ACULEATUS (AUSTRALIAN ECHIDNA)//P35311

F-NT2RP2006456

F-NT2RP2006464//PHOTOSYSTEM I IRON-SULFUR CENTER (PHOTOSYSTEM I SUBUNIT VII) (9 KD POLYPEPTIDE) (PSI-C)//0.91:79:30//SYNECHOCOCCUS SP. (STRAIN PCC 7002) (AGMENELLUM QUADRUPLICATUM)//P31087

45 F-NT2RP2006467//PUTATIVE CUTICLE COLLAGEN F55C10.3//0.15:53:35//CAENORHABDITIS ELEGANS//Q21184

F-NT2RP2006472//HYPOTHETICAL 19 KD PROTEIN (ORF 167)//0.33:98:26//MARCHANTIA POLYMORPHA (LIVERWORT)//P12202

50 F-NT2RP2006534

F-NT2RP2006554//ANTI-SIGMA F FACTOR ANTAGONIST (STAGE II SPORULATION PROTEIN AA)//0.91:50:34//BACILLUS SPHAERICUS//O32723

F-NT2RP2006565//SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 1 (SCAMP 37)//6.0e-66:93:96//RATTUS NORVEGICUS (RAT)//P56603

55 F-NT2RP2006573//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE)//0.53:46:39//BOS TAURUS (BO-

VINE).//P02318

F-NT2RP2006598//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.3e-12:44:77//HOMO SAPIENS (HUMAN).//P39195

F-NT2RP3000002//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.4e-19:60:63//HOMO SAPIENS (HUMAN).//P39192

F-NT2RP3000031//HYPOTHETICAL 89.8 KD PROTEIN F41H10.6 IN CHROMOSOME IV.//2.1e-39:210:42//CAENORHABDITIS ELEGANS.//Q20296

F-NT2RP3000046//POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF.//1.4e-25:149:44//PSEUDOMONAS PUTIDA.//P25755

F-NT2RP3000047//NPL4 PROTEIN.//4.7e-48:275:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33755

F-NT2RP3000050//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//3.2e-72:232:59//HOMO SAPIENS (HUMAN).//P51522

F-NT2RP3000055//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.26:57:36//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643

F-NT2RP3000068//HYPOTHETICAL 182.0 KD PROTEIN IN NMD5-HOM6 INTERGENIC REGION.//0.0014:66:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47170

F-NT2RP3000072//HYPOTHETICAL 6.7 KD PROTEIN IN NOHA-CSPI INTERGENIC REGION.//0.95:49:30//ESCHERICHIA COLI.//P77695

F-NT2RP3000080//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/5.1e-17:64:68//HOMO SAPIENS (HUMAN).//P39188

F-NT2RP3000085//BIOTIN CARBOXYLASE (EC 6.3.4.14) (A SUBUNIT OF ACETYL-COA CARBOXYLASE (EC 6.4.1.2)) (ACC).//4.4e-43:169:51//BACILLUS SUBTILIS.//P49787

F-NT2RP3000092//CELL DIVISION CONTROL PROTEIN 1.//0.00016:103:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40986

F-NT2RP3000109//ACYL CARRIER PROTEIN HOMOLOG (ACP).//0.76:83:28//MYCOPLASMA GENITALIUM.//P47529

F-NT2RP3000134

F-NT2RP3000142//GAR2 PROTEIN.//0.00098:241:20//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P41891

F-NT2RP3000149//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.0014:33:36//PONGO PYGMAEUS ABELII (SUMATRAN ORANGUTAN).//P92694

F-NT2RP3000186//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/8.3e-15:36:83//HOMO SAPIENS (HUMAN).//P39188

F-NT2RP3000197//HYPOTHETICAL 6.0 KD PROTEIN IN THI12 5'REGION.//0.91:21:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53820

F-NT2RP3000207//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//0.026:209:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640

F-NT2RP3000220//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//1.0:26:42//HOMO SAPIENS (HUMAN).//P30808

F-NT2RP3000233//RING CANAL PROTEIN (KELCH PROTEIN).//2.1e-42:249:39//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-NT2RP3000235//HOMEBOX PROTEIN H40 (FRAGMENT).//0.55:45:40//APIS MELLIFERA (HONEYBEE).//P15858

F-NT2RP3000247//HYPOTHETICAL PROTEIN KIAA0218.//1.7e-82:123:69//HOMO SAPIENS (HUMAN).//Q93075

F-NT2RP3000251//SERINE PROTEINASE STUBBLE (EC 3.4.21.-) (STUBBLE-STUBBLOID PROTEIN).//1.0:53:33//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q05319

F-NT2RP3000252//HYPOTHETICAL 40 KD GTP-BINDING PROTEIN IN RIBOSOMAL PROTEIN GENE CLUSTER 5'REGION.//2.2e-06:96:32//HALOBACTERIUM CUTIRUBRUM.//P17103

F-NT2RP3000255//HISTONE H1.1 (FRAGMENT).//0.95:71:33//BOS TAURUS (BOVINE).//P02253

F-NT2RP3000267//HYPOTHETICAL 21.1 KD PROTEIN IN SSR-SERA INTERGENIC REGION (O182).//0.38:77:33//ESCHERICHIA COLI.//P09160

F-NT2RP3000299//MYOSIN IC HEAVY CHAIN.//1.2e-11:147:34//ACANTHAMOEBA CASTELLANI (AMOEBA)

F-NT2RP3000301//HYPOTHETICAL PROTEIN IN NMD5-HOM6 INTERGENIC REGION.//0.0014:66:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214

F-NT2RP3000599//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66)//0.00095:90:37//HOMO
 SAPIENS (HUMAN)//Q15428
 F-NT2RP3000603//5E5 ANTIGEN//1.0e-09:181:34//RATTUS NORVEGICUS (RAT)//Q63003
 F-NT2RP3000605//STEROL REGULATORY ELEMENT BINDING PROTEIN-1 (SREBP-1) (STEROL REGULA-
 5 TORY ELEMENT-BINDING TRANSCRIPTION FACTOR 1)//0.00098:76:34//HOMO SAPIENS (HUMAN)//
 P36956
 F-NT2RP3000622//HYPOTHETICAL PROTEIN MG096 HOMOLOG 5 (P02_ORF427)//0.15:52:36//MYCOPLAS-
 MA PNEUMONIAE//P75277
 F-NT2RP3000624//HYPOTHETICAL PROTEIN KIAA0256//5.4e-16:222:31//HOMO SAPIENS (HUMAN)//
 10 Q93073
 F-NT2RP3000628
 F-NT2RP3000632//ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10)//2.0e-16:52:63//MUS
 MUSCULUS (MOUSE)//Q61967
 F-NT2RP3000644//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/6.7e-40:102:79//HOMO SAPIENS (HU-
 15 MAN)//P39194
 F-NT2RP3000661//HYPOTHETICAL 139.1 KD PROTEIN C08B11.3 IN CHROMOSOME II//6.0e-08:83:36//
 CAENORHABDITIS ELEGANS//Q09441
 F-NT2RP3000665//HOMEBOX PROTEIN PROPHET OF PIT-1 (PROP-1) (PITUITARY SPECIFIC HOMEODO-
 MAIN FACTOR)//0.13:48:35//HOMO SAPIENS (HUMAN)//O75360
 20 F-NT2RP3000685//HYPOTHETICAL 33.5 KD PROTEIN IN CAT1 5'REGION (ORFY)//0.26:202:23//CLOSTRID-
 IUM KLUYVERI//P38943
 F-NT2RP3000690//INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO- HYDRO-
 LASE) (PPASE)//0.99:131:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P00817
 F-NT2RP3000736//HYPOTHETICAL 28.7 KD PROTEIN IN RNR3-ARC15 INTERGENIC REGION//3.5e-27:211:
 25 34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40516
 F-NT2RP3000739//HYPOTHETICAL 33.5 KD PROTEIN C1D4.02C IN CHROMOSOME I//6.0e-23:114:42//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10149
 F-NT2RP3000742//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC
 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III)//6.7e-12:85:36//RATTUS NORVEGICUS
 30 (RAT)//P10688
 F-NT2RP3000753//CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER
 PROTEIN 1)//0.00011:208:28//CLOSTRIDIUM THERMOCELLUM//Q06852
 F-NT2RP3000759//ADP-RIBOSYLATION FACTOR 6//8.1e-28:141:38//GALLUS GALLUS (CHICKEN)//P26990
 F-NT2RP3000815//CYTOCHROME C-551 (C551) (CYTOCHROME C8)//0.24:45:37//PSEUDOMONAS DENI-
 35 TRIFICANS//P00103
 F-NT2RP3000825//ALPHA-LACTALBUMIN (LACTOSE SYNTHASE B PROTEIN (EC 2.4.1.22))//0.82:51:39//
 MACROPUS RUFOGRISEUS (RED-NECKED WALLABY)//P07458
 F-NT2RP3000826//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS)//0.025:79:37//BOS TAURUS (BOVINE)//
 P25508
 40 F-NT2RP3000836//HYPOTHETICAL PROTEIN IN KSGA 3'REGION (ORF L5) (FRAGMENT)//0.85:36:47//MYC-
 OPLASMA CAPRICOLUM//P43040
 F-NT2RP3000841//UDP-GLUCURONOSYLTRANSFERASE 1-7 PRECURSOR, MICROSOMAL (EC 2.4.1.17)
 (UDPGT) (UGT1*7) (UGT1-07) (UGT1.7) (UGT1A7) (UGTP4) (FRAGMENT)//1.0:70:34//MUS MUSCULUS
 (MOUSE)//Q62452
 45 F-NT2RP3000845//PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-)//5.2e-72:247:61//HO-
 MO SAPIENS (HUMAN)//P27448
 F-NT2RP3000847//HYPOTHETICAL PROTEIN KIAA0161//0.037:55:30//HOMO SAPIENS (HUMAN)//P50876
 F-NT2RP3000850//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/7.4e-31:90:75//HOMO SAPIENS (HUMAN)//
 P39194
 50 F-NT2RP3000852//HYDROPHOBIC SEED PROTEIN (HPS)//0.33:23:69//GLYCINE MAX (SOYBEAN)//P24337
 F-NT2RP3000859//IMMEDIATE-EARLY PROTEIN//3.6e-07:189:25//HERPESVIRUS SAIMIRI (STRAIN 11)//
 Q01042
 F-NT2RP3000865
 F-NT2RP3000868//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE ISOFORM (FRAGMENT)//1.4e-09:232:28//
 55 GALLUS GALLUS (CHICKEN)//P29616
 F-NT2RP3000875//HOMEBOX PROTEIN PROPHET OF PIT-1 (PROP-1) (PITUITARY SPECIFIC HOMEODO-
 MAIN FACTOR)//0.13:48:35//HOMO SAPIENS (HUMAN)//O75360
 MUS MUSCULUS (MOUSE)//P43241

F-NT2RP3000901//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS)//0.99:124:33//BOS TAURUS (BOVINE)//
 P02453
 F-NT2RP3000904
 F-NT2RP3000917//DHP1 PROTEIN//6.5e-60:229:55//SCHIZOSACCHAROMYCES POMBE (FISSION
 5 YEAST)//P40848
 F-NT2RP3000919//HYPOTHETICAL 33.5 KD PROTEIN C1D4.02C IN CHROMOSOME I//2.4e-19:159:34//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10149
 F-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A//3.7e-48:73:98//HOMO SAPIENS (HUMAN), AND RAT-
 TUS NORVEGICUS (RAT)//P39027
 10 F-NT2RP3000980//COPA/INCA PROTEIN (REPA3 PROTEIN)//0.24:19:47//ESCHERICHIA COLI//P13946
 F-NT2RP3000994//MATERNAL EFFECT PROTEIN STAUFEN//1.4e-10:78:48//DROSOPHILA MELA-
 NOGASTER (FRUIT FLY)//P25159
 F-NT2RP3001004//HYPOTHETICAL 7.6 KD PROTEIN B0563.8 IN CHROMOSOME X//0.70:50:32//
 CAENORHABDITIS ELEGANS//Q11084
 15 F-NT2RP3001007
 F-NT2RP3001055//N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT HOMOLOG//1.3e-05:
 138:28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD)//P36416
 F-NT2RP3001057//ZINC FINGER PROTEIN 45 (BRC1744)//4.0e-28:141:51//HOMO SAPIENS (HUMAN)//
 Q02386
 20 F-NT2RP3001081//HYPOTHETICAL 46.4 KD PROTEIN T16H12.5 IN CHROMOSOME III//3.8e-08:144:29//
 CAENORHABDITIS ELEGANS//P34568
 F-NT2RP3001084//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT)//3.4e-06:217:32//NEPHILA CLA-
 VIPES (ORB SPIDER)//P46804
 F-NT2RP3001096//SYNAPTONEMAL COMPLEX PROTEIN SC65//1.1e-30:244:33//RATTUS NORVEGICUS
 25 (RAT)//Q64375
 F-NT2RP3001107//ARYLSULFATASE F (EC 3.1.6.-) (ASF) (FRAGMENT)//0.041:47:44//HOMO SAPIENS (HU-
 MAN)//P54793
 F-NT2RP3001109
 F-NT2RP3001111//MALE SPECIFIC SPERM PROTEIN MST84DC//0.17:28:39//DROSOPHILA MELA-
 30 NOGASTER (FRUIT FLY)//Q01644
 F-NT2RP3001113//INVOLUCRIN//0.00036:192:23//MUS MUSCULUS (MOUSE)//P48997
 F-NT2RP3001115
 F-NT2RP3001116//AMINOPEPTIDASE G (EC 3.4.11.-) (FRAGMENT)//0.99:29:51//STREPTOMYCES LIVI-
 DANS//Q54340
 35 F-NT2RP3001119//COLLAGEN ALPHA 4(IV) CHAIN (FRAGMENT)//0.0015:73:39//BOS TAURUS (BOVINE)//
 Q29442
 F-NT2RP3001120//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT)//1.3e-57:229:52//HOMO SAPIENS (HU-
 MAN)//P16415
 F-NT2RP3001126//HYPOTHETICAL 91.2 KD PROTEIN IN RPS4B-SCH9 INTERGENIC REGION//2.8e-07:83:
 40 34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38888
 F-NT2RP3001133//CALCIUM BINDING PROTEIN//2.0e-08:171:32//DICTYOSTELIUM DISCOIDEUM (SLIME
 MOLD)//P35085
 F-NT2RP3001140//F-SPONDIN PRECURSOR//2.0e-147:244:97//RATTUS NORVEGICUS (RAT)//P35446
 F-NT2RP3001147//TROPOMYOSIN 2 (TMII)//0.11:159:23//SCHISTOSOMA MANSONI (BLOOD FLUKE)//
 45 P42638
 F-NT2RP3001150//OCTAPEPTIDE-REPEAT PROTEIN T2//6.2e-09:163:25//MUS MUSCULUS (MOUSE)//
 Q06666
 F-NT2RP3001155//DNA POLYMERASE ALPHA-BINDING PROTEIN (POB1/CTF4 PROTEIN) (CHROMOSOME
 REPLICATION PROTEIN CHL15)//4.1e-05:244:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//
 50 Q01454
 F-NT2RP3001176//LEUKOSIALIN PRECURSOR (LEUCOCYTE SIALOGLYCOPROTEIN) (SIALOPHORIN)
 (CD43) (LY 48) (B CELL DIFFERENTIATION ANTIGEN LP-3)//0.21:136:26//MUS MUSCULUS (MOUSE)//
 P15702
 F-NT2RP3001214//SAP1 PROTEIN//0.058:133:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//
 P39955
 F-NT2RP3001221//GAMMA-BUTYROBETAINE 2-OXOGLUTARATE DIOXYGENASE (EC 1.14.11.1) (GAMMA

BUTYROBETAINE HYDROXYLASE) //4.2e-05:131:26//PSEUDOMONAS SP. (STRAIN AK-1) //P80193
 F-NT2RP3001232//HYPOTHETICAL PROTEIN PRECURSOR IN CS5 3'REGION (FRAGMENT) //0.75:57:31//
 ESCHERICHIA COLI //P33792
 5 F-NT2RP3001236//TRANSFORMING PROTEIN MAF //0.017:136:30//AVIAN MUSCULOAPONEUROTIC FIB-
 ROSARCOMA VIRUS AS42 //P23091
 F-NT2RP3001239//ELECTROMOTOR NEURON-ASSOCIATED PROTEIN 1 (FRAGMENT) //4.2e-55:221:49//
 TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY) //P14400
 F-NT2RP3001245
 10 F-NT2RP3001253//TROPOMYOSIN 2, MUSCLE THORACIC ISOFORM (TROPOMYOSIN I) //0.0042:142:24//
 DROSOPHILA MELANOGASTER (FRUIT FLY) //P09491
 F-NT2RP3001260//COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR //0.0011:89:43//HOMO SAPIENS (HU-
 MAN) //P53420
 F-NT2RP3001268//ZINC FINGER PROTEIN 45 (BRC1744) //9.0e-29:194:44//HOMO SAPIENS (HUMAN) //
 Q02386
 15 F-NT2RP3001272//HYPOTHETICAL 75.2 KD PROTEIN C13F4.08C IN CHROMOSOME I //8.2e-17:183:26//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST) //Q10199
 F-NT2RP3001274//SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOS-
 PHATASE T) (PPT) (FRAGMENT) //1.7e-09:78:39//MUS MUSCULUS (MOUSE) //Q60676
 F-NT2RP3001281//!!!! ALU SUBFAMILY J WARNING ENTRY !!!! //7.7e-08:38:71//HOMO SAPIENS (HUMAN) //
 20 P39188
 F-NT2RP3001297//HYPOTHETICAL PROTEIN KIAA0281 (HA6725) //2.2e-57:159:70//HOMO SAPIENS (HU-
 MAN) //Q92556
 F-NT2RP3001307//SPERM PROTAMINE P1 //0.21:46:39//ORNITHORHYNCHUS ANATINUS (DUCKBILL PLAT-
 YPUS) //P35307
 25 F-NT2RP3001318
 F-NT2RP3001325//ENHANCER OF RUDIMENTARY HOMOLOG //1.0:73:24//BRACHYDANIO RERIO (ZE-
 BRAFISH) (ZEBRA DANIO) //Q98874
 F-NT2RP3001338//ZINC FINGER PROTEIN 29 (ZINC FINGER PROTEIN KOX26) (FRAGMENT) //0.0021:56:
 35//HOMO SAPIENS (HUMAN) //P17037
 30 F-NT2RP3001339//CITRON PROTEIN //3.6e-06:90:33//MUS MUSCULUS (MOUSE) //P49025
 F-NT2RP3001340//HYPOTHETICAL PROTEIN UL61 //7.2e-11:202:34//HUMAN CYTOMEGALOVIRUS
 (STRAIN AD169) //P16818
 F-NT2RP3001355//TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PRO-
 TEIN) (CTP) (TRICARBOXYLATE CARRIER PROTEIN) //7.7e-16:129:33//HOMO SAPIENS (HUMAN) //P53007
 35 F-NT2RP3001356//RAS-RELATED PROTEIN RABA (FRAGMENT) //0.00041:66:28//DICTYOSTELIUM DISCOI-
 DEUM (SLIME MOLD) //P34141
 F-NT2RP3001374
 F-NT2RP3001383//PTB-ASSOCIATED SPLICING FACTOR (PSF) //2.5e-06:190:32//HOMO SAPIENS (HU-
 MAN) //P23246
 40 F-NT2RP3001384//CHORION PROTEIN S15 //0.00079:94:37//DROSOPHILA VIRILIS (FRUIT FLY) //P13424
 F-NT2RP3001392//VPU PROTEIN (ORF-X PROTEIN) (UPX PROTEIN) //1.0:22:45//CAPRINE ARTHRITIS EN-
 CEPHALITIS VIRUS (CAEV) //P31834
 F-NT2RP3001396//HYPOTHETICAL 8.1 KD PROTEIN (ORF4) //1.0:37:32//STRAWBERRY MILD YELLOW
 EDGE-ASSOCIATED VIRUS (SMYEA) //Q00848
 45 F-NT2RP3001398//KRUEPPEL-RELATED ZINC FINGER PROTEIN 2 (HKR2 PROTEIN) (FRAGMENT) //1.9e-
 08:45:37//HOMO SAPIENS (HUMAN) //P10073
 F-NT2RP3001399//SSU72 PROTEIN //7.3e-18:84:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //
 P53538
 F-NT2RP3001407//SCY1 PROTEIN //1.5e-08:143:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //
 50 P53009
 F-NT2RP3001420//HYPOTHETICAL 7.9 KD PROTEIN //0.25:41:26//VACCINIA VIRUS (STRAIN COPENHA-
 GEN) //P20542
 F-NT2RP3001426//DNAJ PROTEIN //7.5e-15:78:43//HAEMOPHILUS INFLUENZAE //P43735
 F-NT2RP3001427//WERNER SYNDROME HELICASE //3.6e-13:159:33//HOMO SAPIENS (HUMAN) //Q14191
 55 F-NT2RP3001428//NUCLEOPROTEIN TPR //1.8e-53:117:99//HOMO SAPIENS (HUMAN) //P12270
 F-NT2RP3001437//HYPOTHETICAL 5.5 KD PROTEIN IN REPLICATION ORIGIN REGION (ORF1) //0.96:45:35//
 TARSUS SYRICHIA (TARSIER) //Q36111
 F-NT2RP3001447//HYPOTHETICAL 5.5 KD PROTEIN IN REPLICATION ORIGIN REGION (ORF1) //0.96:45:35//

ESCHERICHIA COLI//P14505

F-NT2RP3001449//HOMEOBOX PROTEIN SAX-1 (CHOX-3) (FRAGMENT)//0.0043:53:43//GALLUS GALLUS (CHICKEN)//P19601

F-NT2RP3001453//MALE SPECIFIC SPERM PROTEIN MST84DB//0.0048:65:40//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q01643

F-NT2RP3001457//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS28.//0.55:121:20//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q02767

F-NT2RP3001459//MYOSIN IC HEAVY CHAIN//0.10:126:34//ACANTHAMOEBA CASTELLANII (AMOEBA)//
P10569

F-NT2RP3001472//NONHISTONE CHROMOSOMAL PROTEIN 6A//3.0e-14:87:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P11632

F-NT2RP3001490//METALLOTHIONEIN-LIKE PROTEIN LSC54.//1.0:39:35//BRASSICA NAPUS (RAPE).//
P43402

F-NT2RP3001495//UBIQUITIN--PROTEIN LIGASE RSP5 (EC 6.3.2.-)//3.3e-14:148:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P39940

F-NT2RP3001497//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS)//0.13:44:38//BOS TAURUS (BOVINE)//
P25508

F-NT2RP3001527//SPERM PROTAMINE P1.//0.35:29:37//DIDELPHIS MARSUPIALIS VIRGINIANA (NORTH AMERICAN OPOSSUM), AND MONODELPHIS DOMESTICA (SHORT-TAILED GREY OPOSSUM).//P35305

F-NT2RP3001529//HYPOTHETICAL 43.3 KD GTP-BINDING PROTEIN IN DACB-RPMA INTERGENIC REGION//3.3e-21:125:37//ESCHERICHIA COLI//P42641

F-NT2RP3001538//HNF3/FH TRANSCRIPTION FACTOR GENESIS (WINGED HELIX PROTEIN CWH-3).//0.13:
53:39//GALLUS GALLUS (CHICKEN)//P79772

F-NT2RP3001554//ELECTROMOTOR NEURON-ASSOCIATED PROTEIN 2 (FRAGMENT)//2.3e-48:137:52//
TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY)//P14401

F-NT2RP3001580//GERM CELL-LESS PROTEIN.//8.2e-18:100:42//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q01820

F-NT2RP3001587//UBIQUITIN-ACTIVATING ENZYME E1-LIKE (POLYMERASE-INTERACTING PROTEIN 2).//
2.0e-47:188:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P52488

F-NT2RP3001589//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/7.4e-41:87:80//HOMO SAPIENS (HUMAN).//
P39193

F-NT2RP3001607//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//1.0:49:32//DICENTRARCHUS LABRAX (EUROPEAN SEA BASS)//Q36362

F-NT2RP3001608//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN)//0.0013:177:25//ZEA MAYS (MAIZE)//P14918

F-NT2RP3001621//MALE SPECIFIC SPERM PROTEIN MST84DD//0.84:29:37//DROSOPHILA MELA-
NOGASTER (FRUIT FLY)//Q01645

F-NT2RP3001629//RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1 (P21-RAC1) (FRAGMENTS)//0.91:57:24//CAVIA PORCELLUS (GUINEA PIG)//P80236

F-NT2RP3001634//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/8.9e-11:73:54//HOMO SAPIENS (HUMAN).//
P39189

F-NT2RP3001642//HYPOTHETICAL PROTEIN KIAA0210.//1.1e-12:117:29//HOMO SAPIENS (HUMAN).//
Q92609

F-NT2RP3001646//HYPOTHETICAL 29.3 KD PROTEIN (ORF92)//0.0092:69:34//ORGYIA PSEUDOTSUGATA
MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV)//O10341

F-NT2RP3001671//RING CANAL PROTEIN (KELCH PROTEIN).//0.0042:55:41//DROSOPHILA MELA-
NOGASTER (FRUIT FLY)//Q04652

F-NT2RP3001672

F-NT2RP3001676//GTP-BINDING PROTEIN LEPA (FRAGMENT)//1.2e-15:56:62//PSEUDOMONAS FLUORESCENS//P26843

F-NT2RP3001678//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT)//0.054:187:31//NEPHILA CLAVIPES (ORB SPIDER).//P46804

F-NT2RP3001679//HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III.//1.5e-07:63:44//
CAENORHABDITIS ELEGANS//P34679

F-NT2RP3001688//GLUCOAMYLASE S1 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE)

- AST - P04065

NT2RP3001690//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM.//0.021.247.24//HOMO SA-

PIENS (HUMAN)//P12883

F-NT2RP3001698

F-NT2RP3001708//TWISTED GASTRULATION PROTEIN PRECURSOR//7.7e-12:73:43//DROSOPHILA MEL-
ANOGASTER (FRUIT FLY)//P54356

5 F-NT2RP3001712//CEC-1 PROTEIN//1.9e-07:121:29//CAENORHABDITIS ELEGANS//P34618

F-NT2RP3001716//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR//0.89:54:40//DROSOPHILA SIMULANS
(FRUIT FLY)//P13729

F-NT2RP3001724//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1)//7.5e-41:164:48//HO-
MO SAPIENS (HUMAN)//O14646

10 F-NT2RP3001727//HYPOTHETICAL 37.7 KD PROTEIN ZK686.3 IN CHROMOSOME III//1.5e-51:240:41//
CAENORHABDITIS ELEGANS//P34669

F-NT2RP3001730//SEPTIN 2 HOMOLOG (FRAGMENT)//2.4e-122:267:86//HOMO SAPIENS (HUMAN)//
Q14141

15 F-NT2RP3001739//INTESTINAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE
COTRANSPORTER)//0.99:63:34//RATTUS NORVEGICUS (RAT)//P70545

F-NT2RP3001752//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/4.0e-21:60:85//HOMO SAPIENS (HUMAN)//
P39193

F-NT2RP3001753//HYPOTHETICAL PROTEIN KIAA0127//7.9e-12:83:44//HOMO SAPIENS (HUMAN)//
Q14140

20 F-NT2RP3001764//DUAL SPECIFICITY PROTEIN PHOSPHATASE 6 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPE-
CIFICITY PROTEIN PHOSPHATASE PYST1)//7.7e-25:146:36//HOMO SAPIENS (HUMAN)//Q16828

F-NT2RP3001777//SERINE/THREONINE-PROTEIN KINASE STE20 HOMOLOG (EC 2.7.1.-)//0.0096:204:25//
CANDIDA ALBICANS (YEAST)//Q92212

25 F-NT2RP3001782//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//0.91:34:44//PONGO PYGMAEUS ABELII
(SUMATRAN ORANGUTAN)//P92694

F-NT2RP3001792//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP M)//1.8e-33:159:53//
HOMO SAPIENS (HUMAN)//P52272

F-NT2RP3001799//LIGHT-HARVESTING PROTEIN B800/830/1020, ALPHA-2 CHAIN (EHS-ALPHA-2) (ANTEN-
NA PIGMENT PROTEIN, ALPHA-2 CHAIN)//0.14:46:28//ECTOTHIORHODOSPIRA HALOCHLORIS//P80103

30 F-NT2RP3001819//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR//0.00030:77:36//HOMO SAPIENS (HU-
MAN)//P08123

F-NT2RP3001844//OCTAMER-BINDING TRANSCRIPTION FACTOR 1 (OTF-1) (NF-A1) (FRAGMENT)//0.99:
43:34//MACROPUS EUGENII (TAMMAR WALLABY)//Q28466

35 F-NT2RP3001854//FIBRINOGEN- AND IG-BINDING PROTEIN PRECURSOR (MRP PROTEIN)//9.3e-10:213:
24//STREPTOCOCCUS PYOGENES//P30141

F-NT2RP3001855//HOMEBOX PROTEIN PKNOX1 (HOMEBOX PROTEIN PREP-1)//2.6e-61:220:60//HO-
MO SAPIENS (HUMAN)//P55347

F-NT2RP3001857//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1//1.0e-13:213:24//PODOSPORA AN-
SERINA//Q00808

40 F-NT2RP3001896//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66)//0.074:124:34//HOMO SA-
PIENS (HUMAN)//Q15428

F-NT2RP3001898//REGULATORY PROTEIN E2//0.36:131:29//CANINE ORAL PAPILLOMAVIRUS (COPV)//
Q89420

45 F-NT2RP3001915//CHITIN BIOSYNTHESIS PROTEIN CHS5 (CAL3 PROTEIN)//0.0021:237:23//SACCHARO-
MYCES CEREVISIAE (BAKER'S YEAST)//Q12114

F-NT2RP3001926//HYPOTHETICAL 14.0 KD PROTEIN IN RPL15B-GCR3 INTERGENIC REGION//1.0:63:34//
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q03880

F-NT2RP3001929//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.4e-14:35:60//HOMO SAPIENS (HUMAN)//
P39195

50 F-NT2RP3001931//HYPOTHETICAL 59.3 KD PROTEIN IN TAP42-ARP9 INTERGENIC REGION//0.86:162:24//
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q05040

F-NT2RP3001938//GLYCOPROTEIN GP50//0.0036:54:40//PSEUDORABIES VIRUS (STRAIN RICE) (PRV)//
P07645

55 F-NT2RP3001943//33.2 KD PROTEIN IN DIND-RPH INTERGENIC REGION (ORF X)//1.0:113:27//ES-
CHERICHIA COLI//P23839

F-NT2RP3001950

CAENORHABDITIS ELEGANS//Q09428

F-NT2RP3001969//POPH-19-2 PROTEIN PRECURSOR//0.0078:149:26//SCIARA COPROPHILA (FUNGUS)

F-NT2RP3002002//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.2e-44:69:79//HOMO SAPIENS (HUMAN).//
P39195

F-NT2RP3002004//TRANSCRIPTION FACTOR BF-2 (BRAIN FACTOR 2) (BF2)//0.00024:45:40//MUS MUSCULUS (MOUSE)//Q61345

F-NT2RP3002007//TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEM) (JI) (MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225) (TENASCIN-C)//0.21:115:28//HOMO SAPIENS (HUMAN)//P24821

F-NT2RP3002014//HYPOTHEetical 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III.//1.7e-25:139:48//
CAENORHABDITIS ELEGANS//Q09232

F-TN2RP3002033//ACTIVATOR OF APOPTOSIS HARAKIRI (NEURONAL DEATH PROTEIN DP5)//0.14:65:41//HOMO SAPIENS (HUMAN)//O00198

F-NT2RP3002045/ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT)/8.1e-108:192:98/MUS MUSCULUS (MOUSE)./P17427

F-NT2RP3002054//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556//0.046:176:31//STREPTOMYCES FRADIAE//P20186

F-NT2RP3002056//140 KD NUCLEOLAR PHOSPHOPROTEIN (NOPP140).//1.4e-07:245:25//RATTUS NOR-VEGICUS (RAT).//P41777

F-NT2RP3002057//SMALL HYDROPHOBIC PROTEIN.//1.0:12:66//SIMIAN VIRUS 5 (STRAIN W3) (SV5).//P07577

F-NT2RP3002062//PROTEASE A INHIBITOR 3 (PROTEINASE INHIBITOR I(A)3)//1.0:49:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P01094

F-NT2RP3002063//ACYL CARRIER PROTEIN (ACP)//0.99:38:31//HAEMOPHILUS INFLUENZAE//P43709

F-NT2RP3002081//HYPOTHETICAL 100.5 KD PROTEIN C1B9.04 IN CHROMOSOME I//5.8e-35:253:37//
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10429

F-NT2RP3002097//HYPOTHETICAL 98.1 KD PROTEIN IN SPX19-GCR2 INTERGENIC REGION.//6.2e-06:99:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40164

F-NT2RP3002102//HYPOTHETICAL 7.4 KD PROTEIN.//0.68:34:47//THERMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1).//P19302

F-NT2RP3002108//HYPOTHETICAL 105.5 KD PROTEIN R13F6.10 IN CHROMOSOME III.//7.9e-19:179:34//
CAENORHABDITIS ELEGANS//Q21986

F-NT2RP3002142//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.6e-17:37:75//HOMO SAPIENS (HUMAN).//
P39188

F-NT2RP3002146//CUTICLE COLLAGEN 40J//0.00034:90:37//CAENORHABDITIS ELEGANS.//P34804

F-NT2RP3002147//SALIVARY PROLINE-RICH PROTEIN PO PRECURSOR (ALLELE S)//0.011:166:28//HOMO SAPIENS (HUMAN)//P10163

F-NT2RP3002151//G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG (GTP-BINDING PROTEIN GST1-HS)//4.8e-11:60:53//HOMO SAPIENS (HUMAN)//P15170

F-NT2RP3002163//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130)//O.028:191:29//HOMO SAPIENS (HUMAN)//O00268

F-NT2RP3002165//TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP.//2.3e-131:223:91//MUS MUSCULUS (MOUSE) //Q02614

F-NT2RP3002166//D-ALANYL CARRIER PROTEIN (DCP)//1.0:65:33//LACTOBACILLUS CASEI//P55153

F-NT2RP3002173//!!!! ALU SUBFAMILY SQ WARNING ENTRY!!!!/2.4e-26:114:62//HOMO SAPIENS (HUMAN)//P39194

F-NT2RP3002181//MALE SPECIFIC SPERM PROTEIN MST84DD//0.25:31:38//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q01645

F-NT2RP3002244//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE)//0.069:16:62//OVIS ARIES (SHEEP), AND CAPRA HIRCUS (GOAT)//P04102

F-NT2RP3002248//MICROFIBRILLAR-ASSOCIATED PROTEIN 1 (ASSOCIATED MICROFIBRIL PROTEIN) (AMF).//0.0079:187:24//GALLUS GALLUS (CHICKEN).//P55080

F-NT2RP3002255//PROINFL-RICH PROTEIN MP-3 (FRAGMENT) 14-60-10-168-34//MUS MUSCULUS

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F-NT2RP3002276//PROBABLE E4 PROTEIN//0.91:54:29//HUMAN PAPILLOMAVIRUS TYPE 16//P06922
 F-NT2RP3002303//HYPOTHETICAL 30.2 KD PROTEIN C4D7.04C IN CHROMOSOME I//1.7e-42:191:43//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//O14171
 F-NT2RP3002304
 5 F-NT2RP3002330//NNP-1 PROTEIN//0.52:140:18//MUS MUSCULUS (MOUSE)//P56183
 F-NT2RP3002343//5E5 ANTIGEN//0.0056:189:30//RATTUS NORVEGICUS (RAT)//Q63003
 F-NT2RP3002351//NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.15)
 / METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE (EC 3.5.4.9) MITOCHONDRIAL PRECURSOR//
 1.0e-66:196:68//HOMO SAPIENS (HUMAN)//P13995
 10 F-NT2RP3002352//PRESYNAPTIC PROTEIN SAP102 (SYNAPSE-ASSOCIATED PROTEIN 102) (NEUROEN-
 DOCRINE-DLG) (NE-DLG)//0.79:173:27//HOMO SAPIENS (HUMAN)//Q92796
 F-NT2RP3002377//PUTATIVE HELICASE YGR271W//1.0e-56:216:44//SACCHAROMYCES CEREVISIAE
 (BAKER'S YEAST)//P53327
 F-NT2RP3002399//MINICHROMOSOME MAINTENANCE PROTEIN 6//1.4e-19:136:31//SACCHAROMYCES
 15 CEREVISIAE (BAKER'S YEAST)//P53091
 F-NT2RP3002402//EBNA-6 NUCLEAR PROTEIN (EBNA-3C) (EBNA-4B)//0.74:107:36//EPSTEIN-BARR VIRUS
 (STRAIN B95-8) (HUMAN HERPESVIRUS 4)//P03204
 F-NT2RP3002455//DNAJ PROTEIN (FRAGMENT)//5.6e-06:57:42//AGROBACTERIUM TUMEFACIENS//
 P50018
 20 F-NT2RP3002484//HYPOTHETICAL 46.5 KD PROTEIN C12B10.04 IN CHROMOSOME I//0.00032:52:48//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10438
 F-NT2RP3002501//HYPOTHETICAL 34.9 KD PROTEIN IN FRE2-JEN1 INTERGENIC REGION//9.4e-42:209:
 42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P36007
 F-NT2RP3002512//HYPOTHETICAL 37.4 KD PROTEIN IN GPM1-MCR1 INTERGENIC REGION//7.7e-32:162:
 25 37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P36059
 F-NT2RP3002529//PUTATIVE VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN C2G11.03C//2.1e-45:
 241:43//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09805
 F-NT2RP3002545
 F-NT2RP3002549//HYPOTHETICAL 26.6 KD PROTEIN T19C3.4 IN CHROMOSOME III//2.8e-41:161:52//
 30 CAENORHABDITIS ELEGANS//Q10010
 F-NT2RP3002566//IMMEDIATE-EARLY PROTEIN IE180//0.56:130:24//PSEUDORABIES VIRUS (STRAIN KA-
 PLAN) (PRV)//P33479
 F-NT2RP3002587
 F-NT2RP3002590
 35 F-NT2RP3002602//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1) (THIOREDOXIN-
 RELATED GLYCOPROTEIN 1)//0.00091:111:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P17967
 F-NT2RP3002603//HYPOTHETICAL 14.2 KD PROTEIN IN BLAB 3'REGION//1.0:65:40//STREPTOMYCES CA-
 CAO1//P33654
 F-NT2RP3002628//DNAJ-LIKE PROTEIN SLR0093//2.4e-17:101:44//SYNECHOCYSTIS SP. (STRAIN PCC
 40 6803)//P50027
 F-NT2RP3002631//METALLOTHIONEIN-IB (MT-1B)//0.092:36:33//HOMO SAPIENS (HUMAN)//P07438
 F-NT2RP3002650//DUALIN//3.0e-21:184:37//GALLUS GALLUS (CHICKEN)//Q90830
 F-NT2RP3002659//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR//0.00016:223:33//HOMO SAPIENS (HU-
 MAN)//P08123
 45 F-NT2RP3002660//40S RIBOSOMAL PROTEIN S27A//0.16:72:31//CAENORHABDITIS ELEGANS//P37165
 F-NT2RP3002663//OXYSTEROL-BINDING PROTEIN//5.4e-23:168:41//HOMO SAPIENS (HUMAN)//P22059
 F-NT2RP3002671//HYPOTHETICAL 124.5 KD PROTEIN IN SKO1-RPL44A INTERGENIC REGION//6.0e-38:
 203:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53893
 F-NT2RP3002682//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3)//0.25:63:31//ARTEMIA
 50 SALINA (BRINE SHRIMP)//P19049
 F-NT2RP3002687//HYPOTHETICAL 30.4 KD PROTEIN IN LEF3-IAP2 INTERGENIC REGION//0.029:60:36//
 AUTOGRAPHAL CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV)//P41469
 F-NT2RP3002688//KINESIN-LIKE PROTEIN KIF1B//5.3e-61:130:88//MUS MUSCULUS (MOUSE)//Q60575
 F-NT2RP3002701//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS)//7.4e-05:109:33//MUS
 55 MUSCULUS (MOUSE)//P15265
 F-NT2RP3002702//HYPOTHETICAL 31.3 KD PROTEIN C2C6.07 IN CHROMOSOME I//6.7e-11:66:40:
 32//HOMO SAPIENS (HUMAN)//Q13201
 F-NT2RP3002763//HYPOTHETICAL 31.3 KD PROTEIN C2C6.07 IN CHROMOSOME I//6.7e-11:66:40:

SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//O14056

F-NT2RP3002770//COLLAGEN ALPHA 1(IX) CHAIN (FRAGMENT)//0.33:87:34//MUS MUSCULUS (MOUSE)//Q05722

F-NT2RP3002785//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN)//9.7e-36:187:39//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q24371

F-NT2RP3002799//!!!! ALU SUBFAMILY J WARNING ENTRY!!!!/5.6e-08:41:73//HOMO SAPIENS (HUMAN)//P39188

F-NT2RP3002810//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!/0.0034:35:65//HOMO SAPIENS (HUMAN)//P39193

F-NT2RP3002818//MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)//3.2e-17:148:37//MUS MUSCULUS (MOUSE)//P27790

F-NT2RP3002861//HYPOTHETICAL 70.2 KD PROTEIN IN GSH1-CHS6 INTERGENIC REGION//1.7e-05:95:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P42951

F-NT2RP3002869//TRYPSIN INHIBITOR II (BDTI-II)//0.97:23:39//BRYONIA DIOICA (RED BRYONY)//P11968

F-NT2RP3002876//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP33)//0.00017:140:31//RAT-TUS NORVEGICUS (RAT)//P04474

F-NT2RP3002877//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!/2.5e-06:55:60//HOMO SAPIENS (HUMAN)//P39194

F-NT2RP3002909//P53-BINDING PROTEIN 53BP2 (BCL2-BINDING PROTEIN) (BBP)//4.6e-08:129:38//HOMO SAPIENS (HUMAN)//Q13625

F-NT2RP3002911//HYPOTHETICAL PROTEIN C18//0.99:26:50//SWINEPOX VIRUS (STRAIN KASZA) (SPV)//P32217

F-NT2RP3002948//RING CANAL PROTEIN (KELCH PROTEIN)//1.2e-23:113:47//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q04652

F-NT2RP3002953//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN)//0.55:116:27//DROSOPHILA MELANOGASTER (FRUIT FLY)//P33450

F-NT2RP3002955//HYPOTHETICAL 16.5 KD PROTEIN IN BLTR-SPOIIC INTERGENIC REGION//0.87:67:37//BACILLUS SUBTILIS//P54445

F-NT2RP3002969//LONG-CHAIN-FATTY-ACID--COA LIGASE 4 (EC 6.2.1.3) (LONG-CHAIN ACYL-COA SYNTHETASE 4) (LACS 4)//6.7e-56:189:59//HOMO SAPIENS (HUMAN)//O60488

F-NT2RP3002972//HYPOTHETICAL 73.0 KD PROTEIN IN CLA4-MID1 INTERGENIC REGION//0.0028:147:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P48566

F-NT2RP3002978//PROBABLE E5 PROTEIN//0.15:55:36//HUMAN PAPILLOMAVIRUS TYPE 51//P26553

F-NT2RP3002985//METALLOTHIONEIN (MT)//0.0031:49:42//PLEURONECTES PLATESSA (PLAICE)//P07216

F-NT2RP3002988//NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1 PRECURSOR (MOTCH PROTEIN)//1.0:111:29//MUS MUSCULUS (MOUSE)//Q01705

F-NT2RP3003008//HYPOTHETICAL 54.7 KD PROTEIN F37A4.1 IN CHROMOSOME III//0.96:112:25//CAENORHABDITIS ELEGANS//P41879

F-NT2RP3003032

F-NT2RP3003059//HYPOTHETICAL 52.3 KD PROTEIN C56F8.06C IN CHROMOSOME I PRECURSOR//9.7e-27:216:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10254

F-NT2RP3003061//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN)//3.7e-25:167:34//HOMO SAPIENS (HUMAN)//P16157

F-NT2RP3003068//SERYL-TRNA SYNTHETASE (EC 6.1.1.11) (SERINE--TRNA LIGASE) (SERRS) (FRAGMENT)//0.074:82:39//SULFOLOBUS SOLFATARICUS//O33780

F-NT2RP3003071//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP)//0.0085:128:30//HOMO SAPIENS (HUMAN)//P50552

F-NT2RP3003078//SPERM ACROSOMAL PROTEIN FSA-ACR.1 PRECURSOR (FRAGMENT)//0.028:165:31//VULPES VULPES (RED FOX)//P53353

F-NT2RP3003101//TETRACYCLINE RESISTANCE PROTEIN, CLASS C (TETA(C))//1.0e-14:243:25//ESCHERICHIA COLI//P02981

F-NT2RP3003121//SUPPRESSOR PROTEIN SRP40//7.4e-05:143:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32583

F-NT2RP3003133//65 KD YES-ASSOCIATED PROTEIN (YAP65)//0.024:61:42//GALLUS GALLUS (CHICKEN)

F-NT2RP3003138//KINESIN-1A PROTEIN KIF1A//1.1e-13:143:14//MUS MUSCULUS (MOUSE) (F01)

F-NT2RP3003139//ATP-BINDING CASSETTE TRANSPORTER ABC1//1.0:70:30//SCHIZOSACCHAROMYCES

- POMBE (FISSION YEAST)//Q92337
 F-NT2RP3003145//MILK FAT GLOBULE-EGF FACTOR 8 PRECURSOR (MFG-E8) (HMFG) (BREAST EPITHE-
 LIAL ANTIGEN BA46) (MFGM)//2.0e-12:121:37//HOMO SAPIENS (HUMAN)//Q08431
 F-NT2RP3003150
- 5 F-NT2RP3003157//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1)//4.0e-79:260:54//HOMO SA-
 PIENS (HUMAN)//P51522
 F-NT2RP3003185//TROPOMYOSIN//0.077:122:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//
 Q02088
- 10 F-NT2RP3003193//ZINC FINGER PROTEIN 135//7.2e-91:239:65//HOMO SAPIENS (HUMAN)//P52742
 F-NT2RP3003197//HYPOTHETICAL 28.1 KD PROTEIN IN SIPU-PBPC INTERGENIC REGION//1.3e-07:117:
 34//BACILLUS SUBTILIS//P42966
 F-NT2RP3003203//HYPOTHETICAL 33.5 KD PROTEIN C1D4.02C IN CHROMOSOME I//9.9e-23:132:39//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10149
 F-NT2RP3003204//RAS-LIKE PROTEIN RASB//0.92:103:27//DICTYOSTELIUM DISCOIDEUM (SLIME
 15 MOLD)//P32252
 F-NT2RP3003210//VERY HYPOTHETICAL 13.2 KD PROTEIN IN PTC3-SAS3 INTERGENIC REGION//0.23:
 106:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38190
 F-NT2RP3003212//SUPPRESSOR PROTEIN SRP40//0.019:171:23//SACCHAROMYCES CEREVISIAE (BAK-
 ER'S YEAST)//P32583
- 20 F-NT2RP3003230//CORONIN-LIKE PROTEIN P57//8.3e-74:183:73//BOS TAURUS (BOVINE)//Q92176
 F-NT2RP3003242//STANNIOCALCIN PRECURSOR//1.4e-21:127:37//HOMO SAPIENS (HUMAN)//P52823
 F-NT2RP3003251//DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR//3.1e-51:198:52//MUS
 MUSCULUS (MOUSE)//P15533
 F-NT2RP3003264//E6 PROTEIN//1.0:31:41//HUMAN PAPILLOMAVIRUS TYPE 48//Q80920
- 25 F-NT2RP3003278//45.8 KD PROTEIN IN SHM1-MRPL37 INTERGENIC REGION//8.6e-07:80:33//SACCHARO-
 MYCES CEREVISIAE (BAKER'S YEAST)//P38344
 F-NT2RP3003282//DYNAMIN 2 (DYNAMIN UDNM)//8.0e-108:226:88//MUS MUSCULUS (MOUSE)//P39054
 F-NT2RP3003290//BIOH PROTEIN//0.0055:107:30//ESCHERICHIA COLI//P13001
 F-NT2RP3003301//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-)//1.3e-69:
 30 200:55//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)//O64948
 F-NT2RP3003302//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//6.4e-69:102:66//HOMO SAPIENS (HU-
 MAN)//P08547
 F-NT2RP3003311//MYOSIN II HEAVY CHAIN, NON MUSCLE//0.18:225:26//ACANTHAMOEBA CASTELLANII
 (AMOEBA)//P05659
- 35 F-NT2RP3003313//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAG-
 MENT)//0.0014:142:33//HOMO SAPIENS (HUMAN)//P10162
 F-NT2RP3003327//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
 (RO52)//8.8e-18:94:43//MUS MUSCULUS (MOUSE)//Q62191
 F-NT2RP3003330//HYPOTHETICAL PROTEIN KIAA0176 (FRAGMENT)//1.3e-20:123:44//HOMO SAPIENS
 40 (HUMAN)//Q14681
 F-NT2RP3003344//HYPOTHETICAL 8.8 KD PROTEIN IN ICDC-MINE INTERGENIC REGION//1.0:28:42//ES-
 CHERICHIA COLI//P75991
 F-NT2RP3003346//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/6.9e-26:74:78//HOMO SAPIENS (HU-
 MAN)//P39191
- 45 F-NT2RP3003353//HYPOTHETICAL 52.4 KD PROTEIN R08D7.2 IN CHROMOSOME III//3.7e-10:118:33//
 CAENORHABDITIS ELEGANS//P30641
 F-NT2RP3003377//PUTATIVE CUTICLE COLLAGEN F09G8.6//1.5e-05:102:37//CAENORHABDITIS ELE-
 GANS//P34391
 F-NT2RP3003384
- 50 F-NT2RP3003385//SKD3 PROTEIN//5.1e-83:210:69//MUS MUSCULUS (MOUSE)//Q60649
 F-NT2RP3003403
 F-NT2RP3003409//SOX-22 PROTEIN//0.042:173:28//HOMO SAPIENS (HUMAN)//O15370
 F-NT2RP3003411//PROBABLE E3 PROTEIN//0.17:91:31//BOVINE PAPILLOMAVIRUS TYPE 2//P11300
 F-NT2RP3003427//HOLOTRICIN 3 PRECURSOR//0.012:36:41//HOLOTRICIA DIOMPHALIA//Q25055
- 55 F-NT2RP3003433
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F-NT2RP3003491//10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES) (HEAT SHOCK 10 KD PRO-
 TEIN)//0.99:49:34//LEPTOSPIRA INTERROGANS//P35472
 F-NT2RP3003500//SCY1 PROTEIN//6.8e-14:192:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//
 P53009
 5 F-NT2RP3003543//COLLAGEN ALPHA 5(IV) CHAIN PRECURSOR//0.0026:175:30//HOMO SAPIENS (HU-
 MAN)//P29400
 F-NT2RP3003552//ANNEXIN VII (SYNEXIN) (FRAGMENT)//0.19:21:47//BOS TAURUS (BOVINE)//P20072
 F-NT2RP3003555//HYPOTHETICAL 32.6 KD PROTEIN IN MET30-PIG2 INTERGENIC REGION//7.3e-27:159:
 43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40529
 10 F-NT2RP3003564//RNA REPLICASE POLYPROTEIN (EC 2.7.7.48)//1.0:99:30//TURNIP YELLOW MOSAIC VI-
 RUS//P10358
 F-NT2RP3003572//PUTATIVE CUTICLE COLLAGEN F09G8.6//0.33:128:32//CAENORHABDITIS ELEGANS//
 P34391
 F-NT2RP3003576//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//7.1e-28:58:77//HOMO SAPIENS (HUMAN)//
 15 P39195
 F-NT2RP3003589//RAS-RELATED PROTEIN RAB-10//5.4e-54:114:94//CANIS FAMILIARIS (DOG)//P24409
 F-NT2RP3003621//COAGULATION FACTOR XII PRECURSOR (EC 3.4.21.38) (HAGEMAN FACTOR) (HAF)//
 2.0e-15:89:40//HOMO SAPIENS (HUMAN)//P00748
 F-NT2RP3003625//MALE SPECIFIC SPERM PROTEIN MST84DD//0.99:22:50//DROSOPHILA MELA-
 20 NOGASTER (FRUIT FLY)//Q01645
 F-NT2RP3003656//HOMEBOX PROTEIN OTX3 (ZOTX3)//0.30:111:25//BRACHYDANIO RERIO (ZE-
 BRAFISH) (ZEBRA DANIO)//Q90267
 F-NT2RP3003659//HYPOTHETICAL 49.8 KD PROTEIN IN RPL14B-GPA1 INTERGENIC REGION//1.1e-20:127:
 37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38755
 25 F-NT2RP3003665//PENAEIDIN-3C PRECURSOR (P3-C)//0.34:52:34//PENAEUS VANNAMEI (PENOEID
 SHRIMP) (EUROPEAN WHITE SHRIMP)//P81060
 F-NT2RP3003672//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PRO-
 TEIN) (12E7)//8.7e-15:146:42//HOMO SAPIENS (HUMAN)//P14209
 F-NT2RP3003680//HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PES4 INTERGENIC REGION//4.3e-25:159:
 30 40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P43601
 F-NT2RP3003686//NONHISTONE CHROMOSOMAL PROTEIN HMG-17//0.067:63:31//GALLUS GALLUS
 (CHICKEN)//P02314
 F-NT2RP3003701//F-SPONDIN PRECURSOR//1.8e-13:193:27//RATTUS NORVEGICUS (RAT)//P35446
 F-NT2RP3003716//SLIT PROTEIN PRECURSOR//1.3e-12:150:34//DROSOPHILA MELANOGASTER (FRUIT
 35 FLY)//P24014
 F-NT2RP3003726//INSERTION ELEMENT IS136 HYPOTHETICAL 16.9 KD PROTEIN//0.47:109:28//AGRO-
 BACTERIUM TUMEFACIENS//P05680
 F-NT2RP3003746//HYPOTHETICAL 7.7 KD PROTEIN IN FIXX 3'REGION (ORF1)//0.57:34:38//AZORHIZO-
 BIUM CAULINODANS//P26486
 40 F-NT2RP3003795//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//4.3e-10:40:90//HOMO SAPIENS (HUMAN)//
 P39195
 F-NT2RP3003799//MATING-TYPE PHEROMONE BBP1(3) PRECURSOR//0.75:60:36//SCHIZOPHYLLUM
 COMMUNE (BRACKET FUNGUS)//P78744
 F-NT2RP3003800//PROTO-ONCOGENE TYROSINE-PROTEIN KINASE SRC (EC 2.7.1.112) (P60-SRC)//4.2e-
 45 51:72:95//GALLUS GALLUS (CHICKEN)//P00523
 F-NT2RP3003805//HYPOTHETICAL 32.1 KD PROTEIN IN DBP7-GCN3 INTERGENIC REGION//0.00069:160:
 25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P36121
 F-NT2RP3003809//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENTS)//0.028:135:35//GALLUS GALLUS (CHICK-
 EN)//P12105
 50 F-NT2RP3003819//C-HORDEIN (PCP387) (FRAGMENT)//0.0026:90:33//HORDEUM VULGARE (BARLEY)//
 P06472
 F-NT2RP3003825//PHOSPHATIDYLCHOLINE TRANSFER PROTEIN (PC-TP)//5.6e-20:174:31//BOS TAURUS
 (BOVINE)//P02720
 F-NT2RP3003828//ADENYLATE CYCLASE, TYPE V (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (CA(2+)-
 55 INHIBITABLE ADENYLATE CYCLASE)//0.0017:111:38//CANIS FAMILIARIS (DOG)//P30803
 F-NT2RP3003830//HYPOTHETICAL 6.4 KD PROTEIN IN INTPIN INTERGENIC REGION//1.0:38:39//ES-
 CHINUS MUSCULUS (HOUSE MOUSE)//P08600
 F-NT2RP3003833//HYPOTHETICAL 6.4 KD PROTEIN IN INTPIN INTERGENIC REGION//1.0:38:39//ES-

CHERICHIA COLI.//P75979

F-NT2RP3003842

F-NT2RP3003846//RETINAL DEGENERATION B PROTEIN (PROBABLE CALCIUM TRANSPORTER RDGB).//0.61:54:35//DROSOPHILA MELANOGASTER (FRUIT FLY).//P43125

5 F-NT2RP3003870//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.83:51:37//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643

F-NT2RP3003876//PROTEIN TRANSPORT PROTEIN SEC2.//0.0017:151:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P17065

10 F-NT2RP3003914//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//3.3e-23:76:64//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q09332

F-NT2RP3003918//VESICLE-ASSOCIATED MEMBRANE PROTEIN/SYNAPTOBREVIN BINDING PROTEIN (VAP-33).//5.5e-45:127:69//APLYSIA CALIFORNICA (CALIFORNIA SEA HARE).//Q16943

F-NT2RP3003932

15 F-NT2RP3003989//PREPROTEIN TRANSLOCASE SECE SUBUNIT.//0.96:46:32//THERMOTOGA MARITIMA.//P35874

F-NT2RP3003992//NUCLEAR LOCALIZATION SEQUENCE BINDING PROTEIN (P67).//0.0011:170:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P27476

F-NT2RP3004013//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAMINASE) (RNA EDITING ENZYME 1).//3.6e-21:134:45//RATTUS NORVEGICUS (RAT).//P51400

20 F-NT2RP3004016//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION.//0.00021:64:40//AUTOGRAPHAL CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41479

F-NT2RP3004041//SPERM PROTAMINE P1.//0.0028:43:46//ORNITHORHYNCHUS ANATINUS (DUCKBILL PLATYPUS).//P35307

25 F-NT2RP3004051//MICROBIAL COLLAGENASE PRECURSOR (EC 3.4.24.3) (120 KD COLLAGENASE).//0.0079:194:24//CLOSTRIDIUM PERFRINGENS.//P43153

F-NT2RP3004070//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.4e-11:51:72//HOMO SAPIENS (HUMAN).//P39188

F-NT2RP3004078//DNA BINDING PROTEIN RFX2.//2.7e-114:243:87//MUS MUSCULUS (MOUSE).//P48379

30 F-NT2RP3004093//HYPOTHETICAL 32.3 KD PROTEIN IN RHSE-NARV INTERGENIC REGION (ORFB).//8.0e-13:111:41//ESCHERICHIA COLI.//P37757

F-NT2RP3004095//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.5e-17:72:65//HOMO SAPIENS (HUMAN).//P39188

F-NT2RP3004110//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.6e-10:51:72//HOMO SAPIENS (HUMAN).//P39195

35 F-NT2RP3004125//ZINC FINGER PROTEIN 75.//1.1e-28:118:47//HOMO SAPIENS (HUMAN).//P51815

F-NT2RP3004145//AEROLYSIN REGULATORY PROTEIN.//0.012:45:33//AEROMONAS SOBRIA.//P09165

F-NT2RP3004148//METALLOTHIONEIN-I (MT-1).//0.055:18:50//COLUMBA LIVIA (DOMESTIC PIGEON).//P15786

40 F-NT2RP3004155//UBIQUINONE BIOSYNTHESIS PROTEIN COQ7 HOMOLOG.//1.7e-82:178:89//RATTUS NORVEGICUS (RAT).//Q63619

F-NT2RP3004189//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//1.7e-11:215:24//PODOSPORA ANSERINA.//Q00808

F-NT2RP3004206//CROOKED NECK PROTEIN.//3.8e-101:241:73//DROSOPHILA MELANOGASTER (FRUIT FLY).//P17886

45 F-NT2RP3004207//CUTICLE COLLAGEN 12 PRECURSOR.//0.13:130:33//CAENORHABDITIS ELEGANS.//P20630

F-NT2RP3004209//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG).//6.5e-16:207:29//HOMO SAPIENS (HUMAN).//Q13107

50 F-NT2RP3004215//PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT.//1.0:69:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P35179

F-NT2RP3004242//HYPOTHETICAL 30.2 KD PROTEIN ZK632.12 IN CHROMOSOME III.//1.1e-64:191:63//CAENORHABDITIS ELEGANS.//P34657

F-NT2RP3004246//RING3 PROTEIN (KIAA9001).//0.060:101:28//HOMO SAPIENS (HUMAN).//P25440

55 F-NT2RP3004253//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS) //1.1e-07:184:35//BOS TAURUS (BOVINE) //P15786

F-NT2RP3004258//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P32583

F-NT2RP3004262//DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HEAT SHOCK PROTEIN 40) (HSP40)//1.6e-63:210:61//HOMO SAPIENS (HUMAN)//P25685
 F-NT2RP3004282//HYPOTHETICAL PROTEIN F44G4.1 IN CHROMOSOME II (FRAGMENT)//1.6e-29:177:38//CAENORHABDITIS ELEGANS//P54073
 5 F-NT2RP3004332//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT)//0.030:118:36//CRICETULUS GRISEUS (CHINESE HAMSTER)//P11414
 F-NT2RP3004334
 F-NT2RP3004341//ALPHA-INTERNEXIN (ALPHA-INX)//0.91:110:26//MUS MUSCULUS (MOUSE)//P46660
 F-NT2RP3004348//HYPOTHETICAL 105.3 KD PROTEIN C01G6.5 IN CHROMOSOME III//0.60:198:24//10 CAENORHABDITIS ELEGANS//P46012
 F-NT2RP3004349//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.0e-37:60:76//HOMO SAPIENS (HUMAN)//P39193
 F-NT2RP3004378//HYPOTHETICAL 18.8 KD PROTEIN IN GNTR-GGT INTERGENIC REGION (O162)//0.0026:76:28//ESCHERICHIA COLI//P46854
 15 F-NT2RP3004399//LEUCINE-RICH PRIMARY RESPONSE PROTEIN 1 (FOLLICLE-STIMULATING HORMONE PRIMARY RESPONSE PROTEIN)//4.4e-109:212:96//HOMO SAPIENS (HUMAN)//Q92674
 F-NT2RP3004424//JTV-1 PROTEIN//4.5e-18:60:70//HOMO SAPIENS (HUMAN)//Q13155 F-NT2RP3004428//METALLOTHIONEIN-A (MTA)//0.0010:36:47//STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN)//P04734
 20 F-NT2RP3004451//MYOSIN IC HEAVY CHAIN//0.00072:113:34//ACANTHAMOEBA CASTELLANII (AMOEBA)//P10569
 F-NT2RP3004454//VERPROLIN//3.3e-07:156:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P37370
 F-NT2RP3004466//HYPOTHETICAL PROTEIN F-215//0.0013:125:32//HUMAN ADENOVIRUS TYPE 2//25 P03291
 F-NT2RP3004470//HYPOTHETICAL 15.4 KD PROTEIN C16C10.11 IN CHROMOSOME III//1.0:33:51//CAENORHABDITIS ELEGANS//Q09254
 F-NT2RP3004472//GERM CELL-LESS PROTEIN//7.3e-33:170:40//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q01820
 30 F-NT2RP3004475//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131)//8.4e-54:214:46//HOMO SAPIENS (HUMAN)//P98171
 F-NT2RP3004480//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35//3.9e-47:199:49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P34110
 F-NT2RP3004490//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)//0.0013:121:33//35 XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P17437
 F-NT2RP3004498//HYPOTHETICAL 43.5 KD PROTEIN IN COTD-KDUD INTERGENIC REGION PRECURSOR//0.066:87:35//BACILLUS SUBTILIS//P50840
 F-NT2RP3004503//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.0e-34:102:69//HOMO SAPIENS (HUMAN)//P39194
 40 F-NT2RP3004504//SUPPRESSOR PROTEIN SRP40//0.64:93:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32583
 F-NT2RP3004507//MOB1 PROTEIN (MPS1 BINDER 1)//2.2e-16:90:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40484
 F-NT2RP3004527
 45 F-NT2RP3004534//S-PHASE ENTRY CYCLIN 6//0.38:148:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32943
 F-NT2RP3004539//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (IGFBP-1) (IBP-1) (IGF-BINDING PROTEIN 1)//0.38:89:38//RATTUS NORVEGICUS (RAT)//P21743
 F-NT2RP3004544//CYTADHERENCE HIGH MOLECULAR WEIGHT PROTEIN 2 (CYTADHERENCE ACCESSORY PROTEIN 2)//0.0024:200:24//MYCOPLASMA PNEUMONIAE//P75471
 50 F-NT2RP3004566//GASTRULA ZINC FINGER PROTEIN XLCGF17.1 (FRAGMENT)//4.6e-25:126:43//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P18713
 F-NT2RP3004569//ANKYRIN//8.3e-07:150:28//MUS MUSCULUS (MOUSE)//Q02357
 F-NT2RP3004572//TRANSCRIPTION INITIATION FACTOR TFIID 150 KD SUBUNIT (TAFII-150) (TAFII150)//1.6e-70:247:54//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q24325
 55 F-NT2RP3004594//P54 PROTEIN PRECURSOR//0.0044:230:24//ENTEROCOCCUS FAECIUM (STREPTOCOCCUS) (Q0222)

COCCUS FAECIUM) //P13692
 F-NT2RP3004617//DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR //1.5e-14:113:34//MUS
 MUSCULUS (MOUSE) //P15533
 F-NT2RP3004618//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME III //4.5e-08:149:30//
 5 CAENORHABDITIS ELEGANS //P34681
 F-NT2RP3004669//ETHANOLAMINE KINASE (EC 2.7.1.82) (EASILY SHOCKED PROTEIN) //1.0e-24:75:48//
 DROSOPHILA MELANOGASTER (FRUIT FLY) //P54352
 F-NT2RP3004670//CUTICLE COLLAGEN 21/0.00090:159:29//CAENORHABDITIS ELEGANS //P17656
 F-NT2RP4000008//CHLORINE CHANNEL PROTEIN P64 //4.0e-79:243:62//BOS TAURUS (BOVINE) //P35526
 10 F-NT2RP4000023
 F-NT2RP4000035//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.6e-06:46:67//HOMO SAPIENS (HUMAN) //
 P39194
 F-NT2RP4000049//CALDESMON (CDM) //0.41:63:34//GALLUS GALLUS (CHICKEN) //P12957
 F-NT2RP4000051//DUALIN //2.3e-23:195:37//GALLUS GALLUS (CHICKEN) //Q90830
 15 F-NT2RP4000078//RING CANAL PROTEIN (KELCH PROTEIN) //1.2e-24:182:31//DROSOPHILA MELA-
 NOGASTER (FRUIT FLY) //Q04652
 F-NT2RP4000102//XPAR7 PROTEIN //1.0:54:33//BACILLUS LICHENIFORMIS //Q99166
 F-NT2RP4000109//SLIT PROTEIN PRECURSOR //1.9e-60:230:46//DROSOPHILA MELANOGASTER (FRUIT
 FLY) //P24014
 20 F-NT2RP4000111//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100
 KD SUBUNIT) //1.4e-91:157:100//BOS TAURUS (BOVINE) //Q10568
 F-NT2RP4000129//SE5 ANTIGEN //0.00072:124:37//RATTUS NORVEGICUS (RAT) //Q63003
 F-NT2RP4000147//ZINC FINGER PROTEIN GCS1 //1.5e-26:119:43//SACCHAROMYCES CEREVISIAE (BAK-
 ER'S YEAST) //P35197
 25 F-NT2RP4000150
 F-NT2RP4000151//HYPOTHETICAL 31.0 KD PROTEIN R107.2 IN CHROMOSOME III //4.2e-31:180:47//
 CAENORHABDITIS ELEGANS //P32740
 F-NT2RP4000159//SPORE COAT PROTEIN SP96 //0.84:107:28//DICTYOSTELIUM DISCOIDEUM (SLIME
 MOLD) //P14328
 30 F-NT2RP4000167//HYPOTHETICAL 98.1 KD PROTEIN IN SPX19-GCR2 INTERGENIC REGION //2.4e-08:133:
 32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P40164
 F-NT2RP4000185//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN) //5.4e-05:143:
 32//HERBES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52) //P28284
 F-NT2RP4000210//PAIRED AMPHIPATHIC HELIX PROTEIN //1.8e-40:258:35//SACCHAROMYCES CEREVI-
 35 SIAE (BAKER'S YEAST) //P22579
 F-NT2RP4000212//ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA) //1.4e-20:104:40//APLYSIA
 CALIFORNICA (CALIFORNIA SEA HARE) //P15287
 F-NT2RP4000214//FERREDOXIN //1.0:19:42//MOORELLA THERMOACETICA (CLOSTRIDIUM THERMOACE-
 TICUM) //P00203
 40 F-NT2RP4000218//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.7e-15:48:60//HOMO SAPIENS (HUMAN) //
 P39188
 F-NT2RP4000243//DUALIN //5.8e-78:192:70//GALLUS GALLUS (CHICKEN) //Q90830
 F-NT2RP4000246//NPC DERIVED PROLINE RICH PROTEIN 1 (NDPP-1) //3.1e-83:207:76//MUS MUSCULUS
 (MOUSE) //Q03173
 45 F-NT2RP4000259//GLUTATHIONE PEROXIDASE 2 (EC 1.11.1.9) //5.5e-29:153:43//HELIANTHUS ANNUUS
 (COMMON SUNFLOWER) //O23968
 F-NT2RP4000263//ANNEXIN VII (SYNEXIN) (FRAGMENT) //0.98:42:40//BOS TAURUS (BOVINE) //P20072
 F-NT2RP4000290//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I //3.5e-71:209:66//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST) //P87115
 50 F-NT2RP4000312//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1) //8.9e-22:166:37//HO-
 MO SAPIENS (HUMAN) //Q15404
 F-NT2RP4000321//VERPROLIN //0.00018:260:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //
 P37370
 F-NT2RP4000323//ANTHOPLEURIN B (TOXIN AP-B) //0.42:15:46//ANTHOPLEURA XANTHOGRAMMICA (GI-
 55 ANT GREEN SEA ANEMONE) //P01531
 F-NT2RP4000355//HYPOTHETICAL 30.9 KD PROTEIN IN CHROMOSOME III //4.2e-31:180:47//
 CAENORHABDITIS ELEGANS //P32740
 F-NT2RP4000359//DUALIN //5.8e-78:192:70//GALLUS GALLUS (CHICKEN) //Q90830
 F-NT2RP4000360//ACIDIC PROLINE RICH PROTEIN PRECURSOR (ILOXN-PP25) (FRAGMENT) //0.27:92:

F-NT2RP4000367//HYPOTHETICAL 7.3 KD PROTEIN IN 100 KD PROTEIN REGION.//0.99:52:32//HUMAN AD-
ENOVIRUS TYPE 41//P23691

5 163:52/HOMO SAPIENS (HUMAN).//O75570

F-NT2RP4000376//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP).//4.2e-59:125:80//RATTUS NOR-VEGICUS (RAT).//P54319

F-NT2RP4000381//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H)//
0.00058:194:30//MUS MUSCULUS (MOUSE)//P19246

10 F-NT2RP4000398//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.2e-45:153:39//HOMO SAPIENS (HUMAN).//
Q99676

F-NT2RP4000415//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR//
0.00066:201:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P47179

15 F-NT2RP4000417//PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2-MANNOSIDASE 1B).//
1.8e-25:196:40//MUS MUSCULUS (MOUSE)//P39098

F-NT2RP4000424//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.0e-15:72:61//HOMO SAPIENS (HUMAN).//
P39195

F-NT2RP4000448//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/7.0e-23:63:82/HOMO SAPIENS (HUMAN).//
P39192

20 F-NT2RP4000449//REGULATORY PROTEIN SIR2 (SILENT INFORMATION REGULATOR 2)//1.3e-41:102:45//
KLUYVEROMYCES LACTIS (YEAST)//P33294

F-NT2RP4000455//HOMEBOX PROTEIN SAX-1 (CHOX-3) (FRAGMENT).//0.00014:92:30//GALLUS GALLUS (CHICKEN)//P19601

25 F-NT2RP4000457//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 7 (EC 3.1.2.15) (UBIQUITIN THIOLESTE-
RASE 7) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 7) (DEUBIQUITINATING ENZYME 7) (HERPESVI-

RUS ASSOCIATED UBIQUITIN-SPECIFIC PROTEASE) //1.0e-29:218:38//HOMO SAPIENS (HUMAN) //Q93009
F-NT2RP4000480//TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULATORY PROTEIN

ALGR3)//0.049:117:29//PSEUDOMONAS AERUGINOSA//P15276
F-NT2RP4000481//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III//2.3e-05:152:23//

30 CAENORHABDITIS ELEGANS //Q09475
F-NT2RP4000498//MOB1 PROTEIN (MPS1 BINDER 1)//2.3e-48:172:52//SACCHAROMYCES CEREVISIAE

(BAKER'S YEAST).//P40484
F-NT2RP4000500//HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III.//1.3e-23:165:35//

CAENORHABDITIS ELEGANS//P34535
35 F-NT2RP4000515//PHOSPHODIESTERASE I (EC 3.1.4.1) (5'-EXONUCLEASE) (5'-NUCLEOTIDE PHOS-

PHODIESTERASE) (FRAGMENT)//1.0:48:37//BOS TAURUS (BOVINE)//P15396
F-NT2RP4000517//METALLOTHIONEIN-LIKE PROTEIN TYPE 2//1.0:41:36//VICIA FABA (BROAD BEAN)//

Q41657
F-NT2RP4000518//ATP-DEPENDENT RNA HELICASE ROK1.//1.1e-11:93:36//SACCHAROMYCES CEREVISIAE

40 SIAE (BAKER'S YEAST)//P45818
F-NT2RP4000519//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS)//0.68:55:40//BOS TAURUS (BOVINE)//

P25508
F-NT2RP4000524//IGA FC RECEPTOR PRECURSOR (BETA ANTIGEN) (B ANTIGEN)//0.37:187:24//STREP-

45 F-NT2RP4000528//NPL4 PROTEIN//2.1e-45:305:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)///

P33755
F-NT2RP4000541//HOMEBOX PROTEIN CHOX-1 (FRAGMENT)//0.23:28:50//GALLUS GALLUS (CHICK-

F-NT2RP4000556//HYPOTHETICAL 34.1 KD PROTEIN C40H1.4 IN CHROMOSOME III//4.3e-14:174:34//

CAENORHABDITIS ELEGANS //Q03574
F-NAT2RP4000560//HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III.//2.1e-19:155:36//

CAENORHABDITIS ELEGANS//P34679
F-NT2R2P4000588//HYPOTHETICAL PROTEIN E-115.//0.014:64:35//HUMAN ADENOVIRUS TYPE 2.//P03290

55 F-NT2RP4000614//SPlicing FACTOR, ARGinine/SERine-RICH 2 (SPlicing FACTOR SC35) (SC-35)
(SPlicing COMPONENT, 35 KD) (PR264 PROTEIN).//2.7e-27.188.44//GALLUS GALLUS (CHICKEN)//P30352

NT2RP4000638: FAP
BEAN: Q05544

CPD:RP4000648; RFL:CCB-FAMILY WARNING EXP: 2024-06-30 17:47/HOMO SAPIENS (HUMAN);

P39188

F-NT2RP46000657//HYPOTHETICAL PROTEIN MJ1065//2.5e-40:237:40//METHANOCOCCUS JANNAS-CHII//Q58465

F-NT2RP4000704

5 F-NT2RP4000713//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556//4.0e-07:134:40//STREPTOMYCES FRADIAE//P20186

F-NT2RP4000724//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE]//1.1e-62:109:88//HOMO SAPIENS (HUMAN)//P10266

10 F-NT2RP4000728//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR//0.0033:190:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32323

F-NT2RP4000737//PTB-ASSOCIATED SPLICING FACTOR (PSF)//1.0e-05:114:34//HOMO SAPIENS (HUMAN)//P23246

F-NT2RP4000739//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//1.0:20:50//ANAS PLATYRHYNCHOS (DOMESTIC DUCK)//P50655

15 F-NT2RP4000781//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION//0.0013:67:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53915

F-NT2RP4000787//POLLEN SPECIFIC PROTEIN SF3//1.3e-13:79:39//HELIANTHUS ANNUUS (COMMON SUNFLOWER)//P29675

20 F-NT2RP4000817//SUPPRESSOR PROTEIN SRP40//1.3e-05:255:21//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32583

F-NT2RP4000833

F-NT2RP4000837//MALE SPECIFIC SPERM PROTEIN MSTS4DB//0.18:38:44//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q01643

25 F-NT2RP4000839//TRANSCRIPTION INITIATION FACTOR TFIID 90 KD SUBUNIT (TAFII-90)//0.026:38:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38129

F-NT2RP4000855//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B)//2.8e-64:229:53//RATTUS NORVEGICUS (RAT)//O09175

30 F-NT2RP4000865//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT)//3.6e-84:174:54//HOMO SAPIENS (HUMAN)//P16415

F-NT2RP4000878//MYELOID UPREGULATED PROTEIN//8.2e-88:227:74//MUS MUSCULUS (MOUSE)//O35682

F-NT2RP4000879//UBIQUITIN-ACTIVATING ENZYME E1 (A1S9 PROTEIN)//9.1e-55:268:43//HOMO SAPIENS (HUMAN)//P22314

35 F-NT2RP4000907//BDNF / NT-3 GROWTH FACTORS RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKB TYROSINE KINASE) (GP145-TRKB) (TRK-B)//5.4e-10:220:25//HOMO SAPIENS (HUMAN)//Q16620

F-NT2RP4000915//60S ACIDIC RIBOSOMAL PROTEIN P2 (FRAGMENT)//0.46:23:60//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)//P51407

40 F-NT2RP4000918//METHYL-ACCEPTING CHEMOTAXIS PROTEIN TLPB//0.00010:148:32//BACILLUS SUBTILIS//P39217

F-NT2RP4000925//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN)//3.5e-27:220:36//HOMO SAPIENS (HUMAN)//Q06828

F-NT2RP4000927//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6)//0.64:75:37//BOVINE HERPESVIRUS TYPE 1 (STRAIN JURA)//P29128

45 F-NT2RP4000928//PHOSPHATIDATE CYTIDYLYLTRANSFERASE (EC 2.7.7.41) (CDP-DIGLYCERIDE SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE) (CDP-DIACYLGLYCEROL SYNTHASE) (CDS) (CTP:PHOSPHATIDATE CYTIDYLYLTRANSFERASE) (CDP-DAG SYNTHASE)//3.1e-104:263:66//HOMO SAPIENS (HUMAN)//Q92903

F-NT2RP4000929//HYPOTHETICAL 22.2 KD PROTEIN IN NSR1-TIF4631 INTERGENIC REGION//0.93:107:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53288

50 F-NT2RP4000955//PUTATIVE CUTICLE COLLAGEN F09G8.6//2.0e-05:102:37//CAENORHABDITIS ELEGANS//P34391

F-NT2RP4000973//HYPOTHETICAL 48.6 KD PROTEIN IN BET1-PAN1 INTERGENIC REGION//2.3e-17:78:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40564

55 F-NT2RP4000975//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT) //0.0041:140:33//HOMO SAPIENS (HUMAN) //P1461

F-NT2RP4000979//HYPOTHETICAL 10.5 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION//0.0013:67:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53915

F-NT2RP4000984//HYPOTHETICAL 124.8 KD PROTEIN C29E4.4 IN CHROMOSOME III//0.90:94:25//
 CAENORHABDITIS ELEGANS//P34343
 F-NT2RP4000989//ANTHOPLEURIN B (TOXIN AP-B)//0.76:41:41//ANTHOPLEURA XANTHOGRAMMICA (GI-
 ANT GREEN SEA ANEMONE)//P01531
 5 F-NT2RP4000996//PROTEIN Q300//0.00024:41:53//MUS MUSCULUS (MOUSE)//Q02722
 F-NT2RP4000997//DNA-DIRECTED RNA POLYMERASE I135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMER-
 ASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUBUNIT)//8.7e-115:261:82//RATTUS NORVEGI-
 CUS (RAT)//O54888
 F-NT2RP4001004//EC PROTEIN HOMOLOG 2 (FRAGMENT)//0.50:61:34//ARABIDOPSIS THALIANA
 10 (MOUSE-EAR CRESS)//Q42377
 F-NT2RP4001006//HYPOTHETICAL 43.5 KD PROTEIN IN COTD-KDUD INTERGENIC REGION PRECUR-
 SOR//0.010:152:29//BACILLUS SUBTILIS//P50840
 F-NT2RP4001010//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-
 DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)//9.9e-05:247:25//SACCHAROMYCES CEREVISIAE
 15 (BAKER'S YEAST)//P08640
 F-NT2RP4001029//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIV-
 ITY) (TRANSCRIPTION FACTOR NTF-1)//1.1e-14:175:31//DROSOPHILA MELANOGASTER (FRUIT FLY)//
 P13002
 F-NT2RP4001041//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE)
 20 (LEURS)//1.5e-74:272:55//CAENORHABDITIS ELEGANS//Q09996
 F-NT2RP4001057//HYPOTHETICAL 62.2 KD PROTEIN ZK652.6 IN CHROMOSOME III//0.0064:76:38//
 CAENORHABDITIS ELEGANS//P34664
 F-NT2RP4001064//DUALIN//2.5e-24:199:38//GALLUS GALLUS (CHICKEN)//Q90830
 F-NT2RP4001078//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135)
 25 (TAFII-130) (TAFII130)//0.11:139:38//HOMO SAPIENS (HUMAN)//O00268
 F-NT2RP4001079//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (GOLGI CA2+-ATPASE)//1.5e-22:242:
 31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P13586
 F-NT2RP4001080//POLYPYRIMIDINE TRACT-BINDING PROTEIN (PTB) (HETEROGENEOUS NUCLEAR RI-
 BONUCLEOPROTEIN I) (HNRNP I)//1.7e-82:178:69//SUS SCROFA (PIG)//Q29099
 30 F-NT2RP4001086//LEUCINE-RICH ACIDIC NUCLEAR PROTEIN//0.00039:141:26//RATTUS NORVEGICUS
 (RAT)//P49911
 F-NT2RP4001095//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAM-
 INASE) (RNA EDITING ENZYME 1)//9.9e-07:79:43//HOMO SAPIENS (HUMAN)//P78563
 F-NT2RP4001100//HYPOTHETICAL 74.0 KD PROTEIN IN CAJ1-HOM3 INTERGENIC REGION//4.4e-16:207:
 35 35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40032
 F-NT2RP4001117//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT//8.1e-115:224:99//RATTUS
 NORVEGICUS (RAT)//P38378
 F-NT2RP4001122//TIPD PROTEIN//7.5e-11:129:31//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD)//O15736
 F-NT2RP4001126//TRICHOHYALIN//1.4e-19:257:28//OVIS ARIES (SHEEP)//P22793
 40 F-NT2RP4001138//PUTATIVE F420-DEPENDENT NADP REDUCTASE (EC 1.-.-.-)//0.00010:204:25//METH-
 ANOCOCCUS JANNASCHII//Q58896
 F-NT2RP4001143//HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION//4.5e-34:
 168:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P43616
 F-NT2RP4001148//SOF1 PROTEIN//2.4e-41:158:41//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//
 45 P33750
 F-NT2RP4001149//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)//1.3e-08:106:41//VOLVOX CART-
 ERI//P21997
 F-NT2RP4001150//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO)//
 3.6e-24:194:32//GALLUS GALLUS (CHICKEN)//P35331
 50 F-NT2RP4001159//MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2)//0.0056:117:25//PLASMODI-
 UM FALCIPARUM (ISOLATE K1 / THAILAND)//Q03643
 F-NT2RP4001174//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT)//
 5.9e-24:184:34//BRASSICA OLERACEA (CAULIFLOWER)//P52178
 F-NT2RP4001206//MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2)//0.0029:117:26//PLASMODI-
 UM FALCIPARUM (ISOLATE K1 / THAILAND)//Q03642
 55 F-NT2RP4001210//DERMORPHIN 1 PRECURSOR (CONTAINS DELTORPHIN (DERMENKEPHALIN), DER-
 REVISIAE (BAKER'S YEAST)//P33307

MORPHIN]//0.019:130:30//PHYLLomedusa SAUVAGEI (SAUVAGE'S LEAF FROG)//P05422
 F-NT2RP4001213//ZINC FINGER PROTEIN 177//3.2e-28:176:39//HOMO SAPIENS (HUMAN)//Q13360
 F-NT2RP4001219//DISULFIDE ISOMERASE MPD1 PRECURSOR (EC 5.3.4.1)//2.4e-13:108:37//SACCHARO-
 MYCES CEREVISIAE (BAKER'S YEAST)//Q12404
 5 F-NT2RP4001228//RING CANAL PROTEIN (KELCH PROTEIN)//2.7e-56:242:40//DROSOPHILA MELA-
 NOGASTER (FRUIT FLY)//Q04652
 F-NT2RP4001235//REGULATORY PROTEIN E2//0.0080:100:38//HUMAN PAPILLOMAVIRUS TYPE 25//
 P36787
 F-NT2RP4001256//CUTICLE COLLAGEN 1//0.014:104:31//CAENORHABDITIS ELEGANS//P08124
 10 F-NT2RP4001260//BACTERIOCIN MICROCIN B17 PRECURSOR (MCB17)//0.00077:16:68//ESCHERICHIA
 COLI//P05834
 F-NT2RP4001274//HISTONE H1.M6.1//0.98:65:35//TRYPANOSOMA CRUZI//P40273
 F-NT2RP4001276//ELAV PROTEIN//0.00054:134:33//DROSOPHILA VIRILIS (FRUIT FLY)//P23241
 F-NT2RP4001313//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)//
 15 0.014:71:35//NICOTIANA TABACUM (COMMON TOBACCO)//P13983
 F-NT2RP4001315//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS9//2.3e-12:190:27//SAC-
 CHAROMYCES CEREVISIAE (BAKER'S YEAST)//P54787
 F-NT2RP4001336//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1//0.0037:108:31//PODOSPORA AN-
 SERINA//Q00808
 20 F-NT2RP4001339//HYPOTHETICAL PROTEIN MJ0810//1.2e-09:150:34//METHANOCOCCUS JANNASCHII//
 Q58220
 F-NT2RP4001343//HYPOTHETICAL 85.2 KD PROTEIN F52C9.3 IN CHROMOSOME III//1.4e-18:244:27//
 CAENORHABDITIS ELEGANS//Q10123
 F-NT2RP4001345//PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43)
 25 (LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL ACYLTRANSFERASE)
 (FRAGMENT)//4.0e-49:212:50//GALLUS GALLUS (CHICKEN)//P53760
 F-NT2RP4001351//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1//5.7e-11:229:26//SACCHARO-
 MYCES CEREVISIAE (BAKER'S YEAST)//P25386
 F-NT2RP4001353//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1)//0.00088:84:28//HO-
 30 MO SAPIENS (HUMAN)//Q15404
 F-NT2RP4001372//IRREGULAR CHIASM C-ROUGHEST PROTEIN PRECURSOR (IRREC PROTEIN)//1.0e-
 22:222:30//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q08180
 F-NT2RP4001373//OV-17 ANTIGEN PRECURSOR (IMMUNODOMINANT HYPODERMAL ANTIGEN)//0.51:92:
 26//ONCHOCERCA VOLVULUS//P36991
 35 F-NT2RP4001375//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE- PRO-
 TEIN KINASE 1)//3.5e-13:146:35//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD)//P18160
 F-NT2RP4001379//HYPOTHETICAL 64.2 KD PROTEIN IN SLT2-PUT2 INTERGENIC REGION//1.2e-14:207:
 28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38767
 F-NT2RP4001389//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAG-
 40 MENT)//0.073:112:33//CRICETULUS GRISEUS (CHINESE HAMSTER)//P11414
 F-NT2RP4001407//CENTROMERIC PROTEIN E (CENP-E PROTEIN)//0.0019:233:24//HOMO SAPIENS (HU-
 MAN)//Q02224
 F-NT2RP4001414//SEPTIN 2 HOMOLOG (FRAGMENT)//6.2e-89:195:81//HOMO SAPIENS (HUMAN)//Q14141
 F-NT2RP4001433//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6)//1.5e-85:216:56//HOMO SAPIENS (HU-
 45 MAN)//P28160
 F-NT2RP4001442//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (VERSION 1)//
 0.012:107:35//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)//P18616
 F-NT2RP4001447//60S ACIDIC RIBOSOMAL PROTEIN P2 (EL12)//0.0046:69:33//ARTEMIA SALINA (BRINE
 SHRIMP)//P02399
 50 F-NT2RP4001474//CBP3 PROTEIN PRECURSOR//0.0011:111:29//SACCHAROMYCES CEREVISIAE (BAK-
 ER'S YEAST)//P21560
 F-NT2RP4001483//2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSOR (EC 1.2.4.2) (AL-
 PHA-KETOGLUTARATE DEHYDROGENASE)//6.2e-60:146:61//HOMO SAPIENS (HUMAN)//Q02218
 F-NT2RP4001498//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I//2.3e-24:137:37//
 55 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09701
 F-NT2RP4001500//HYPOTHETICAL 100.5 KD PROTEIN C2F7.10 IN CHROMOSOME I//2.3e-24:137:37//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09701
 F-NT2RP4001503//HYPOTHETICAL 100.5 KD PROTEIN C2F7.10 IN CHROMOSOME I//2.3e-24:137:37//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09701
 F-NT2RP4001507//CUTICLE COLLAGEN 40//0.00029:166:31//CAENORHABDITIS ELEGANS//P34804

F-NT2RP4001524//LACTOCOCCIN A IMMUNITY PROTEIN//0.74:96:30//LACTOCOCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS), AND LACTOCOCCUS LACTIS (SUBSP. CREMORIS) (STREPTOCOCCUS CREMORIS)//Q00561

5 F-NT2RP4001529//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1)//2.8e-06:79:41//DROSOPHILA MELANOGASTER (FRUIT FLY)//P13002

F-NT2RP4001547//HYPOTHETICAL 45.0 KD PROTEIN IN NOT1/CDC39-HMR INTERGENIC REGION//5.4e-34:88:46//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P25656

10 F-NT2RP4001551//CELL DIVISION CONTROL PROTEIN 68//1.5e-18:243:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32558

F-NT2RP4001555//PUTATIVE ENDONUCLEASE VIII (EC 3.2.-.-)//0.00030:158:24//MYCOBACTERIUM TUBERCULOSIS//P96902

F-NT2RP4001567//IMPORTIN ALPHA-1 SUBUNIT (KARYOPHERIN ALPHA-1 SUBUNIT)//0.00013:147:29//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P52170

15 F-NT2RP4001568//HYPOTHETICAL PROTEIN KIAA0041 (FRAGMENT)//8.0e-22:119:42//HOMO SAPIENS (HUMAN)//Q15057

F-NT2RP4001571//NEUROMODULIN (AXONAL MEMBRANE PROTEIN GAP-43) (PP46) (B-50) (PROTEIN F1) (CALMODULIN-BINDING PROTEIN P-57)//0.012:167:28//BOS TAURUS (BOVINE)//P06836

20 F-NT2RP4001574//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP)//6.8e-115:208:98//BOS TAURUS (BOVINE)//P53620

F-NT2RP4001575//M-RELATED PROTEIN PRECURSOR//0.22:184:25//STREPTOCOCCUS PYOGENES//P16946

F-NT2RP4001592//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS)//7.4e-45:229:39//SYNECHOCYSTIS SP. (STRAIN PCC 6803)//P73505

25 F-NT2RP4001610//APOLIPOPROTEIN C-III PRECURSOR (APO-CIII)//0.41:74:28//SUS SCROFA (PIG)//P27917

F-NT2RP4001614//BASIC PROLINE-RICH PEPTIDE P-E (IB-9)//1.0:29:37//HOMO SAPIENS (HUMAN)//P02811

30 F-NT2RP4001634//MYOSIN HEAVY CHAIN, PERINATAL SKELETAL MUSCLE (FRAGMENT)//0.16:233:23//RATTUS NORVEGICUS (RAT)//P04462

F-NT2RP4001638//DNA REPAIR/TRANSCRIPTION PROTEIN MET18/34MS19//4.2e-21:249:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40469

F-NT2RP4001644//MYOSIN LIGHT CHAIN KINASE (EC 2.7.1.117) (MLCK)//4.5e-18:111:44//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD)//P25323

35 F-NT2RP4001656//HYPOTHETICAL 108.5 KD PROTEIN R06F6.2 IN CHROMOSOME II//3.4e-13:175:32//CAENORHABDITIS ELEGANS//Q09600

F-NT2RP4001677//HYPOTHETICAL 73.6 KD PROTEIN CY49.21//0.065:66:43//MYCOBACTERIUM TUBERCULOSIS//Q10690

40 F-NT2RP4001679//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.3e-36:103:72//HOMO SAPIENS (HUMAN)//P39194

F-NT2RP4001696//PHOTOSYSTEM II REACTION CENTRE J PROTEIN//0.93:37:37//CHLORELLA VULGARIS//P56338

F-NT2RP4001725//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT//4.3e-11:128:32//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10282

45 F-NT2RP4001730//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT)//4.1e-22:201:27//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q09332

F-NT2RP4001739//HOMEBOX PROTEIN HOX-A10 (HOX-1H) (HOX-1.8) (PL)//1.0:67:34//HOMO SAPIENS (HUMAN)//P31260

50 F-NT2RP4001753//ZINC FINGER PROTEIN 10 (ZINC FINGER PROTEIN KOX1) (FRAGMENT)//1.2e-19:72:62//HOMO SAPIENS (HUMAN)//P21506

F-NT2RP4001760//BREAKPOINT CLUSTER REGION PROTEIN//1.8e-13:179:28//HOMO SAPIENS (HUMAN)//P11274

F-NT2RP4001790//ZINC FINGER PROTEIN 38 (ZFP-38) (CTFIN51) (TRANSCRIPTION FACTOR RU49)//7.9e-38:147:49//MUS MUSCULUS (MOUSE)//Q07231

55 F-NT2RP4001803//CUTICLE COLLAGEN 12 PRECURSOR//0.40:48:39//CAENORHABDITIS ELEGANS//P10630

F-NT2RP4001822//PUTATIVE COLLAGEN PRECURSOR//0.36:16:152:42//HOMO SAPIENS (HUMAN)//Q10481

F-NT2RP4001823//PUTATIVE COLLAGEN PRECURSOR//0.98:6:152:42//CAENORHABDITIS ELEGANS//P10630

F-NT2RP4001838//METASTASIS-ASSOCIATED PROTEIN MTA1 //1.2e-07:95:31//HOMO SAPIENS (HUMAN).//
Q13330

F-NT2RP4001849//SH3-BINDING PROTEIN 3BP-1.//5.6e-52:276:45//MUS MUSCULUS (MOUSE)//P55194

F-NT2RP4001861//HYPOTHETICAL 10.6 KD PROTEIN IN GALE-PEPT INTERGENIC REGION.//0.92:39:51//
BACILLUS SUBTILIS//P55185

10 F-NT2RP4001889//HYPOTHETICAL BHLF1 PROTEIN//0.32:97:31//EPSTEIN-BARR VIRUS (STRAIN B95-8)
(HUMAN HERPESVIRUS 4)//P03181

F-NT2RP4001893//2-5A-DEPENDENT RIBONUCLEASE (EC 3.1.26.-) (2-5A-DEPENDENT RNAASE) (RNASE L) (RIBONUCLEASE 4) (FRAGMENT)//3.6e-07:124:29//MUS MUSCULUS (MOUSE)//Q05921

15 F-NT2RP4001896/HYPOTHETICAL 89.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMT6-PCT1
INTERGENIC REGION.//3.9e-10;210:28/SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P42935

F-NT2RP4001901//ACROSIN PRECURSOR (EC 3.4.21.10)//2.4e-07:53:45//ORYZOLAGUS CUNICULUS (RABBIT)//P48038

F-NT2RP4001927//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//3.1e-19:170:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q12024

20 F-NT2RP4001938//ZINC FINGER PROTEIN MOK-2//1.3e-28:72:50//MUS MUSCULUS (MOUSE)//P24399

F-NT2RP4001946//PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (EC 2.1.1.77) (PROTEIN- BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISO-ASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE)//4.8e-14:183:30//TRITICUM AESTIVUM (WHEAT)//Q43209

25 F-NT2RP4001950//HYPOTHETICAL PROTEIN ORF-1137.//3.7e-07:115:29//MUS MUSCULUS (MOUSE).//
P11260

F-NT2RP4001953

F-NT2RP4001966//WALL-ASSOCIATED PROTEIN PRECURSOR.//0.13:151:27//BACILLUS SUBTILIS.//
Q07833

30 F-NT2RP4001975//FIBRIL-FORMING COLLAGEN ALPHA CHAIN//0.00031:190:31//RIFTIA PACHYPTILA
(TUBE WORM)//P30754

F-NT2RP4002018//RING CANAL PROTEIN (KELCH PROTEIN)//3.5e-18:185:29//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q04652

35 F-NT2RP4002047//GTP-BINDING PROTEIN GUF1 (GTPASE GUF1)//4.0e-49:158:65//SACCHAROMYCES
CEREVISIAE (BAKER'S YEAST)//P46943

F-NT2RP4002052//HYPOTHETICAL 54.3 KD PROTEIN C23D3.03C IN CHROMOSOME I.//0.0047:148:27//
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09844

F-NT2RP4002058//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE F56D2.6//
0.057:66:30//CAENORHABDITIS ELEGANS//Q20875

40 F-NT2RP4002071//VERY HYPOTHETICAL 13.2 KD PROTEIN CY251.09.//0.94:45:46//MYCOBACTERIUM TU-
BERCULOSIS.//Q10888

F-NT2RP4002075//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.44:36:38//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE) (HIV-1)//P18804

F-NT2RP4002078//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7)//2.6e-19:46:76//HOMO SAPIENS (HUMAN)//Q05481

F-NT2RP4002081//MHC CLASS II REGULATORY FACTOR RFX1 (RFX) (ENHANCER FACTOR C) (EF-C).//
2.8e-05:196:31//HOMO SAPIENS (HUMAN)//P22670

F-NT2RP4002083//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT)//0.0064:29:55//OWENIA FUSIFORMIS//P21260

50 F-NT2RP4002408//PROTEIN KINASE CEK1 (EC 2.7.1.-)//1.1e-37:159:53//SCHIZOSACCHAROMYCES
POMBE (FISSION YEAST)//P38938

F-NT2RP4002791//30S RIBOSOMAL PROTEIN S20//1.0:73:26//HELICOBACTER PYLORI (CAMPYLO-
BACTER PYLORI)//P56027

F-NT2RP4002888//HYPOTHETICAL PROTEIN TP0352.//0.98:52:26//TREPONEMA PALLIDUM.//O83371

55 E-NT2RP4002905//G2/MITOTIC-SPECIFIC CYCLIN S13-7 (B-LIKE CYCLIN) (FRAGMENT) //5 9p-05 138 27"

ICRP5003459/HOMEOBOX/P02831
-MOUSE)://P02831

F-NT2RP5003461//HYPOTHETICAL PROTEIN C22F3.14C IN CHROMOSOME I (FRAGMENT)//1.1e-12:142:35//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09779
 F-NT2RP5003477//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1//5.3e-13:215:28//PODOSPORA ANSERINA//Q00808
 5 F-NT2RP5003492//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)//0.0055:144:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P08640
 F-NT2RP5003500//PROLINE-RICH PROTEIN MP-2 PRECURSOR//9.0e-05:103:38//MUS MUSCULUS (MOUSE)//P05142
 10 F-NT2RP5003506//MALE SPECIFIC SPERM PROTEIN MST87F//0.53:21:38//DROSOPHILA MELANOGASTER (FRUIT FLY)//P08175
 F-NT2RP5003512//HYPOTHETICAL PROTEIN IN CYCB3'REGION PRECURSOR (ORF2) (FRAGMENT)//0.92:49:32//PARACOCCLUS DENITRIFICANS//P29969
 F-NT2RP5003522//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR)//2.7e-18:165:39//PHASEOLUS AUREUS (MUNG BEAN) (VIGNA RADIATA)//P37116
 15 F-NT2RP5003524//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS)//6.0e-08:125:41//RATTUS NORVEGICUS (RAT)//P02454
 F-NT2RP5003534//ATP SYNTHASE, SUBUNIT F (EC 3.6.1.34)//0.88:37:45//HALOBACTERIUM VOLCANII (HALOFERAX VOLCANII)//Q48331
 20 F-OVARC1000001//GAR22 PROTEIN//1.9e-05:41:58//HOMO SAPIENS (HUMAN)//Q99501
 F-OVARC1000004//70 KD EXOCYST COMPLEX PROTEIN//3.7e-08:186:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P19658
 F-OVARC1000006//HISTONE H2A.1//4.7e-55:117:98//RATTUS NORVEGICUS (RAT)//P02262
 F-OVARC1000013//WD-REPEAT PROTEIN POP1//0.00022:126:28//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//P87060
 25 F-OVARC1000014//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR//2.3e-05:220:30//GALLUS GALLUS (CHICKEN)//P02457
 F-OVARC1000017//CUTICLE COLLAGEN DPY-13//2.6e-05:97:30//CAENORHABDITIS ELEGANS//P17657
 F-OVARC1000035
 30 F-OVARC1000058//RAS-RELATED PROTEIN RABC//0.00015:110:24//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD)//P34143
 F-OVARC1000060//EXTRACELLULAR RIBONUCLEASE LE PRECURSOR (EC 3.1.27.1) (RNASE LE)//6.8e-09:60:45//LYCOPERSICON ESCULENTUM (TOMATO)//P80022
 F-OVARC1000068//CYTOTOXIN 4 (CARDIOTOXIN V-II-4)//1.0:27:44//NAJA MOSSAMBICA (MOZAMBIQUE COBRA)//P01452
 35 F-OVARC1000071//NUCLEAR TRANSPORT FACTOR 2 (NTF-2) (PLACENTAL PROTEIN 15) (PP15)//5.2e-06:115:29//HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT)//P13662
 F-OVARC1000085
 F-OVARC1000087//HISTONE MACRO-H2A.1//1.2e-13:174:26//RATTUS NORVEGICUS (RAT)//Q02874
 40 F-OVARC1000091//OCTAPEPTIDE-REPEAT PROTEIN T2//0.0013:137:32//MUS MUSCULUS (MOUSE)//Q06666
 F-OVARC1000092//MITOCHONDRIAL RIBOSOMAL PROTEIN S7//0.97:46:39//ACANTHAMOEBA CASTELLANI (AMOEBA)//P46756
 F-OVARC1000106//HYPOTHETICAL 141.5 KD PROTEIN IN YPT53-RHO2 INTERGENIC REGION//0.0012:165:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53935
 45 F-OVARC1000109//PROLINE RICH 33 KD EXTENSIN-RELATED PROTEIN PRECURSOR (FRAGMENT)//0.18:35:34//DAUCUS CAROTA (CARROT)//P06600
 F-OVARC1000113//HYPOTHETICAL PROTEIN C18//1.0:26:26//SWINEPOX VIRUS (STRAIN KASZA) (SPV)//P32217
 50 F-OVARC1000114//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.6e-28:57:63//HOMO SAPIENS (HUMAN)//P39194
 F-OVARC1000133
 F-OVARC1000139//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG) //1.9e-09:200:29//HOMO SAPIENS (HUMAN) //Q13107
 55

F-OVARC1000148//HYPHAL WALL PROTEIN 1 CELL ELONGATION PROTEIN 27//0.12:175:29//CANDIDA ALBICANS (YEAST) //P39194

BICANS (YEAST)//P46593

F-OVARC1000151//HYPOTHETICAL PROTEIN KIAA0161//5.6e-20:197:30//HOMO SAPIENS (HUMAN)//P50876

F-OVARC1000168//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.0030:77:38//HOMO SAPIENS (HUMAN)//P39188

F-OVARC1000191//COLANIC ACID BIOSYNTHESIS PROTEIN WCAH//0.95:56:35//ESCHERICHIA COLI//P32056

F-OVARC1000198//HISTONE H1.C2//0.96:70:25//TRYPANOSOMA CRUZI//P40268

F-OVARC1000209//HYPOTHETICAL 20.9 KD PROTEIN IN PLB1-HXT2 INTERGENIC REGION//2.5e-33:178:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q03677

F-OVARC1000212//PROLINE-RICH PROTEIN MP-2 PRECURSOR//1.7e-05:66:46//MUS MUSCULUS (MOUSE)//P05142

F-OVARC1000240//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.8e-10:41:78//HOMO SAPIENS (HUMAN)//P39193

F-OVARC1000241//ENDOTHELIAL PAS DOMAIN PROTEIN 1 (EPAS-1) (HIF-1 ALPHA-LIKE FACTOR) (MHLF) (HIF-RELATED FACTOR) (HRF)//7.4e-54:177:54//MUS MUSCULUS (MOUSE)//P97481

F-OVARC1000288//HYPOTHETICAL 54.2 KD PROTEIN IN ERP5-ORC6 INTERGENIC REGION//2.9e-20:115:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38821

F-OVARC1000302//CORTICOSTEROID-BINDING GLOBULIN PRECURSOR (CBG) (TRANSCORTIN)//1.0:79:25//MUS MUSCULUS (MOUSE)//Q06770

F-OVARC1000304//PROTEIN MOV-10//1.6e-79:181:83//MUS MUSCULUS (MOUSE)//P23249

F-OVARC1000309//THREONINE SYNTHASE (EC 4.2.99.2)//6.9e-36:156:42//ASHBYA GOSSYP II (EREMOTH-ECIUM GOSSYP II)//Q00063

F-OVARC1000321//HYPOTHETICAL 28.1 KD PROTEIN C4F8.03 IN CHROMOSOME I//5.2e-45:159:53//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//O14179

F-OVARC1000326//BASIC PROLINE-RICH PEPTIDE IB-1//0.036:67:35//HOMO SAPIENS (HUMAN)//P04281

F-OVARC1000335//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION//1.2e-16:200:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40004

F-OVARC1000347//HYPOTHETICAL 7.6 KD PROTEIN YCF33//0.69:41:43//CYANOPHORA PARADOXA//P48273

F-OVARC1000384//ANTIFREEZE PEPTIDE 4 PRECURSOR//0.98:49:34//PSEUDOPLEURONECTA AMERICANUS (WINTER FLOUNDER)//P02734

F-OVARC1000408//INTEGUMENTARY MUCIN C.1 (FIM-C.1) (FRAGMENT)//8.1e-05:115:33//XENOPUS LAE-VIS (AFRICAN CLAWED FROG)//Q05049

F-OVARC1000411//DYNACTIN, 150 KD ISOFORM (150 KD DYNEIN-ASSOCIATED POLYPEPTIDE) (DP-150) (DAP-150) (P150-GLUED)//0.00076:100:29//RATTUS NORVEGICUS (RAT)//P28023

F-OVARC1000414//HYPOTHETICAL 7.0 KD PROTEIN IN BLTR-SPOIII C INTERGENIC REGION//1.0:46:34//BACILLUS SUBTILIS//P54431

F-OVARC1000420//COLLAGEN ALPHA 2(VIII) CHAIN (ENDOTHELIAL COLLAGEN) (FRAGMENT)//0.0028:97:37//HOMO SAPIENS (HUMAN)//P25067

F-OVARC1000427//HYPOTHETICAL 13.9 KD PROTEIN IN PRFA-SPOIIR INTERGENIC REGION//0.70:21:47//BACILLUS SUBTILIS//P39150

F-OVARC1000431

F-OVARC1000437//TENSIN//9.2e-42:195:52//GALLUS GALLUS (CHICKEN)//Q04205

F-OVARC1000440//PINCH PROTEIN (PARTICULARLY INTERESTING NEW CYS-HIS PROTEIN)//3.4e-31:37:97//HOMO SAPIENS (HUMAN)//P48059

F-OVARC1000442

F-OVARC1000443//CUTICLE COLLAGEN 2C (FRAGMENT)//0.0056:163:34//HAEMONCHUS CONTORTUS//P16252

F-OVARC1000461//FIXU PROTEIN//0.36:36:44//RHIZOBIUM LEGUMINOSARUM (BIOVAR TRIFOLII)//P42710

F-OVARC1000465//PROTEIN TRANSPORT PROTEIN SEC7//2.4e-14:222:26//SACCHAROMYCES CEREVI-SIAE (BAKER'S YEAST)//P11075

F-OVARC1000466//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/2.3e-08:29:93//HOMO SAPIENS (HUMAN)//P39192

F-OVARC1000467

F-OVARC1000468//THREONINE SYNTHASE (EC 4.2.99.2) (FRAGMENT)//6.9e-36:156:42//RATTUS NORVEGICUS (RAT)//P28023

F-OVARC1000787//40S RIBOSOMAL PROTEIN S14 (FRAGMENT)//0.96:37:48//SUS SCROFA (PIG)//Q29303
F-OVARC1000800//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/2.5e-31:47:82//HOMO SAPIENS (HUMAN)//
P39189

5 F-OVARC1000802//HYPOTHETICAL 8.8 KD PROTEIN B0302.2 IN CHROMOSOME X//0.16:55:40//
CAENORHABDITIS ELEGANS//Q10926

F-OVARC1000834//SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA (EC 2.7.1.-) (P68-PAK) (P21- ACTI-
VATED KINASE) (ALPHA-PAK) (PROTEIN KINASE MUK2)//0.87:140:31//RATTUS NORVEGICUS (RAT)//
P35465

10 F-OVARC1000846//NUCLEOLIN (PROTEIN C23)//7.0e-07:109:30//MESOCRICETUS AURATUS (GOLDEN
HAMSTER)//P08199

F-OVARC1000850//HYPOTHETICAL 56.2 KD PROTEIN IN ERG8-UBP8 INTERGENIC REGION//6.9e-09:180:
28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q04991

15 F-OVARC1000862//UBIQUITIN-CONJUGATING ENZYME E2-17.5 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN
LIGASE) (UBIQUITIN CARRIER PROTEIN)//0.0020:74:28//SACCHAROMYCES CEREVISIAE (BAKER'S
YEAST)//P52490

F-OVARC1000876//MOB1 PROTEIN (MPS1 BINDER 1)//9.8e-39:154:55//SACCHAROMYCES CEREVISIAE
(BAKER'S YEAST)//P40484

F-OVARC1000883//METALLOTHIONEIN-I//0.87:38:36//CANDIDA GLABRATA (YEAST) (TORULOPSIS GLA-
BRATA)//P15113

20 F-OVARC1000885//OXIDOREDUCTASE UCPA (EC 1.-.-.-)//2.8e-18:170:34//ESCHERICHIA COLI//P37440

F-OVARC1000886//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENT)//0.00033:60:45//BOS TAURUS (BOVINE)//
P02465

F-OVARC1000890//PROBABLE E5 PROTEIN//0.92:7:71//HUMAN PAPILLOMAVIRUS TYPE 70//P50774

25 F-OVARC1000891//HYPOTHETICAL 8.3 KD PROTEIN (ORF5)//1.0:36:36//PARAMECIUM TETRAURELIA//
P15606

F-OVARC1000897//HYPOTHETICAL 6.1 KD PROTEIN PRECURSOR (ORF87)//1.0:34:44//ORGYIA PSEU-
DOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV)//O10337

F-OVARC1000912//PUTATIVE CUTICLE COLLAGEN C09G5.4//4.0e-07:98:35//CAENORHABDITIS ELE-
GANS//Q09455

30 F-OVARC1000915//HYPOTHETICAL PROTEIN KIAA0288 (HA6116)//1.7e-47:115:76//HOMO SAPIENS (HU-
MAN)//P56524

F-OVARC1000924//CYTOCHROME B (EC 1.10.2.2) (FRAGMENT)//0.99:54:24//BOA CONSTRICTOR (BOA)//
P92848

35 F-OVARC1000936//HYPOTHETICAL 7.5 KD PROTEIN IN INAA-GLPQ INTERGENIC REGION//1.0:48:33//ES-
CHERICHIA COLI//P45505

F-OVARC1000937//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR//1.0:135:31//HOMO SAPIENS (HU-
MAN)//P02452

F-OVARC1000945//EARLY E1A 11 KD PROTEIN//0.087:81:24//MOUSE ADENOVIRUS TYPE 1 (MAV-1)//
P12533

40 F-OVARC1000948

F-OVARC1000959//HYPOTHETICAL PROTEIN MJ0933//0.99:67:28//METHANOCOCCUS JANNASCHII//
Q58343

F-OVARC1000960//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.8e-32:56:75//HOMO SAPIENS (HUMAN)//
P39193

45 F-OVARC1000964//MAMBIN (GLYCOPROTEIN IIB-IIA ANTAGONIST) (PLATELET AGGREGATION INHIBITOR)
(DENDROASPIN)//1.0:30:36//DENDROASPIS JAMESONI KAIMOSAE (EASTERN JAMESON'S MAMBA)//
P28375

F-OVARC1000971

50 F-OVARC1000984//HYPOTHETICAL 52.3 KD PROTEIN IN MRPL10-ERG24 INTERGENIC REGION PRECUR-
SOR//0.093:36:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53832

F-OVARC1000996//MO25 PROTEIN//1.9e-39:80:95//MUS MUSCULUS (MOUSE)//Q06138

F-OVARC1000999//BRAIN-SPECIFIC HOMEOBOX/POU DOMAIN PROTEIN 1 (BRN-1 PROTEIN)//0.00020:50:
40//HOMO SAPIENS (HUMAN)//P20264

55 F-OVARC1001000//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.4e-16:43:90//HOMO SAPIENS (HUMAN)//
P39195

F-OVARC1001001//MA
KASTER-ERG24-UBP8

F-OVARC1001002//HYPOTHETICAL PROTEIN MJ0926//0.50:71:23//METHANOCOCCUS JANNASCHII//

Q58336

F-OVARC1001011//CORTISTATIN PRECURSOR//0.81:45:37//RATTUS NORVEGICUS (RAT)//Q62949

F-OVARC1001032//FERREDOXIN LIKE PROTEIN//1.0:26:46//RHIZOBIUM LEGUMINOSARUM (BIOVAR PHASEOLI)//Q05561

5 F-OVARC1001034//METALLOTHIONEIN-IG (MT-1G)//0.14:9:77//HOMO SAPIENS (HUMAN)//P13640

F-OVARC1001038//NUCLEOLIN (PROTEIN C23)//3.2e-07:36:80//HOMO SAPIENS (HUMAN)//P19338

F-OVARC1001040//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.5e-18:45:60//HOMO SAPIENS (HUMAN)//P39194

10 F-OVARC1001044//BIS(5'-NUCLEOSYL)-TETRAPHOSPHATASE (SYMMETRICAL) (EC 3.6.1.41) (DIADENOSINE TETRAPHOSPHATASE)//0.88:43:39//ESCHERICHIA COLI//P05637

F-OVARC1001051//SERINE PROTEINASE STUBBLE (EC 3.4.21.-) (STUBBLE-STUBBLOID PROTEIN)//0.34:117:25//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q05319

F-OVARC1001055//PRE-B CELL ENHANCING FACTOR PRECURSOR//1.6e-33:43:97//HOMO SAPIENS (HUMAN)//P43490

15 F-OVARC1001062

F-OVARC1001065//METHIONYL-TRNA SYNTHETASE (EC 6.1.1.10) (METHIONINE--TRNA LIGASE) (METRS)//0.79:76:39//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE)//Q44951

F-OVARC1001068//GTP-BINDING PROTEIN ERA HOMOLOG (FRAGMENT)//5.3e-15:100:44//BRADYRHIZOBIUM JAPONICUM//O69162

20 F-OVARC1001072//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.0076:41:56//HOMO SAPIENS (HUMAN)//P39188

F-OVARC1001074//60S RIBOSOMAL PROTEIN L38//1.0:32:40//LYCOPERSICON ESCULENTUM (TOMATO)//P46291

25 F-OVARC1001085//HYPOTHETICAL 126.5 KD PROTEIN C13F4.06 IN CHROMOSOME I//0.73:135:25//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10197

F-OVARC1001092//HYPOTHETICAL 51.2 KD PROTEIN IN PET54-DIE2 INTERGENIC REGION//5.6e-05:30:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P50079

F-OVARC1001107//SHK1 KINASE-BINDING PROTEIN 1//1.8e-08:52:51//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//P78963

30 F-OVARC1001113//DIAPHANOUS PROTEIN//1.9e-33:218:35//DROSOPHILA MELANOGASTER (FRUIT FLY)//P48608

F-OVARC1001117//GENE 7 PROTEIN//0.68:12:50//SPIROPLASMA VIRUS 4 (SPV4)//P11339

F-OVARC1001118

F-OVARC1001129//30S RIBOSOMAL PROTEIN S17//0.15:57:22//AQUIFEX AEOLICUS//O66439

35 F-OVARC1001154//GRANULINS PRECURSOR (ACROGRANIN)//2.3e-95:99:77//MUS MUSCULUS (MOUSE)//P28798

F-OVARC1001161//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT//0.17:87:34//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)//P49177

F-OVARC1001162

40 F-OVARC1001167//TRBD PROTEIN//0.92:24:45//ESCHERICHIA COLI//P41070

F-OVARC1001169//FRUCTOSE-1,6-BISPHOSPHATASE (EC 3.1.3.11) (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) (FRAGMENT)//0.82:35:40//MUS MUSCULUS (MOUSE)//P97323

F-OVARC1001170//PROLINE-RICH PEPTIDE P-B//0.17:27:37//HOMO SAPIENS (HUMAN)//P02814

45 F-OVARC1001171//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.00023:28:75//HOMO SAPIENS (HUMAN)//P39188

F-OVARC1001173

F-OVARC1001176//HYPOTHETICAL BHLF1 PROTEIN//2.7e-05:158:31//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4)//P03181

50 F-OVARC1001180//UBIQUITIN-LIKE PROTEIN DSK2//1.4e-12:208:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P48510

F-OVARC1001188//HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION//3.3e-31:129:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53215

F-OVARC1001200//HYPOTHETICAL 49.0 KD PROTEIN IN NSP1-KAR2 INTERGENIC REGION//0.018:148:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P47057

55 F-OVARC1001232//HYPOTHETICAL PROTEIN MJ1236//2.5e-27:141:39//METHANOCOCCUS JANNASCHII//P8633

F-OVARC1001244

F-OVARC1001246

- F-OVARC1001244//RING3 PROTEIN (KIAA9001)//1.7e-13:37:91//HOMO SAPIENS (HUMAN)//P25440
 F-OVARC1001261//OCTAPEPTIDE-REPEAT PROTEIN T2//1.3e-07:109:35//MUS MUSCULUS (MOUSE)//Q06666
 5 F-OVARC1001268//HYPOTHETICAL 57.4 KD PROTEIN IN PILT REGION (ORF4)//0.71:43:41//PSEUDOMONAS AERUGINOSA//P24563
 F-OVARC1001270//HYPOTHETICAL 9.0 KD PROTEIN IN UVSW-UVSY INTERGENIC REGION//1.0:44:29//BACTERIOPHAGE T4//P32281
 F-OVARC1001271//HYPOTHETICAL 104.7 KD PROTEIN F23F12.8 IN CHROMOSOME III PRECURSOR//0.00015:188:23//CAENORHABDITIS ELEGANS//P46504
 10 F-OVARC1001282
 F-OVARC1001296//WEB1 PROTEIN (PROTEIN TRANSPORT PROTEIN SEC31)//0.022:101:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38968
 F-OVARC1001306//HYPOTHETICAL 52.9 KD SERINE-RICH PROTEIN C11G7.01 IN CHROMOSOME I//0.023:134:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//O13695
 15 F-OVARC1001329//CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT)//1.3e-14:150:28//ZEA MAYS (MAIZE)//P49133
 F-OVARC1001330
 F-OVARC1001339//RIBONUCLEOPROTEIN RB97D//0.0013:55:38//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q02926
 20 F-OVARC1001341//HYPOTHETICAL 74.0 KD PROTEIN IN CAJ1-HOM3 INTERGENIC REGION//4.9e-17:110:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40032
 F-OVARC1001342
 F-OVARC1001344//PREPROTEIN TRANSLOCASE SECE SUBUNIT//0.99:39:23//STAPHYLOCOCCUS CARNOSUS//P36253
 25 F-OVARC1001357//METALLOTHIONEIN//0.99:28:42//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//Q05890
 F-OVARC1001360//LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)//0.86:109:31//HOMO SAPIENS (HUMAN)//P48634
 F-OVARC1001369//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENT)//6.7e-05:124:36//BOS TAURUS (BOVINE)//P02465
 30 F-OVARC1001372//HYPOTHETICAL 34.5 KD PROTEIN IN CLCB-CLCD INTERGENIC REGION PRECURSOR//0.75:33:48//PSEUDOMONAS PUTIDA, AND PSEUDOMONAS SP. (STRAIN B13)//Q47100
 F-OVARC1001376//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.8e-24:96:61//HOMO SAPIENS (HUMAN)//P39188
 35 F-OVARC1001381//MEMBRANE-ASSOCIATED ATPASE EPSILON CHAIN (EC 3.6.1.34) (SUL-ATPASE EPSILON)//0.96:46:39//SULFOLOBUS ACIDOCALDARIUS//P23039
 F-OVARC1001391//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT)//0.00024:189:29//HOMO SAPIENS (HUMAN)//P10162
 F-OVARC1001399//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//0.062:18:77//HOMO SAPIENS (HUMAN)//P39195
 40 F-OVARC1001417//HYPOTHETICAL 157.0 KD PROTEIN C38C10.5 IN CHROMOSOME III//0.010:185:23//CAENORHABDITIS ELEGANS//Q03570
 F-OVARC1001419//A-TYPE INCLUSION PROTEIN (ATI)//0.50:135:28//CAMELPOX VIRUS (STRAIN CP-1)//Q05482
 45 F-OVARC1001425//COLLAGEN ALPHA 1(X) CHAIN PRECURSOR//0.43:85:40//HOMO SAPIENS (HUMAN)//Q03692
 F-OVARC1001436//HYPOTHETICAL 11.4 KD PROTEIN (C4 PROTEIN)//0.031:100:30//TOMATO YELLOW LEAF CURL VIRUS (STRAIN AUSTRALIA) (TYLCV)//P36283
 F-OVARC1001442//HOMEBOX PROTEIN HTR-A2 (FRAGMENT)//1.0:32:34//HELOBDELLA TRISERIALIS (LEECH)//P17138
 50 F-OVARC1001453//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF)//0.74:19:47//MUS MUSCULUS (MOUSE)//P28184
 F-OVARC1001476//GTP-BINDING PROTEIN GTR2//3.0e-12:114:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53290
 55 F-OVARC1001480//COLLAGEN ALPHA 2(VI) CHAIN PRECURSOR//0.00019:134:32//MUS MUSCULUS (FRUIT FLY)
 F-OVARC1001489//HYPOTHETICAL PROTEIN H101//1.8e-04:43//HAEMOPHILUS NEUTRIZANS
 F-OVARC1001496//C-TERMINAL BINDING PROTEIN 2//4.0e-65:132:100//HOMO SAPIENS (HUMAN)

P56545

F-OVARC1001506//POLYCYSTIN PRECURSOR (AUTOSOMAL DOMINANT POLYCYSTIC KIDNEY DISEASE PROTEIN 1)//3.2e-70:159:94//HOMO SAPIENS (HUMAN)//P98161

F-OVARC1001525//FIBROBLAST GROWTH FACTOR INDUCIBLE PROTEIN 14 (FIN14)//1.0:36:33//MUS MUSCULUS (MOUSE)//Q61077

F-OVARC1001542//SMALL PROLINE-RICH PROTEIN 2B (SPR-2B)//0.69:57:33//HOMO SAPIENS (HUMAN)//P35325

F-OVARC1001547

F-OVARC1001555//NGG1-INTERACTING FACTOR 3//7.6e-16:148:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53081

F-OVARC1001577//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN)//8.8e-38:94:81//GALLUS GALLUS (CHICKEN)//P30352

F-OVARC1001600//GENE 7 PROTEIN//0.80:38:39//SPIROPLASMA VIRUS SPV1-R8A2 B//P15898

F-OVARC1001610//DIACYLGLYCEROL CHOLINEPHOSPHOTRANSFERASE (EC 2.7.8.2) (SN-1,2- DIACYLGLYCEROL CHOLINEPHOSPHOTRANSFERASE) (CHOPT)//1.6e-22:122:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P17898

F-OVARC1001611

F-OVARC1001615//HYPOTHETICAL 6.1 KD PROTEIN C03B1.10 IN CHROMOSOME X//0.30:43:34//CAENORHABDITIS ELEGANS//Q11116

F-OVARC1001668/////ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.0e-19:45:82//HOMO SAPIENS (HUMAN)//P39192

F-OVARC1001702//SOX-20 PROTEIN//2.4e-28:71:83//HOMO SAPIENS (HUMAN)//O60248

F-OVARC1001703//INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GUANINE NUCLEOTIDE-BINDING PROTEIN 1) (INTERFERON-GAMMA INDUCIBLE PROTEIN MAG-1)//0.00018:88:36//MUS MUSCULUS (MOUSE)//Q01514

F-OVARC1001711//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1 B)//2.7e-05:98:32//MUS MUSCULUS (MOUSE)//Q62267

F-OVARC1001713//ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM BINDING INHIBITOR) (MA-DBI)//4.5e-20:46:67//BOS TAURUS (BOVINE)//P07106

F-OVARC1001726//ALPHA-AMYLASE INHIBITOR PAIM I (PIG PANCREATIC ALPHA-AMYLASE INHIBITOR OF MICROBES I)//0.59:23:56//STREPTOMYCES OLIVACEOVIRIDIS (STREPTOMYCES CORCHORUSII)//P09921

F-OVARC1001731//TROPOMYOSIN ALPHA CHAIN, SKELETAL MUSCLE//2.1e-75:176:87//XENOPUS LAEVIS (AFRICAN CLAWED FROG)//Q01173

F-OVARC1001745//GENE 11 PROTEIN//0.31:36:52//SPIROPLASMA VIRUS SPV1-R8A2 B//P15902

F-OVARC1001762//N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA- AMINO, ACETYLTRANSFERASE 1)//2.8e-23:197:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P12945

F-OVARC1001766//FK506-BINDING NUCLEAR PROTEIN (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PPIASE) (EC 5.2.1.8) (PROLINE ROTAMASE) (NUCLEOLAR PROLINE ISOMERASE) (FKBP-70)//2.2e-06:99:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38911

F-OVARC1001767//33.2 KD PROTEIN IN DIND-RPH INTERGENIC REGION (ORF X)//0.99:113:27//ESCHERICHIA COLI//P23839

F-OVARC1001768

F-OVARC1001791//HYPOTHETICAL 63.3 KD PROTEIN IN MPT5-SAE2 INTERGENIC REGION//0.090:75:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P46945

F-OVARC1001795//HYPOTHETICAL 7.5 KD PROTEIN IN RPBA-GP46 INTERGENIC REGION//0.81:21:38//BACTERIOPHAGE T4//P07878

F-OVARC1001802//PLECTOXIN VIII (PLT-VIII) (PLTVIII)//0.41:19:36//PLECTREURYS TRISTIS (SPIDER)//P36984

F-OVARC1001805//60S RIBOSOMAL PROTEIN L40 (CEP52)//0.67:24:58//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P14796

F-OVARC1001809//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS)//0.23:111:31//RATTUS NORVEGICUS (RAT)//P02454

F-OVARC1001812//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L) //0.99:28:42//HALICHOERUS GRYPHUS GRAY SEAL

F-OVARC1001813//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L) //0.99:28:42//HALICHOERUS GRYPHUS GRAY SEAL

F-OVARC1001814//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L) //0.99:28:42//HALICHOERUS GRYPHUS GRAY SEAL

F-OVARC1001820//HYPOTHETICAL PROTEIN ORF-1137.//0.80:58:29//MUS MUSCULUS (MOUSE).//P11260
 F-OVARC1001828
 F-OVARC1001846
 F-OVARC1001861//METALLOTHIONEIN (MT).//0.18:11:54//PLEURONECTES PLATESSA (PLAICE).//P07216
 5 F-OVARC1001873
 F-OVARC1001879//HYPOTHETICAL 55.9 KD PROTEIN EEED8.6 IN CHROMOSOME II.//2.3e-05:73:31//
 CAENORHABDITIS ELEGANS.//Q09296
 F-OVARC1001880//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CONTAINS: BASIC
 PEPTIDE P-F] (FRAGMENT).//2.4e-11:203:32//HOMO SAPIENS (HUMAN).//P02812
 10 F-OVARC1001883//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.3e-16:86:59//HOMO SAPIENS (HUMAN).//
 P39188
 F-OVARC1001900//HYPOTHETICAL 105.9 KD PROTEIN F22B7.5 IN CHROMOSOME III.//0.0053:48:47//
 CAENORHABDITIS ELEGANS.//P34408
 F-OVARC1001901
 15 F-OVARC1001911//40S RIBOSOMAL PROTEIN S28.//1.0:33:36//ARABIDOPSIS THALIANA (MOUSE-EAR
 CRESS).//P34789
 F-OVARC1001916//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-
 CIOGENITAL DYSPLASIA PROTEIN).//0.00082:114:27//HOMO SAPIENS (HUMAN).//P98174
 F-OVARC1001928//FERREDOXIN III (FDIII).//1.0:64:29//ANABAENA VARIABILIS.//P46050
 20 F-OVARC1001942//N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA- AMI-
 NO, ACETYLTRANSFERASE 1).//3.0e-07:93:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//
 P12945
 F-OVARC1001943//HYPOTHETICAL 62.2 KD PROTEIN ZK652.6 IN CHROMOSOME III.//1.7e-23:147:43//
 CAENORHABDITIS ELEGANS.//P34664
 25 F-OVARC1001949//ZINC FINGER PROTEIN 177.//2.0e-23:56:66//HOMO SAPIENS (HUMAN).//Q13360
 F-OVARC1001950//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.011:57:47//HOMO SAPIENS (HUMAN).//
 P39188
 F-OVARC1001987//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE).//0.39:14:64//MUS MUSCULUS
 (MOUSE).//P02319
 30 F-OVARC1001989//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.4e-13:55:72//HOMO SAPIENS (HUMAN).//
 P39188
 F-OVARC1002044
 F-OVARC1002050//UTROPHIN (DYSTROPHIN-RELATED PROTEIN 1) (DRP1) (DRP).//3.6e-12:221:25//HOMO
 SAPIENS (HUMAN).//P46939
 35 F-OVARC1002066
 F-OVARC1002082
 F-OVARC1002107//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//0.99:149:24//SACCHARO-
 MYCES CEREVISIAE (BAKER'S YEAST).//P25386
 F-OVARC1002112//HISTONE MACRO-H2A.1.//2.8e-64:133:98//RATTUS NORVEGICUS (RAT).//Q02874
 40 F-OVARC1002127//60S RIBOSOMAL PROTEIN L22.//0.0023:95:35//DROSOPHILA MELANOGASTER (FRUIT
 FLY).//P50887
 F-OVARC1002138//PROBABLE 26S PROTEASE SUBUNIT YTA6 (TAT-BINDING HOMOLOG 6).//6.4e-51:198:
 56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40328
 F-OVARC1002143
 45 F-OVARC1002156//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION.//0.00010:64:
 34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53915
 F-OVARC1002158//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION.//8.2e-07:119:35//
 AUTOGRAPHIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41479
 F-OVARC1002165//EBNA-6 NUCLEAR PROTEIN (EBNA-3C) (EBNA-4B).//0.00023:90:45//EPSTEIN-BARR VI-
 50 RUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03204
 F-OVARC1002182//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHRO-
 MOSOME II.//1.3e-34:165:35//CAENORHABDITIS ELEGANS.//Q18964
 F-PLACE1000004//HYPOTHETICAL 180.2 KD PROTEIN C31A2.05C IN CHROMOSOME I.//8.8e-05:148:25//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09725
 55 F-PLACE1000005//PROTEIN Q300.//0.30:10:100//MUS MUSCULUS (MOUSE).//Q02722
 F-PLACE1000007//PROBABLE UBIQUITIN CARBOXYL TERMINAL HYDROLASE P1.//1.0e-05:100:100//
 CAENORHABDITIS ELEGANS.//P3454
 F-PLACE1000008//PROBABLE UBIQUITIN CARBOXYL TERMINAL HYDROLASE P1.//1.0e-05:100:100//
 CAENORHABDITIS ELEGANS.//P3454

F-PLACE1000014//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))//
0.00036:63:39//HOMO SAPIENS (HUMAN)//P19474

F-PLACE1000031

F-PLACE1000040//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//4.4e-12:97:41//HOMO SAPIENS (HUMAN)//
P39194

F-PLACE1000048//50S RIBOSOMAL PROTEIN L15 (FRAGMENT)//0.98:31:38//BACILLUS SP. (STRAIN C-
125)//P38373

F-PLACE1000050//COLLAGEN ALPHA 1(III) CHAIN//0.00062:190:33//BOS TAURUS (BOVINE)//P04258

F-PLACE1000061//60S RIBOSOMAL PROTEIN L37A//6.4e-19:51:86//GALLUS GALLUS (CHICKEN)//P32046

F-PLACE1000066//SSU72 PROTEIN//2.3e-39:165:49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//
P53538

F-PLACE1000078//BAD PROTEIN (BCL-2 BINDING COMPONENT 6)//1.7e-06:21:95//HOMO SAPIENS (HU-
MAN)//Q92934

F-PLACE1000081//HOMEBOX PROTEIN HOX-A4 (HOX-1.4) (MH-3)//0.0053:146:33//MUS MUSCULUS
(MOUSE)//P06798

F-PLACE1000094

F-PLACE1000133//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3)//
1.8e-62:158:81//HOMO SAPIENS (HUMAN)//P20290

F-PLACE1000142//ENOYL-COA HYDRATASE, MITOCHONDRIAL PRECURSOR (EC 4.2.1.17) (SHORT CHAIN
ENOYL-COA HYDRATASE) (SCEH) (ENOYL-COA HYDRATASE 1)//9.8e-12:104:34//HOMO SAPIENS (HU-
MAN)//P30084

F-PLACE1000184//AC PROTEIN//0.44:31:29//BACTERIOPHAGE T4//P18924

F-PLACE1000185//HYPOTHETICAL GLYCINE-RICH 49.6 KD PROTEIN CY130.10C PRECURSOR//0.11:48:
33//MYCOBACTERIUM TUBERCULOSIS//Q10637

F-PLACE1000213//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-
DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)//3.4e-05:194:26//SACCHAROMYCES CEREVISIAE
(BAKER'S YEAST)//P08640

F-PLACE1000214

F-PLACE1000236//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR//0.027:63:34//GALLUS GALLUS
(CHICKEN)//P02457

F-PLACE1000246//TEGUMENT PROTEIN (GENE 11 PROTEIN)//0.78:100:26//EQUINE HERPESVIRUS TYPE
4 (STRAIN 1942) (EHV-4) (EQUINE HERPESVIRUS TYPE 1 SUBTYPE 2)//Q00039

F-PLACE1000292

F-PLACE1000308//EARLY NODULIN 75 (N-75) (NGM-75) (FRAGMENT)//0.049:28:42//MEDICAGO SATIVA
(ALFALFA)//P11728

F-PLACE1000332

F-PLACE1000347//HYPOTHETICAL PROTEIN TP0420//0.15:24:54//TREPONEMA PALLIDUM//O83435

F-PLACE1000374//LYSOZYME C (EC 3.2.1.17) (1,4-BETA-N-ACETYLMURAMIDASE C)//1.0:63:25//ORYC-
TOLAGUS CUNICULUS (RABBIT)//P16973

F-PLACE1000380//MATING PROCESS PROTEIN MID2 (SERINE-RICH PROTEIN SMS1) (PROTEIN KINASE
A INTERFERENCE PROTEIN)//0.018:169:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P36027

F-PLACE1000383//MYOTUBULARIN//1.2e-65:215:57//HOMO SAPIENS (HUMAN)//Q13496

F-PLACE1000401//ELASTIN PRECURSOR (TROPOELASTIN)//0.00023:145:30//MUS MUSCULUS
(MOUSE)//P54320

F-PLACE1000406//54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB))//3.4e-27:90:63//HOMO SAPIENS
(HUMAN)//Q15233

F-PLACE1000420//7,8-DIHYDRO-8-OXOGUANINE TRIPHOSPHATASE (EC 3.1.6.-) (8-OXO-DGTPASE)//4.7e-
07:134:29//MUS MUSCULUS (MOUSE)//P53368

F-PLACE1000421//HYPOTHETICAL 8.8 KD PROTEIN C11D3.01C IN CHROMOSOME I//0.48:72:27//
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10080

F-PLACE1000424

F-PLACE1000435

F-PLACE1000444//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//2.0e-31:129:63//HOMO SAPIENS (HU-
MAN)//P39195

F-PLACE1000453//PROTEIN Q300//0.013:16:68//MUS MUSCULUS (MOUSE)//Q02722

F-PLACE1000481//LINE 1 REVERSE TRANSCRIPTASE HOMOLOG 116336134M

F-PLACE1000540

F-PLACE1000547//MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP-MANNOSE-1-PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE)//1.8e-21:87:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P41940

5 F-PLACE1000562//HYPOTHETICAL PROTEIN MJ0562//1.0:35:34//METHANOCOCCUS JANNASCHII//Q57982

F-PLACE1000564//ADRENAL SPECIFIC 30 KD PROTEIN (CLONE PG2)//0.13:66:37//HOMO SAPIENS (HUMAN)//P15803

10 F-PLACE1000583//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1)//7.0e-45:192:47//HOMO SAPIENS (HUMAN)//P51522

F-PLACE1000588//INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GUANINE NUCLEOTIDE-BINDING PROTEIN 1)//5.3e-63:122:88//HOMO SAPIENS (HUMAN)//P32455

F-PLACE1000596//RING CANAL PROTEIN (KELCH PROTEIN)//2.6e-12:120:38//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q04652

15 F-PLACE1000599//EARLY E3B 12.7 KD PROTEIN PRECURSOR//0.83:53:32//HUMAN ADENOVIRUS TYPE 12//P36707

F-PLACE1000610

F-PLACE1000611//HYPOTHETICAL 33.6 KD PROTEIN IN MCK1-RPS19B INTERGENIC REGION//9.4e-07:64:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P48558

20 F-PLACE1000636//MALE STERILITY PROTEIN 2//3.7e-09:83:43//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)//Q08891

F-PLACE1000653//PUTATIVE PHOSPHOACETYLGLUCOSAMINE MUTASE (EC 5.4.2.3) (ACETYLGLUCOSAMINE PHOSPHOMUTASE) (N-ACETYLGLUCOSAMINE-PHOSPHATE MUTASE)//1.9e-30:203:41//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09667

25 F-PLACE1000656//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)//0.0029:75:33//NICOTIANA TABACUM (COMMON TOBACCO)//P13983

F-PLACE1000706//TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (NUCLEAR COREPRESSOR KAP-1) (KRAB-ASSOCIATED PROTEIN 1)//1.1e-38:180:42//HOMO SAPIENS (HUMAN)//Q13263

30 F-PLACE1000712//VERY HYPOTHETICAL 8.9 KD PROTEIN CY441.05 PRECURSOR//0.93:49:34//MYCOBACTERIUM TUBERCULOSIS//P71934

F-PLACE1000716

F-PLACE1000748//HYPOTHETICAL 10.4 KD PROTEIN IN SPAT 3'REGION (ORF-11)//0.90:53:37//SHIGELLA FLEXNERI//P55794

35 F-PLACE1000749//HYPOTHETICAL PROTEIN MG148//0.0014:142:27//MYCOPLASMA GENITALIUM//P47394

F-PLACE1000755//HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III//1.1e-15:98:48//CAENORHABDITIS ELEGANS//P34529

F-PLACE1000769//VIGILIN//0.51:60:33//GALLUS GALLUS (CHICKEN)//P81021

40 F-PLACE1000785//PROBABLE COLD SHOCK PROTEIN CY15C10.04//1.0:22:45//MYCOBACTERIUM TUBERCULOSIS//O06360

F-PLACE1000786//HYPOTHETICAL 30.2 KD PROTEIN ZK632.12 IN CHROMOSOME III//2.6e-38:159:51//CAENORHABDITIS ELEGANS//P34657

F-PLACE1000793//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP)//0.0097:128:30//HOMO SAPIENS (HUMAN)//P50552

45 F-PLACE1000798//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//9.4e-07:47:61//HOMO SAPIENS (HUMAN)//P39188

F-PLACE1000841

F-PLACE1000849//ELAV PROTEIN//3.5e-05:140:35//DROSOPHILA VIRILIS (FRUIT FLY)//P23241

50 F-PLACE1000856//HYPOTHETICAL PROTEIN MJ0008//0.95:100:23//METHANOCOCCUS JANNASCHII//Q60319

F-PLACE1000863//PUTATIVE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN YHR148W//2.3e-46:172:54//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32899

F-PLACE1000909//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN)//0.00022:105:35//HOMO SAPIENS (HUMAN)//P16157

55 F-PLACE1000931//KILLER TOXIN HM-1//0.95:24:33//WILLIOPSIS MRAKII (YEAST) (HANSENULA MRAKII)//P10410

- F-PLACE1000972//MYOSIN ID HEAVY CHAIN.//1.9e-06:79:43//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P34109
- F-PLACE1000977//HYPOTHETICAL 94.2 KD PROTEIN C38D4.5 IN CHROMOSOME III.//2.5e-23:105:41//CAENORHABDITIS ELEGANS.//P46941
- 5 F-PLACE1000979//ZINC FINGER PROTEIN 7 (ZINC FINGER PROTEIN KOX4) (ZINC FINGER PROTEIN HF. 16).//0.91:83:30//HOMO SAPIENS (HUMAN).//P17097
- F-PLACE1000987//HYPOTHETICAL 111.5 KD PROTEIN C22G7.02 IN CHROMOSOME I.//0.10:128:24//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09796
- F-PLACE1001000
- 10 F-PLACE1001007//ZYXIN.//2.2e-05:135:30//GALLUS GALLUS (CHICKEN).//Q04584
- F-PLACE1001010//BETA-1 BUNGAROTOXIN B CHAIN, MAJOR COMPONENT PRECURSOR (BUNGAROTOXIN, B1 CHAIN).//1.0:30:40//BUNGARUS MULTICINCTUS (MANY-BANDED KRAIT).//P00987
- F-PLACE1001015
- F-PLACE1001024
- 15 F-PLACE1001036
- F-PLACE1001054//HOLOTRICIN 3 PRECURSOR.//0.0044:56:39//HOLOTRICHIA DIOMPHALIA.//Q25055
- F-PLACE1001062//SACCHAROPINE DEHYDROGENASE [NADP+, L-GLUTAMATE FORMING] (EC 1.5.1.10).//0.0013:38:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38999
- F-PLACE1001076
- 20 F-PLACE1001088//EARLY NODULIN 75 (N-75) (NGM-75) (FRAGMENT).//0.95:32:50//MEDICAGO SATIVA (ALFALFA).//P11728
- F-PLACE1001092//HYPOTHETICAL 49.0 KD PROTEIN IN NSP1-KAR2 INTERGENIC REGION.//0.0026:81:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47057
- F-PLACE1001104//HYPOTHETICAL 131.5 KD PROTEIN C02F12.7 IN CHROMOSOME X.//0.00063:125:32//CAENORHABDITIS ELEGANS.//Q11102
- 25 F-PLACE1001118//ZINC FINGER PROTEIN MLZ-4 (ZINC FINGER PROTEIN 46).//2.6e-77:209:63//MUS MUSCULUS (MOUSE).//Q03309
- F-PLACE1001136//ALPHA-N-ACETYL GALACTOSAMINIDASE PRECURSOR (EC 3.2.1.49) (ALPHA- GALACTOSIDASE B).//0.99:107:30//HOMO SAPIENS (HUMAN).//P17050
- 30 F-PLACE1001168
- F-PLACE1001171//RETROVIRUS-RELATED POL POLYPROTEIN (FRAGMENT).//0.00012:37:59//HOMO SAPIENS (HUMAN).//P12895
- F-PLACE1001185//HYPOTHETICAL 56.6 KD PROTEIN IN URE2-SSU72 INTERGENIC REGION.//3.6e-12:88:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53867
- 35 F-PLACE1001238
- F-PLACE1001241//METALLOTHIONEIN B (MTB) (FRAGMENT).//0.13:30:53//COLINUS VIRGINIANUS (BOBWHITE QUAIL) (COMMON BOBWHITE).//P27087
- F-PLACE1001257//RING CANAL PROTEIN (KELCH PROTEIN).//4.1e-24:125:46//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
- 40 F-PLACE1001272//HYPOTHETICAL PROTEIN IN KSGA 3'REGION (ORF L5) (FRAGMENT).//1.0:24:45//MYCOPLASMA CAPRICOLUM.//P43040
- F-PLACE1001279//CYTOTOXIN 3 (CYTOTOXIN V-II-3).//0.98:31:41//NAJA MOSSAMBICA (MOZAMBIQUE COBRA).//P01470
- F-PLACE1001280//PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS: CHONDROCALCIN].//0.0051:156:32//MUS MUSCULUS (MOUSE).//P28481
- 45 F-PLACE1001294//GAMETOGENESIS EXPRESSED PROTEIN GEG-154.//3.7e-56:109:93//MUS MUSCULUS (MOUSE).//P50636
- F-PLACE1001304//ZINC FINGER PROTEIN 35 (ZFP-35).//3.2e-30:75:57//MUS MUSCULUS (MOUSE).//P15620
- F-PLACE1001311//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//2.7e-31:66:66//HOMO SAPIENS (HUMAN).//P39189
- 50 F-PLACE1001323
- F-PLACE1001351//REV PROTEIN (ANTI-REPRESSION TRANSACTIVATOR PROTEIN) (ART/TRS).//0.11:66:27//SIMIAN IMMUNODEFICIENCY VIRUS (AGM155 ISOLATE) (SIV-AGM).//P27971
- F-PLACE1001366//SHORT NEUROTOXIN 2 (TOXIN CM-14) (TOXIN V-N-12).//0.070:18:33//NAJA HAJE ANNU-LIFERA (BANDED EGYPTIAN COBRA).//P01422
- 55 F-PLACE1001377//DISINTEGRIN TRIGRAMIN BETA (PLATELET AGGREGATION ACTIVATION INHIBITOR)

- 0.00050:213:23//RATTUS NORVEGICUS (RAT)//P12839
 F-PLACE1001740//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.4e-17:90:56//HOMO SAPIENS (HUMAN)//
 P39188
 F-PLACE1001745//HYPOTHETICAL PROTEIN KIAA0125//0.96:38:36//HOMO SAPIENS (HUMAN)//Q14138
 5 F-PLACE1001746//CONGLUTIN DELTA-2 SMALL CHAIN//0.98:23:43//LUPINUS ANGUSTIFOLIUS (NARROW-
 LEAVED BLUE LUPINE)//P09930
 F-PLACE1001748//HYPOTHETICAL 99.0 KD PROTEIN SPBC119.17//2.9e-28:167:38//SCHIZOSACCHARO-
 MYCES POMBE (FISSION YEAST)//O42908
 F-PLACE1001756//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/9.2e-43:126:77//HOMO SAPIENS (HU-
 10 MAN)//P39189
 F-PLACE1001761//50S RIBOSOMAL PROTEIN L35//0.26:42:38//HELICOBACTER PYLORI (CAMPYLO-
 BACTER PYLORI)//P56057
 F-PLACE1001771//TRANSIENT-RECEPTOR-POTENTIAL LIKE PROTEIN//4.8e-35:223:40//DROSOPHILA
 MELANOGASTER (FRUIT FLY)//P48994
 15 F-PLACE1001781//HYPOTHETICAL 71.1 KD PROTEIN IN DSK2-CAT8 INTERGENIC REGION//9.5e-41:194:
 46//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q03262
 F-PLACE1001799
 F-PLACE1001810
 F-PLACE1001817//SUCCINYL-COA LIGASE [GDP-FORMING], BETA-CHAIN PRECURSOR (EC 6.2.1.4) (SUC-
 20 CINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA)//2.8e-40:115:61//NEOCALLIMASTIX FRONTALIS (RU-
 MEN FUNGUS)//P53587
 F-PLACE1001821
 F-PLACE1001844//IG KAPPA CHAIN V-I REGION (HAU)//0.59:89:35//HOMO SAPIENS (HUMAN)//P01600
 F-PLACE1001845
 25 F-PLACE1001869//MPA43 PROTEIN//3.5e-14:153:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//
 P53583
 F-PLACE1001897//LIGATOXIN A//1.0:43:27//PHORADENDRON LIGA (ARGENTINE MISTLETOE)//P01540
 F-PLACE1001912//LONG NEUROTOXIN 2 (TOXIN C)//0.57:44:45//ASTROTIA STOKESI (STOKES'S SEA
 SNAKE) (DITEIRA STOKESI)//P01381
 30 F-PLACE1001920//LATE GENES ACTIVATOR (EARLY PROTEIN GP4) (GPF)//0.89:75:29//BACTERIOPHAGE
 NF//P09877
 F-PLACE1001928
 F-PLACE1001983//IMMEDIATE-EARLY PROTEIN IE180//0.0049:51:45//PSEUDORABIES VIRUS (STRAIN KA-
 PLAN) (PRV)//P33479
 35 F-PLACE1001989//PUTATIVE AMIDASE (EC 3.5.1.4)//8.9e-08:125:36//MORAXELLA CATARRHALIS//Q49091
 F-PLACE1002004
 F-PLACE1002046//LIGATIN (FRAGMENT)//1.6e-84:191:84//MUS MUSCULUS (MOUSE)//Q61211
 F-PLACE1002052
 F-PLACE1002066
 40 F-PLACE1002072//ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR//0.16:77:31//ARABIDOP-
 SIS THALIANA (MOUSE-EAR CRESS)//P40602
 F-PLACE1002073//HYPOTHETICAL 118.2 KD PROTEIN F43C.1 IN CHROMOSOME III//4.0e-11:174:28//
 CAENORHABDITIS ELEGANS//Q09564
 F-PLACE1002090//SIGNAL RECOGNITION PARTICLE 72 KD PROTEIN (SRP72)//2.8e-57:112:99//HOMO SA-
 45 PIENS (HUMAN)//O76094
 F-PLACE1002115//P8 MTCP-1 PROTEIN (MATURE T-CELL PROLIFERATION-1 TYPE A) (MTCP-1 TYPE A)
 (P8MTCP1)//1.0:49:30//MUS MUSCULUS (MOUSE)//Q61908
 F-PLACE1002119//T-LYMPHOCYTE ACTIVATED PROTEIN (CYCLOHEXIMIDE-INDUCED) (CHX1) (IMMEDI-
 50 ATE EARLY RESPONSE 2 PROTEIN)//2.7e-11:118:36//MUS MUSCULUS (MOUSE)//P17950
 F-PLACE1002140//HYPOTHETICAL 12.3 KD PROTEIN IN MOBL 3'REGION (ORF 4)//0.0086:39:46//THIOBA-
 CILLUS FERROOXIDANS//P20088
 F-PLACE1002150
 F-PLACE1002157//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/2.4e-34:56:82//HOMO SAPIENS (HUMAN)//
 P39189
 55 F-PLACE1002163//NEUROTOXIN 1//1.0:17:52//CENTRUROIDES SCULPTURATUS (BARK SCORPION)//
 P01492

SWI3) (TRANSCRIPTION FACTOR

TYE2).//0.00023:179:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32591

F-PLACE1002205//HYPOTHETICAL 13.5 KD PROTEIN IN MOB1-SGA1 INTERGENIC REGION.//0.77:21:47//
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40490

5 F-PLACE1002213//HISTONE H4 (FRAGMENT).//0.62:31:32//BLEPHARISMA JAPONICUM.//P80738

F-PLACE1002227//HYPOTHETICAL 7.9 KD PROTEIN IN FIXW 5'REGION.//0.41:49:36//RHIZOBIUM LEGUMI-
NOSARUM.//P14310

F-PLACE1002256//CYTOCHROME B (EC 1.10.2.2).//0.61:95:29//CAENORHABDITIS ELEGANS.//P24890

10 F-PLACE1002259//HYPOTHETICAL 9.2 KD PROTEIN IN SPS1-QCR7 INTERGENIC REGION.//0.99:22:45//
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P56508F-PLACE1002319//HYPOTHETICAL 56.6 KD PROTEIN IN URE2-SSU72 INTERGENIC REGION.//0.91:18:72//
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53867F-PLACE1002342//HYPOTHETICAL PROTEIN C16.//1.0:53:32//SWINEPOX VIRUS (STRAIN KASZA) (SPV).//
P3221915 F-PLACE1002395//CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).//6.4e-05:127:37//PLASMODIUM
VIVAX.//P08677

F-PLACE1002399

F-PLACE1002433//DYNAMACTIN, 150 KD ISOFORM (150 KD DYNEIN-ASSOCIATED POLYPEPTIDE) (DP-150)
(DAP-150) (P150-GLUED).//0.00094:182:25//RATTUS NORVEGICUS (RAT).//P2802320 F-PLACE1002437//ATP-BINDING CASSETTE TRANSPORTER 1.//4.5e-19:62:77//MUS MUSCULUS
(MOUSE).//P41233F-PLACE1002438//HYPOTHETICAL 141.5 KD ZINC FINGER PROTEIN IN TUB1-CPR3 INTERGENIC RE-
GION.//0.014:63:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q0454525 F-PLACE1002450//OOCYTE ZINC FINGER PROTEIN XLCOF6 (FRAGMENT).//3.9e-28:159:38//XENOPUS
LAEVIS (AFRICAN CLAWED FROG).//P18749F-PLACE1002465//LARIAT DEBRANCHING ENZYME (EC 3.1.-.-).//0.0014:148:28//SCHIZOSACCHAROMY-
CES POMBE (FISSION YEAST).//O13765

F-PLACE1002474//FIBRILLIN 2 PRECURSOR.//2.1e-24:203:33//MUS MUSCULUS (MOUSE).//Q61555

F-PLACE1002477//ALU SUBFAMILY SP WARNING ENTRY !!!!!//0.15:65:41//HOMO SAPIENS (HUMAN).//
P3919330 F-PLACE1002493//SEMENOGELIN II PRECURSOR (SGII).//1.0:72:31//MACACA MULATTA (RHESUS
MACAQUE).//Q95196F-PLACE1002499//HYPOTHETICAL 39.3 KD PROTEIN C02B8.6 IN CHROMOSOME X.//2.9e-11:67:35//
CAENORHABDITIS ELEGANS.//Q1109635 F-PLACE1002500//COBALT-ZINC-CADMIUM RESISTANCE PROTEIN CZCD (CATION EFFLUX SYSTEM PRO-
TEIN CZCD).//8.4e-11:143:32//ALCALIGENES EUTROPHUS.//P13512F-PLACE1002514//HYPOTHETICAL 8.1 KD PROTEIN IN SPEA-METK INTERGENIC REGION (O71).//1.0:15:
60//ESCHERICHIA COLI.//P46878

F-PLACE1002529

40 F-PLACE1002532//HOMEBOX PROTEIN DLX-5.//1.1e-76:183:81//MUS MUSCULUS (MOUSE).//P70396

F-PLACE1002537//ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.6e-18:51:86//HOMO SAPIENS (HUMAN).//
P39195F-PLACE1002571//ACTIN-LIKE PROTEIN 13E.//6.0e-56:140:47//DROSOPHILA MELANOGASTER (FRUIT
FLY).//P45890

45 F-PLACE1002578

F-PLACE1002583

F-PLACE1002591//CORONIN-LIKE PROTEIN P57.//5.5e-26:78:69//BOS TAURUS (BOVINE).//Q92176

F-PLACE1002598

F-PLACE1002604

50 F-PLACE1002625//HYPOTHETICAL 180.2 KD PROTEIN IN FAA4-HOR7 INTERGENIC REGION.//6.4e-08:193:
23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04781F-PLACE1002655//ADSEVERIN (GELSOLIN-LIKE PROTEIN).//7.1e-100:210:89//MUS MUSCULUS (MOUSE).//
Q60604

F-PLACE1002665//MOBILIZATION PROTEIN MOBS.//0.35:60:30//THIOBACILLUS FERROOXIDANS.//P20086

55 F-PLACE1002685//ACTIN BINDING PROTEIN.//0.052:115:29//SACCHAROMYCES EXIGUUS (YEAST).//
P38479

F-PLACE1002768//FOLLICLE STIMULATING HORMONE RECEPTOR PRECURSOR (FSH-R) (FOLLITROPIN RECEPTOR) (FRAGMENT).//0.43:40:35//MUS MUSCULUS (MOUSE).//P35378

F-PLACE1002775//CENTROMERE/MICROTUBULE BINDING PROTEIN CBF5 (CENTROMERE-BINDING FACTOR 5) (NUCLEOLAR PROTEIN CBF5)//4.8e-07:96:29//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//O14007

F-PLACE1002794//CUTICLE COLLAGEN 12 PRECURSOR//0.0068:98:39//CAENORHABDITIS ELEGANS//P20630

F-PLACE1002815//C-HORDEIN (CLONE PC HOR1-3) (FRAGMENT)//0.46:35:42//HORDEUM VULGARE (BARLEY)//P17991

F-PLACE1002834/ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1)//1.6e-30:54:96/HOMO SAPIENS (HUMAN)//P51522

F-PLACE1002851//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR (VAI)//0.77:35:37//VICIA ANGUSTIFOLIA
(COMMON VETCH).//P01065

F-PLACE1002881//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.1e-27:91:70//HOMO SAPIENS (HUMAN)//P39188

F-PLACE1002941//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.6e-11:40:85//HOMO SAPIENS (HUMAN).//
P39195

F-PLACE1002968//TOXIN IV-5 PRECURSOR (TITYUSTOXIN) (FRAGMENT)//0.97:26:38//TITYUS SERRULATUS (BRAZILIAN SCORPION)//P01496

F-PLACE1002993//HYPOTHETICAL 17.8 KD PROTEIN IN SMPA-SMPB INTERGENIC REGION (F158).//
0.00045:93:23//ESCHERICHIA COLI//P52121

F-PLACE1003025//SUPPRESSOR PROTEIN SRP40.//0.0079:214:24//SACCHAROMYCES CEREVISIAE (BAK-ER'S YEAST)//P32583

F-PLACE1003044//SPORE COAT PROTEIN D.//0.97:24:45//BACILLUS SUBTILIS //P07791
F-PLACE1003045

F-PLACE1003100/

F-PLACE1003136

E-PLACE1003153//HUNCHBACK PROTEIN (FRAGMENT) //1.0:23:23//LOCUSTA MIGRATORIA (MIGRATORIA)

E-PI ACE1003174//UBIQUITIN-CONJUGATING ENZYME 53.18 KD (EC 6.2.2.19) (UBIQUITIN-PROTEIN)

DOI: 10.1002/for

- SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38319
 F-PLACE1003190//SOF1 PROTEIN.//1.0e-52:158:41//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//
 P33750
 F-PLACE1003200
 5 F-PLACE1003205//SPERM PROTAMINE P1.//0.074:20:45//CAENOLESTES FULIGINOSUS.//P42131
 F-PLACE1003238//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001.//0.013:20:55//HOMO SAPIENS
 (HUMAN).//Q15391
 F-PLACE1003249//HYPOTHETICAL PROTEIN KIAA0125.//0.98:48:37//HOMO SAPIENS (HUMAN).//Q14138
 F-PLACE1003256//OMEGA-CONOTOXINS GVIA, GVIB AND GVIC PRECURSOR (SHAKER PEPTIDE).//0.84:
 10 53:30//CONUS GEOGRAPHUS (GEOGRAPHY CONE).//P01522
 F-PLACE1003258//EARLY EMBRYOGENESIS ZYG-11 PROTEIN.//4.1e-18:70:47//CAENORHABDITIS ELE-
 GANS.//P21541
 F-PLACE1003296//SPECTRIN BETA CHAIN, ERYTHROCYTE.//0.063:160:24//HOMO SAPIENS (HUMAN).//
 P11277
 15 F-PLACE1003302//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//9.4e-69:84:94//HOMO SAPI-
 ENS (HUMAN).//P51522
 F-PLACE1003334//NUCLEOBINDIN PRECURSOR (NUCB1) (BONE 63 KD CALCIUM-BINDING PROTEIN).//
 0.029:125:24//RATTUS NORVEGICUS (RAT).//Q63083
 F-PLACE1003342//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.97:44:40//DROSOPHILA MELA-
 20 NOGASTER (FRUIT FLY).//Q01643
 F-PLACE1003343//GENE 11 PROTEIN.//1.0:37:37//SPIROPLASMA VIRUS SPV1-R8A2 B.//P15902
 F-PLACE1003353//SH2/SH3 ADAPTOR CRK (ADAPTER MOLECULE CRK) (CRK2).//6.4e-05:69:40//XENOPUS
 LAEVIS (AFRICAN CLAWED FROG).//P87378
 F-PLACE1003361/////ALU SUBFAMILY SC WARNING ENTRY /////1.6e-23:66:75//HOMO SAPIENS (HUMAN).//
 25 P39192
 F-PLACE1003366//SMALL PROLINE-RICH PROTEIN 2-1.//0.62:19:57//HOMO SAPIENS (HUMAN).//P35326
 F-PLACE1003369//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//4.3e-06:102:42//SACCHAROMY-
 CES CEREVISIAE (BAKER'S YEAST).//P32323
 F-PLACE1003373//PROTEIN Q300.//0.042:29:37//MUS MUSCULUS (MOUSE).//Q02722
 30 F-PLACE1003375//OLFACTORY RECEPTOR 11 (M49) (FRAGMENT).//0.99:46:34//MUS MUSCULUS
 (MOUSE).//Q60890
 F-PLACE1003383
 F-PLACE1003394//RAS-RELATED PROTEIN RAB-14.//2.8e-80:166:89//RATTUS NORVEGICUS (RAT).//
 P35287
 35 F-PLACE1003401
 F-PLACE1003420//PUTATIVE MITOCHONDRIAL CARRIER YIL006W.//8.1e-17:138:37//SACCHAROMYCES
 CEREVISIAE (BAKER'S YEAST).//P40556
 F-PLACE1003454
 F-PLACE1003478
 40 F-PLACE1003493//ENDOTHELIAL CELL MULTIMERIN PRECURSOR.//3.4e-11:123:32//HOMO SAPIENS (HU-
 MAN).//Q13201
 F-PLACE1003516//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.0e-32:68:76//HOMO SAPIENS (HU-
 MAN).//P08547
 F-PLACE1003519/////ALU SUBFAMILY J WARNING ENTRY /////9.2e-17:77:50//HOMO SAPIENS (HUMAN).//
 45 P39188
 F-PLACE1003521//HYPOTHETICAL BAMHI-ORF9 PROTEIN.//1.0:38:42//FOWLPOX VIRUS (ISOLATE HP-438
 [MUNICH]).//P14366
 F-PLACE1003528//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.96:32:40//XENOPUS LAEVIS (AFRI-
 CAN CLAWED FROG).//P03931
 50 F-PLACE1003537//CEF PROTEIN.//0.92:47:29//BACTERIOPHAGE T4.//Q01436
 F-PLACE1003553
 F-PLACE1003566//HYPOTHETICAL BAMHI-ORF9 PROTEIN.//1.0:32:34//FOWLPOX VIRUS (ISOLATE HP-438
 [MUNICH]).//P14366
 F-PLACE1003575
 55 F-PLACE1003583//PROBABLE E5 PROTEIN.//0.16:64:31//HUMAN PAPILLOMAVIRUS TYPE 35.//P27226
 F-PLACE1003584

1003582:1003583:1003584:1003585:1003586:1003587:1003588:1003589:1003590:1003591:1003592:1003593:1003594:1003595:1003596:1003597:1003598:1003599:1003600:1003601:1003602:1003603:1003604:1003605:1003606:1003607:1003608:1003609:1003610:1003611:1003612:1003613:1003614:1003615:1003616:1003617:1003618:1003619:1003620:1003621:1003622:1003623:1003624:1003625:1003626:1003627:1003628:1003629:1003630:1003631:1003632:1003633:1003634:1003635:1003636:1003637:1003638:1003639:1003640:1003641:1003642:1003643:1003644:1003645:1003646:1003647:1003648:1003649:1003650:1003651:1003652:1003653:1003654:1003655:1003656:1003657:1003658:1003659:1003660:1003661:1003662:1003663:1003664:1003665:1003666:1003667:1003668:1003669:1003670:1003671:1003672:1003673:1003674:1003675:1003676:1003677:1003678:1003679:1003680:1003681:1003682:1003683:1003684:1003685:1003686:1003687:1003688:1003689:1003690:1003691:1003692:1003693:1003694:1003695:1003696:1003697:1003698:1003699:1003700:1003701:1003702:1003703:1003704:1003705:1003706:1003707:1003708:1003709:1003710:1003711:1003712:1003713:1003714:1003715:1003716:1003717:1003718:1003719:1003720:1003721:1003722:1003723:1003724:1003725:1003726:1003727:1003728:1003729:1003730:1003731:1003732:1003733:1003734:1003735:1003736:1003737:1003738:1003739:1003740:1003741:1003742:1003743:1003744:1003745:1003746:1003747:1003748:1003749:1003750:1003751:1003752:1003753:1003754:1003755:1003756:1003757:1003758:1003759:1003760:1003761:1003762:1003763:1003764:1003765:1003766:1003767:1003768:1003769:1003770:1003771:1003772:1003773:1003774:1003775:1003776:1003777:1003778:1003779:1003780:1003781:1003782:1003783:1003784:1003785:1003786:1003787:1003788:1003789:1003790:1003791:1003792:1003793:1003794:1003795:1003796:1003797:1003798:1003799:1003800:1003801:1003802:1003803:1003804:1003805:1003806:1003807:1003808:1003809:1003810:1003811:1003812:1003813:1003814:1003815:1003816:1003817:1003818:1003819:1003820:1003821:1003822:1003823:1003824:1003825:1003826:1003827:1003828:1003829:1003830:1003831:1003832:1003833:1003834:1003835:1003836:1003837:1003838:1003839:1003840:1003841:1003842:1003843:1003844:1003845:1003846:1003847:1003848:1003849:1003850:1003851:1003852:1003853:1003854:1003855:1003856:1003857:1003858:1003859:1003860:1003861:1003862:1003863:1003864:1003865:1003866:1003867:1003868:1003869:1003870:1003871:1003872:1003873:1003874:1003875:1003876:1003877:1003878:1003879:1003880:1003881:1003882:1003883:1003884:1003885:1003886:1003887:1003888:1003889:1003890:1003891:1003892:1003893:1003894:1003895:1003896:1003897:1003898:1003899:1003900:1003901:1003902:1003903:1003904:1003905:1003906:1003907:1003908:1003909:1003910:1003911:1003912:1003913:1003914:1003915:1003916:1003917:1003918:1003919:1003920:1003921:1003922:1003923:1003924:1003925:1003926:1003927:1003928:1003929:1003930:1003931:1003932:1003933:1003934:1003935:1003936:1003937:1003938:1003939:1003940:1003941:1003942:1003943:1003944:1003945:1003946:1003947:1003948:1003949:1003950:1003951:1003952:1003953:1003954:1003955:1003956:1003957:1003958:1003959:1003960:1003961:1003962:1003963:1003964:1003965:1003966:1003967:1003968:1003969:1003970:1003971:1003972:1003973:1003974:1003975:1003976:1003977:1003978:1003979:1003980:1003981:1003982:1003983:1003984:1003985:1003986:1003987:1003988:1003989:1003990:1003991:1003992:1003993:1003994:1003995:1003996:1003997:1003998:1003999:1004000:1004001:1004002:1004003:1004004:1004005:1004006:1004007:1004008:1004009:1004010:1004011:1004012:1004013:1004014:1004015:1004016:1004017:1004018:1004019:1004020:1004021:1004022:1004023:1004024:1004025:1004026:1004027:1004028:1004029:1004030:1004031:1004032:1004033:1004034:1004035:1004036:1004037:1004038:1004039:1004040:1004041:1004042:1004043:1004044:1004045:1004046:1004047:1004048:1004049:1004050:1004051:1004052:1004053:1004054:1004055:1004056:1004057:1004058:1004059:1004060:1004061:1004062:1004063:1004064:1004065:1004066:1004067:1004068:1004069:1004070:1004071:1004072:1004073:1004074:1004075:1004076:1004077:1004078:1004079:1004080:1004081:1004082:1004083:1004084:1004085:1004086:1004087:1004088:1004089:1004090:1004091:1004092:1004093:1004094:1004095:1004096:1004097:1004098:1004099:1004100:1004101:1004102:1004103:1004104:1004105:1004106:1004107:1004108:1004109:1004110:1004111:1004112:1004113:1004114:1004115:1004116:1004117:1004118:1004119:1004120:1004121:1004122:1004123:1004124:1004125:1004126:1004127:1004128:1004129:1004130:1004131:1004132:1004133:1004134:1004135:1004136:1004137:1004138:1004139:1004140:1004141:1004142:1004143:1004144:1004145:1004146:1004147:1004148:1004149:1004150:1004151:1004152:1004153:1004154:1004155:1004156:1004157:1004158:1004159:1004160:1004161:1004162:1004163:1004164:1004165:1004166:1004167:1004168:1004169:1004170:1004171:1004172:1004173:1004174:1004175:1004176:1004177:1004178:1004179:1004180:1004181:1004182:1004183:1004184:1004185:1004186:1004187:1004188:1004189:1004190:1004191:1004192:1004193:1004194:1004195:1004196:1004197:1004198:1004199:1004200:1004201:1004202:1004203:1004204:1004205:1004206: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ANA 1451 10/19/95 11:51:02 36. SACCAROMYCES CEREVISIAE, BAKER'S YEAST, Q0550p

F-PLACE1003923//HISTIDYL-TRNA SYNTHETASE (EC 6.1.1.21) (HISTIDINE--TRNA LIGASE) (HISRS)//0.94:
65:29//STREPTOCOCCUS EQUISIMILIS//P30053
F-PLACE1003932//HYPOTHETICAL 17.3 KD PROTEIN IN SEC15-SAP4 INTERGENIC REGION//0.098:79:31//
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53074
F-PLACE1003936
F-PLACE1003968//5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN)//
4.7e-68:164:78//RATTUS NORVEGICUS (RAT)//P80385
F-PLACE1004103/////ALU SUBFAMILY SC WARNING ENTRY /////1.9e-14:60:73//HOMO SAPIENS (HUMAN)//
P39192
F-PLACE1004104//EXOCYST COMPLEX COMPONENT SEC5//0.020:202:20//SACCHAROMYCES CEREV
ISAE (BAKER'S YEAST)//P89102
F-PLACE1004114/////ALU SUBFAMILY J WARNING ENTRY /////2.1e-15:69:60//HOMO SAPIENS (HUMAN)//
P39188
F-PLACE1004118//REGULATORY PROTEIN E2//0.73:58:36//CANINE ORAL PAPILLOMAVIRUS (COPV)//
Q89420
F-PLACE1004128//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 4 (TRANSDUCIN BETA
CHAIN 4)//7.7e-62:108:100//MUS MUSCULUS (MOUSE)//P29387
F-PLACE1004149//PROBABLE NUCLEAR ANTIGEN//0.0011:73:42//PSEUDORABIES VIRUS (STRAIN KAP-
LAN) (PRV)//P33485
F-PLACE1004156//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT)//0.00061:39:48//OWENIA FUSI-
FORMIS//P21260
F-PLACE1004161//PLASMINOGEN-BINDING PROTEIN PAM PRECURSOR (FRAGMENT)//0.033:108:27//
STREPTOCOCCUS PYOGENES//P49054
F-PLACE1004183//HYPOTHETICAL 64.3 KD PROTEIN IN CDC12-EHP5 INTERGENIC REGION//4.0e-07:146:
35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38817
F-PLACE1004197//BUTYROPHILIN PRECURSOR (BT)//5.9e-11:208:27//MUS MUSCULUS (MOUSE)//
Q62556
F-PLACE1004203//PROTEIN A39//8.5e-18:139:33//VACCINIA VIRUS (STRAIN COPENHAGEN)//P21062
F-PLACE1004242//PHOTOSYSTEM II REACTION CENTRE J PROTEIN//1.0:28:42//PISUM SATIVUM (GAR-
DEN PEA)//P13555
F-PLACE1004256//MYOSIN HEAVY CHAIN D (MHC D)//0.73:134:25//CAENORHABDITIS ELEGANS//P02567
F-PLACE1004257//HYPOTHETICAL PROTEIN HI0490//0.13:75:29//HAEMOPHILUS INFLUENZAE//P44006
F-PLACE1004258//COLLAGEN ALPHA 2(VIII) CHAIN (ENDOTHELIAL COLLAGEN) (FRAGMENT)//0.027:128:
35//HOMO SAPIENS (HUMAN)//P25067
F-PLACE1004270//LARGE TEGUMENT PROTEIN//1.8e-10:100:44//EPSTEIN-BARR VIRUS (STRAIN B95-8)
(HUMAN HERPESVIRUS 4)//P03186
F-PLACE1004274//HYPOTHETICAL PROTEIN E-95//0.44:61:42//HUMAN ADENOVIRUS TYPE 2//P03286
F-PLACE1004277//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS)//0.0013:55:38//BOS TAURUS (BOVINE)//
P25508
F-PLACE1004284//7 KD PROTEIN (ORF 4)//1.0:63:23//CHRYSANthemum VIRUS B (CVB)//P37990
F-PLACE1004289//SPERM PROTAMINE P3//0.00057:22:77//MUS MUSCULUS (MOUSE)//Q62100
F-PLACE1004302//SERINE/THREONINE PROTEIN KINASE AFSK (EC 2.7.1.-)//0.0065:148:29//STREPTOMY-
CES COELICOLOR//P54741
F-PLACE1004316//AUTOPHAGY PROTEIN APG5//8.8e-06:117:29//SACCHAROMYCES CEREVISIAE (BAK-
ER'S YEAST)//Q12380
F-PLACE1004336//COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR//0.0027:83:36//HOMO SAPIENS (HU-
MAN)//P53420
F-PLACE1004358//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR//2.9e-05:200:33//GALLUS GALLUS
(CHICKEN)//P02457
F-PLACE1004376//AXONEME-ASSOCIATED PROTEIN MST101(2)//2.4e-05:179:29//DROSOPHILA HYDEI
(FRUIT FLY)//Q08696
F-PLACE1004384/////ALU SUBFAMILY SQ WARNING ENTRY /////1.6e-28:46:76//HOMO SAPIENS (HUMAN)//
P39194
F-PLACE1004388//HYPOTHETICAL 75.2 KD PROTEIN IN ACS1-GCV3 INTERGENIC REGION//5.7e-34:202:
37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P39722
F-PLACE1004405//NEURAMINYLLACTOSE BINDING - MEMBRANE ANCHORED - POLYMERIZING
- WITH A SHORT CYTOSOLIC EXTENSION - GLYCOPROTEIN - CELL SURFACE - BINDING - SUBUNIT - CLBF - FLAGELLAR
HEATH ADHESIN - ADHESIN - FRAGMENT - FROM ESCHERICHIA COLI OCBACTER ACINONYX//Q4794

- F-PLACE1004425//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.81:70:42//HOMO SAPIENS (HUMAN)//P39195
- F-PLACE1004428//PRISTANOYL-COA OXIDASE (EC 1.3.3.-)/1.9e-31:203:39//RATTUS NORVEGICUS (RAT)//Q63448
- 5 F-PLACE1004437//ISOCITRATE DEHYDROGENASE [NAD], MITOCHONDRIAL SUBUNIT BETA PRECURSOR (EC 1.1.1.41) (ISOCITRIC DEHYDROGENASE) (NAD⁺-SPECIFIC ICDH) (FRAGMENT)//4.2e-93:140:100//MACACA FASCICULARIS (CRAB EATING MACAQUE) (CYNOMOLGUS MONKEY)//Q28479
- F-PLACE1004451//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.00013:40:62//HOMO SAPIENS (HUMAN)//P39188
- 10 F-PLACE1004460//MATERNAL TUDOR PROTEIN//0.0066:218:23//DROSOPHILA MELANOGASTER (FRUIT FLY)//P25823
- F-PLACE1004467//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/7.8e-10:33:87//HOMO SAPIENS (HUMAN)//P39193
- F-PLACE1004471//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1)//7.0e-56:92:58//HOMO SAPIENS (HUMAN)//P51522
- 15 F-PLACE1004473//HYPOTHETICAL 54.3 KD PROTEIN C23D3.03C IN CHROMOSOME I//0.019:136:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09844
- F-PLACE1004491//LYSIS PROTEIN//0.95:53:30//BACTERIOPHAGE FR//P19903
- F-PLACE1004506//AUTOIMMUNOGENIC CANCER/TESTIS ANTIGEN NY-ESO-1 (LAGE-1)//0.58:66:34//HOMO SAPIENS (HUMAN)//P78358
- 20 F-PLACE1004510//TRANSCRIPTION INITIATION FACTOR TFIID 150 KD SUBUNIT (TAFII-150) (TAFII150)//3.0e-07:63:46//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q24325
- F-PLACE1004516//HYPOTHETICAL PROTEIN 5' TO ASP-RICH AND HIS-RICH PROTEINS (FRAGMENT)//0.95:62:29//PLASMODIUM FALCIPARUM (ISOLATE FCM17 / SENEGAL)//P14587
- 25 F-PLACE1004518//METALLOTHIONEIN 10-III (MT-10-III)//0.91:28:42//MYTILUS EDULIS (BLUE MUSSEL)//P80248
- F-PLACE1004548//DIHYDROPYRIDINE-SENSITIVE L-TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT//0.94:75:32//ORYCTOLAGUS CUNICULUS (RABBIT)//P19518
- F-PLACE1004550//CUTICLE COLLAGEN 2//0.90:155:31//CAENORHABDITIS ELEGANS//P17656
- 30 F-PLACE1004564//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT)//3.2e-70:121:100//BOS TAURUS (BOVINE)//Q10568
- F-PLACE1004629//PROTEIN OS-9 PRECURSOR//1.7e-10:132:36//HOMO SAPIENS (HUMAN)//Q13438
- F-PLACE1004645//TRANSCRIPTION INITIATION FACTOR IIB HOMOLOG (TFIIB)//0.00036:100:30//PYROCOCCUS FURIOSUS//Q51731
- 35 F-PLACE1004646//PROBABLE UDP-GALACTOPYRANOSE MUTASE (EC 5.4.99.9)//0.91:58:29//KLEBSIELLA PNEUMONIAE//Q48481
- F-PLACE1004658//GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 4 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2D) (NR2D) (NMDAR2D)//0.031:134:32//MUS MUSCULUS (MOUSE)//Q03391
- 40 F-PLACE1004664//HYPOTHETICAL 180.2 KD PROTEIN IN FAA4-HOR7 INTERGENIC REGION//0.025:125:20//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q04781
- F-PLACE1004672//HYPOTHETICAL 36.7 KD PROTEIN C2F7:14C IN CHROMOSOME I//7.6e-52:158:56//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09704
- F-PLACE1004674//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257)//1.4e-88:144:93//MUS MUSCULUS (MOUSE)//P12815
- 45 F-PLACE1004681//CCR4-ASSOCIATED FACTOR 1 (CAF1)//1.0e-34:70:100//MUS MUSCULUS (MOUSE)//Q60809
- F-PLACE1004686//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/3.4e-08:48:62//HOMO SAPIENS (HUMAN)//P39192
- 50 F-PLACE1004691//METALLOTHIONEIN (MT)//0.064:24:45//ARIANTA ARBUSTORUM//P55946
- F-PLACE1004693
- F-PLACE1004716//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//1.0:27:37//PAN PANISCUS (PYGMY CHIMPANZEE) (BONOBO)//Q35587
- F-PLACE1004722//HYPOTHETICAL 61.5 KD PROTEIN IN CLA4-MID1 INTERGENIC REGION//0.95:53:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P48565
- 55 F-PLACE1004736//NEURONAL LAYONIN MEMBRANE PROTEIN 1
- F-PLACE1004740//ALU SUBFAMILY SC WARNING ENTRY !!!!!/7.0e-07:70:70//HOMO SAPIENS (HUMAN)

P39194

F-PLACE1004743//HYPOTHETICAL 12.6 KD PROTEIN IN ALGR3 3'REGION.//0.99:72:33//PSEUDOMONAS AERUGINOSA.//P21484

F-PLACE1004751//CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (EC 2.4.99.-) (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ST3GALIII) (ALPHA 2,3-ST) (GAL-NAC6S) (STZ) (SIAT4-C) (SAT-3) (ST-4).//2.2e-08:90:38//HOMO SAPIENS (HUMAN).//Q11206

F-PLACE1004773//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//3.2e-25:233:32//HOMO SAPIENS (HUMAN).//P16157

F-PLACE1004777//N-CHIMAERIN (NC) (N-CHIMERIN) (ALPHA CHIMERIN) (A-CHIMAERIN).//8.1e-26:210:30//RATTUS NORVEGICUS (RAT).//P30337

F-PLACE1004793//ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36].//0.00062:106:25//MOUSE MAMMARY TUMOR VIRUS (STRAIN BR6).//P10259

F-PLACE1004804

F-PLACE1004813//HYPOTHETICAL PROTEIN UL12.//1.0:22:40//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16777

F-PLACE1004814//HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II.//2.8e-06:136:25//CAENORHABDITIS ELEGANS.//Q09217

F-PLACE1004815

F-PLACE1004824//HYPOTHETICAL 106.7 KD PROTEIN IN MUP1-SPR3 INTERGENIC REGION.//2.3e-09:70:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53236

F-PLACE1004827//HYPOTHETICAL 9.4 KD PROTEIN IN FLAL 3'REGION (ORF3).//0.54:25:56//BACILLUS LICHENIFORMIS.//P22754

F-PLACE1004836//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.0066:12:66//BOS TAURUS (BOVINE).//P20072

F-PLACE1004838

F-PLACE1004840

F-PLACE1004868//MALE STERILITY PROTEIN 2.//4.0e-16:172:30//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q08891

F-PLACE1004885

F-PLACE1004900//MAST CELL DEGRANULATING PEPTIDE PRECURSOR (MCDP) (MCD) (PEPTIDE 401).//1.0:23:47//APIS MELLIFERA (HONEYBEE).//P01499

F-PLACE1004902//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//7.3e-15:94:47//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q42643

F-PLACE1004913//HYPOTHETICAL 7.2 KD PROTEIN IN BCSA-DEGR INTERGENIC REGION.//1.0:42:33//BACILLUS SUBTILIS.//P54165

F-PLACE1004918//HYPOTHETICAL 12.4 KD PROTEIN IN RPS21B-MRS3 INTERGENIC REGION.//0.98:50:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47012

F-PLACE1004930//HYPOTHETICAL PROTEIN MJ0562.//0.82:44:36//METHANOCOCCUS JANNASCHII.//Q57982

F-PLACE1004934

F-PLACE1004937//HYPOTHETICAL 67.1 KD TRP-ASP REPEATS CONTAINING PROTEIN C57A10.05C IN CHROMOSOME I.//9.0e-10:87:33//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P87053

F-PLACE1004969//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//4.0e-14:184:25//CAENORHABDITIS ELEGANS.//Q11073

F-PLACE1004972//BROMELAIN INHIBITOR 2 (BI-II) (BROMELAIN INHIBITOR VI) (BI-VI).//1.0:35:37//ANANAS COMOSUS (PINEAPPLE).//P27478

F-PLACE1004979//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//5.3e-30:55:72//HOMO SAPIENS (HUMAN).//P39192

F-PLACE1004982//M PROTEIN, SEROTYPE 12 PRECURSOR (FRAGMENT).//0.00049:124:27//STREPTOCOCCUS PYOGENES.//P19401

F-PLACE1004985//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:26:34//LUMBRICUS TERRESTRIS (COMMON EARTHWORM).//Q34942

F-PLACE1005026//TELOMERE-BINDING PROTEIN HOMOLOG.//0.0011:179:27//EUPLOTES CRASSUS.//Q06183

F-PLACE1005027

F-PLACE1005046//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.082:44:36//BOS TAURUS (BOVINE).//P20072

F-PLACE1005052//MA F SPECIFIC PROTEIN (PROTEIN 1005052) (PROTEIN 1005052) (PROTEIN 1005052)

PLACE1005052

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GULL)//P02451

F-PLACE1005471//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3)//0.23:49:32//PHYTOPHTHORA INFESTANS (POTATO LATE BLIGHT FUNGUS)//Q37598

F-PLACE1005477//HYPOTHETICAL PROTEIN ORF-1137//9.6e-13:115:38//MUS MUSCULUS (MOUSE)//P11260

F-PLACE1005480//C-HORDEIN (CLONE PC HOR1-3) (FRAGMENT)//0.97:33:30//HORDEUM VULGARE (BARLEY)//P17991

F-PLACE1005481//HUNCHBACK PROTEIN (FRAGMENT)//0.30:52:38//APIS MELLIFERA (HONEYBEE)//P31504

F-PLACE1005494//TRANSIENT-RECEPTOR-POTENTIAL PROTEIN//3.9e-05:87:33//DROSOPHILA MELANOGASTER (FRUIT FLY)//P19334

F-PLACE1005502

F-PLACE1005526//IMMEDIATE-EARLY PROTEIN IE180//4.6e-05:132:32//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV)//P33479

F-PLACE1005528//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//3.4e-09:31:74//HOMO SAPIENS (HUMAN)//P39195

F-PLACE1005530//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III//9.7e-50:148:58//CAENORHABDITIS ELEGANS//Q09251

F-PLACE1005550//HYPOTHETICAL 40.2 KD PROTEIN K12H4.3 IN CHROMOSOME III//3.0e-21:127:37//CAENORHABDITIS ELEGANS//P34524

F-PLACE1005554//CYTOCHROME B (EC 1.10.2.2) (FRAGMENT)//0.84:38:31//DIPODOMYS CALIFORNICUS (KANGAROO RAT)//P16359

F-PLACE1005557//60S RIBOSOMAL PROTEIN L27//4.8e-09:60:48//CRYPTOCOCCUS NEOFORMANS (FILOBASIDIELLA NEOFORMANS) //P46288

F-PLACE1005574//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//0.89:44:29//BOS TAURUS (BOVINE)//P03929

F-PLACE1005584//MALE SPECIFIC SPERM PROTEIN MST87F//0.00030:33:48//DROSOPHILA MELANOGASTER (FRUIT FLY)//P08175

F-PLACE1005595//IMMEDIATE-EARLY PROTEIN IE180//0.00048:162:30//PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV)//P11675

F-PLACE1005603//HIGH-MOBILITY-GROUP PROTEIN (NONHISTONE CHROMOSOMAL PROTEIN)//0.00034:83:30//TETRAHYMENA PYRIFORMIS//P40625

F-PLACE1005611//DNAJ PROTEIN//8.6e-20:108:48//CLOSTRIDIUM ACETOBUTYLICUM//P30725

F-PLACE1005623//EXTRACELLULAR SIGNAL-REGULATED KINASE 5 (EC 2.7.1.-) (ERK5) (ERK4) (BMK1 KINASE)//0.80:116:31//HOMO SAPIENS (HUMAN)//Q13164

F-PLACE1005630//INTERLEUKIN-14 PRECURSOR (IL-14) (HIGH MOLECULAR WEIGHT B-CELL GROWTH FACTOR) (HMW-BCGF)//0.0024:74:39//HOMO SAPIENS (HUMAN)//P40222

F-PLACE1005639//EXTRACELLULAR MATRIX PROTEIN 1 (SECRETORY COMPONENT P85) (FRAGMENT)//0.72:18:61//RATTUS NORVEGICUS (RAT)//Q62894

F-PLACE1005646//RNA HELICASE-LIKE PROTEIN DB10//4.8e-29:172:45//NICOTIANA SYLVESTRIS (WOOD TOBACCO)//P46942

F-PLACE1005656//RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE)//3.7e-64:133:75//MESOCRICETUS AURATUS (GOLDEN HAMSTER)//Q60561

F-PLACE1005666//CHLOROPLAST 50S RIBOSOMAL PROTEIN L28//0.57:36:41//PORPHYRA PURPUREA//P51224

F-PLACE1005698//HYPOTHETICAL PROTEIN IN SIGD 3'REGION (ORFC) (FRAGMENT)//0.50:61:29//BACILLUS SUBTILIS//P40405

F-PLACE1005727//ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX) (FRAGMENT)//0.46:27:51//BRASSICA NAPUS (RAPE)//P40603

F-PLACE1005730//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENT)//0.95:21:52//ORYCTOLAGUS CUNICULUS (RABBIT)//P02456

F-PLACE1005739//INTERFERON-GAMMA INDUCIBLE PROTEIN MG11//3.4e-46:111:53//MUS MUSCULUS (MOUSE)//Q60710

F-PLACE1005755//HYPOTHETICAL 70.2 KD PROTEIN IN GSH1-CHS6 INTERGENIC REGION//2.6e-12:66:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P42951

F-PLACE1005763//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 2.3.1.16) (FATTY ACID SYNTHASE) (FAC) (FAC1) (FAC2) (FAC3) (FAC4) (FAC5) (FAC6) (FAC7) (FAC8) (FAC9) (FAC10) (FAC11) (FAC12) (FAC13) (FAC14) (FAC15) (FAC16) (FAC17) (FAC18) (FAC19) (FAC20) (FAC21) (FAC22) (FAC23) (FAC24) (FAC25) (FAC26) (FAC27) (FAC28) (FAC29) (FAC30) (FAC31) (FAC32) (FAC33) (FAC34) (FAC35) (FAC36) (FAC37) (FAC38) (FAC39) (FAC40) (FAC41) (FAC42) (FAC43) (FAC44) (FAC45) (FAC46) (FAC47) (FAC48) (FAC49) (FAC50) (FAC51) (FAC52) (FAC53) (FAC54) (FAC55) (FAC56) (FAC57) (FAC58) (FAC59) (FAC60) (FAC61) (FAC62) (FAC63) (FAC64) (FAC65) (FAC66) (FAC67) (FAC68) (FAC69) (FAC70) (FAC71) (FAC72) (FAC73) (FAC74) (FAC75) (FAC76) (FAC77) (FAC78) (FAC79) (FAC80) (FAC81) (FAC82) (FAC83) (FAC84) (FAC85) (FAC86) (FAC87) (FAC88) (FAC89) (FAC90) (FAC91) (FAC92) (FAC93) (FAC94) (FAC95) (FAC96) (FAC97) (FAC98) (FAC99) (FAC100) (FAC101) (FAC102) (FAC103) (FAC104) (FAC105) (FAC106) (FAC107) (FAC108) (FAC109) (FAC110) 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SAPIENS (HUMAN)//P26371

F-PLACE1005802//PROTEIN PROSPERO//0.86:64:42//DROSOPHILA MELANOGASTER (FRUIT FLY)//P29617

F-PLACE1005803//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116//1.0:95:25//MUS MUSCULUS (MOUSE)//P17564

F-PLACE1005804//PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2-MANNOSIDASE 1B)//2.8e-73:198:73//MUS MUSCULUS (MOUSE)//P39098

F-PLACE1005813//HYPOTHETICAL 49.0 KD PROTEIN IN NSP1-KAR2 INTERGENIC REGION//0.022:78:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P47057

F-PLACE1005828//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.8e-23:56:76//HOMO SAPIENS (HUMAN)//P39195

F-PLACE1005834//LATE CONTROL GENE B PROTEIN (GPB)//0.97:33:39//BACTERIOPHAGE 186//P08711

F-PLACE1005845

F-PLACE1005850//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/5.5e-28:96:73//HOMO SAPIENS (HUMAN)//P39194

F-PLACE1005851

F-PLACE1005876//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT)//2.2e-99:155:95//BOS TAURUS (BOVINE)//Q10568

F-PLACE1005884

F-PLACE1005890//BEM46 PROTEIN (FRAGMENT)//1.8e-33:137:49//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//P54069

F-PLACE1005898//NADH-UBIQUINONE OXIDOREDUCTASE MLRQ SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-MLRQ) (CI-MLRQ)//0.77:58:34//HOMO SAPIENS (HUMAN)//O00483

F-PLACE1005921//AIG1 PROTEIN//1.4e-23:165:38//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)//P54120

F-PLACE1005923//HYPOTHETICAL 22.4 KD PROTEIN (ORF16)//0.90:118:28//PARAMECIUM TETRAURELIA//P15617

F-PLACE1005925//HYPOTHETICAL GENE 30 PROTEIN//0.94:57:29//HERPESVIRUS SAIMIRI (STRAIN 11)//Q01010

F-PLACE1005932//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)//0.42:128:32//NICOTIANA TABACUM (COMMON TOBACCO)//P13983

F-PLACE1005934//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6)(RPB1) (FRAGMENT)//0.40:76:35//CRICETULUS GRISEUS (CHINESE HAMSTER)//P11414

F-PLACE1005936//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN)//0.50:15:66//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (CLONE 12) (HIV-1)//P04326

F-PLACE1005951//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)//0.0025:135:32//NICOTIANA TABACUM (COMMON TOBACCO)//P13983

F-PLACE1005953//HIGH POTENTIAL IRON-SULFUR PROTEIN (HIPIP)//0.64:57:33//RHODOFERAX FERMENTANS//P80882

F-PLACE1005955//HYPOTHETICAL 54.2 KD PROTEIN IN ERP5-ORC6 INTERGENIC REGION//1.0e-32:110:50//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38821

F-PLACE1005966//TACHYPLESIN II PRECURSOR//0.97:31:35//TACHYPLEUS TRIDENTATUS (JAPANESE HORSESHOE CRAB)//P14214

F-PLACE1005968//GATA FACTOR SREP//0.17:52:40//PENICILLIUM CHRYSOGENUM//Q92259

F-PLACE1005990//CELL PATTERN FORMATION-ASSOCIATED PROTEIN//0.36:55:36//EMERICELLA NIDULANS (ASPERGILLUS NIDULANS)//P36011

F-PLACE1006002//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.5e-36:102:75//HOMO SAPIENS (HUMAN)//P39192

F-PLACE1006003//HYPOTHETICAL 6.8 KD PROTEIN IN COX3-NAD1 INTERGENIC REGION (ORF 61)//1.0:22:40//MARCHANTIA POLYMORPHA (LIVERWORT)//P38473

F-PLACE1006011//POLY [ADP-RIBOSE] POLYMERASE (EC 2.4.2.30) (PARP) (ADPRT) (NAD(+)) ADP-RIBOSYLTRANSFERASE) (POLY[ADP-RIBOSE] SYNTHETASE)//2.8e-21:163:36//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)//Q11207

F-PLACE1006017//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.1e-10:43:67//HOMO SAPIENS (HUMAN)//P39192

F-PLACE1006037//HYPOTHETICAL 1.8 KD PROTEIN IN COX3-NAD1 INTERGENIC REGION (ORF 61)//1.0:22:40//MARCHANTIA POLYMORPHA (LIVERWORT)//P38473

F-PLACE1006040//CAMP-REGULATED PHOSPHOPROTEIN 19 (ARPP-19)//3.2e-40:110:76//HOMO SAPIENS (HUMAN)//P56211
 F-PLACE1006076//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR A-II//0.99:30:40//ARACHIS HYPOGAEA (PEANUT)//P01066
 5 F-PLACE1006119//IMPORTIN BETA-3 SUBUNIT (KARYOPHERIN BETA-3 SUBUNIT) (RAN-BINDING PROTEIN 5)//8.8e-94:218:76//HOMO SAPIENS (HUMAN)//O00410
 F-PLACE1006129//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR//0.00092:228:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32323
 F-PLACE1006139//HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION//5.9e-55:128:50//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P43616
 10 F-PLACE1006143//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.4e-25:107:63//HOMO SAPIENS (HUMAN)//P39194
 F-PLACE1006157//E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E)//1.3e-21:168:32//SUS SCROFA (PIG)//P98110
 15 F-PLACE1006159//COLD SHOCK INDUCED PROTEIN TIR1 PRECURSOR (SERINE-RICH PROTEIN 1)//0.46:98:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P10863
 F-PLACE1006164//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3)//0.70:28:42//ARTEMIA SALINA (BRINE SHRIMP)//P19049
 20 F-PLACE1006167//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)//8.9e-05:167:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P08640
 F-PLACE1006170//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAP T IN ALPHA C SUBUNIT)//1.1e-67:157:88//MUS MUSCULUS (MOUSE)//P17427
 25 F-PLACE1006187//G1/S-SPECIFIC CYCLIN E//5.6e-75:224:62//HOMO SAPIENS (HUMAN)//P24864
 F-PLACE1006195//T-RELATED PROTEIN (TRP) (BRACHYENTERON PROTEIN)//0.99:177:29//DROSOPHILA MELANOGASTER (FRUIT FLY)//P55965
 F-PLACE1006196//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06//2.0e-33:183:46//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09747
 30 F-PLACE1006205
 F-PLACE1006223//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS)//0.00015:22:50//MUS MUSCULUS (MOUSE)//P15265
 F-PLACE1006225//VIRION INFECTIVITY FACTOR (SOR PROTEIN)//1.0:63:34//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE) (HIV-1)//P18805
 35 F-PLACE1006236
 F-PLACE1006239//60S ACIDIC RIBOSOMAL PROTEIN P2 (FRAGMENT)//0.48:23:52//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)//P51407
 F-PLACE1006246//CMP-SIALIC ACID TRANSPORTER (CMP-SIA-TR)//0.012:84:30//MUS MUSCULUS (MOUSE)//Q61420
 40 F-PLACE1006248//140 KD NUCLEOLAR PHOSPHOPROTEIN (NOPP140)//0.017:203:22//RATTUS NORVEGICUS (RAT)//P41777
 F-PLACE1006262//L-FUCULOSE PHOSPHATE ALDOLASE (EC 4.1.2.17)//0.84:25:52//HAEMOPHILUS INFLUENZAE//P44777
 45 F-PLACE1006288
 F-PLACE1006318//CYSTEINE-RICH ANTIFUNGAL PROTEIN 1 (AFP1) (M1)//1.0:29:48//SINAPIS ALBA (WHITE MUSTARD) (BRASSICA HIRTA)//P30231
 F-PLACE1006325//CYCLIN-DEPENDENT KINASE INHIBITOR 1C (CYCLIN-DEPENDENT KINASE INHIBITOR P57) (P57KIP2)//0.99:97:32//HOMO SAPIENS (HUMAN)//P49918
 50 F-PLACE1006335//PROLINE-RICH PEPTIDE P-B//0.56:19:52//HOMO SAPIENS (HUMAN)//P02814
 F-PLACE1006357
 F-PLACE1006360
 F-PLACE1006368//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110)//0.0057:122:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32380
 55 F-PLACE1006371//ARS BINDING PROTEIN 1//0.00030:142:30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST) //P49777

- F-PLACE1006385//HYPOTHETICAL 45.1 KD PROTEIN IN RPS5-ZMS1 INTERGENIC REGION.//3.1e-35:165:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47160
- F-PLACE1006412//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.3e-08:40:47//HOMO SAPIENS (HUMAN).//P08547
- 5 F-PLACE1006414//FORKHEAD-RELATED TRANSCRIPTION FACTOR 4 (FREAC-4).//3.8e-05:123:39//HOMO SAPIENS (HUMAN).//Q16676
- F-PLACE1006438//ZINC FINGER PROTEIN 165.//2.8e-21:76:64//HOMO SAPIENS (HUMAN).//P49910
- F-PLACE1006445//SUPPRESSOR OF HAIRY WING PROTEIN.//0.058:99:29//DROSOPHILA VIRILIS (FRUIT FLY).//Q08876
- 10 F-PLACE1006469//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//1.8e-64:177:50//ESCHERICHIA COLI.//P27550
- F-PLACE1006470
- F-PLACE1006482//TRANSCRIPTION FACTOR MAFF.//2.0e-47:120:85//GALLUS GALLUS (CHICKEN).//Q90595
- 15 F-PLACE1006488//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//1.8e-85:173:95//CANIS FAMILIARIS (DOG).//Q00004
- F-PLACE1006492//VERY HYPOTHETICAL 11.2 KD PROTEIN C56F8.13 IN CHROMOSOME I.//0.75:32:56//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10261
- F-PLACE1006506
- 20 F-PLACE1006521
- F-PLACE1006531//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME III.//1.3e-53:167:61//CAENORHABDITIS ELEGANS.//P34681
- F-PLACE1006534
- F-PLACE1006540
- 25 F-PLACE1006552//MYOSIN HEAVY CHAIN, CLONE 203 (FRAGMENT).//1.3e-07:242:23//HYDRA ATTENUATA (HYDRA) (HYDRA VULGARIS).//P39922
- F-PLACE1006598//!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!//0.17:43:51//HOMO SAPIENS (HUMAN).//P39190
- F-PLACE1006615//ACROSIN PRECURSOR (EC 3.4.21.10).//3.6e-05:66:43//ORYCTOLAGUS CUNICULUS (RABBIT).//P48038
- 30 F-PLACE1006617//HYPOTHETICAL 14.6 KD PROTEIN (READING FRAME C) (REPUCATION).//1.0:74:29//STAPHYLOCOCCUS AUREUS.//P03861
- F-PLACE1006626//HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III.//2.9e-10:73:46//CAENORHABDITIS ELEGANS.//P34529
- 35 F-PLACE1006629//HYPOTHETICAL PROTEIN BB0410.//1.0:23:43//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE).//O51371
- F-PLACE1006640
- F-PLACE1006673
- F-PLACE1006678//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENT).//1.0:36:41//ORYCTOLAGUS CUNICULUS (RABBIT).//P02456
- 40 F-PLACE1006704//BROAD-COMPLEX CORE-TNT1-Q1-Z1 PROTEIN (BRCORE-TNT1-Q1-Z1) [CONTAINS: BROAD-COMPLEX CORE-Q1-Z1 PROTEIN].//0.00062:157:26//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01295
- F-PLACE1006731//RIBOFLAVIN KINASE (EC 2.7.1.26) (FLAVOKINASE) / FMN ADENYLYLTRANSFERASE (EC 2.7.7.2) (FAD PYROPHOSPHORYLASE) (FAD SYNTHETASE).//1.3e-07:127:36//CORYNEBACTERIUM AMMONIAGENES (BREVIBACTERIUM AMMONIAGENES).//Q59263
- 45 F-PLACE1006754//CARCINOEMBRYONIC ANTIGEN CGM1 PRECURSOR (CD66D ANTIGEN).//1.9e-19:78:53//HOMO SAPIENS (HUMAN).//P40198
- F-PLACE1006760//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENT).//0.21:107:30//RATTUS NORVEGICUS (RAT).//P13941
- 50 F-PLACE1006779//CYTOTOXIN 5 (CTX V).//1.0:20:30//NAJA MOSSAMBICA (MOZAMBIQUE COBRA).//P25517
- F-PLACE1006782//ZINC FINGER PROTEIN 1.//0.00052:178:28//CANDIDA ALBICANS (YEAST).//P28875
- F-PLACE1006792
- F-PLACE1006795//VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN SHAW (SHAW2).//1.0:80:30//DROSOPHILA MELANOGASTER (FRUIT FLY).//P17972
- 55 F-PLACE1006800//HYPOTHETICAL 3.4 KD PROTEIN C56F8.13 IN CHROMOSOME I.//0.75:32:56//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10261

- F-PLACE1006815//HYPOTHETICAL PROTEIN UL61.//0.038:146:32//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16818
- F-PLACE1006819//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.3e-98:239:76//HOMO SAPIENS (HUMAN).//P08547
- 5 F-PLACE1006829//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 8 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 8) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 8) (DEUBIQUITINATING ENZYME 8).//0.061:34:58//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P50102
- F-PLACE1006860
- F-PLACE1006867
- 10 F-PLACE1006878//HYPOTHETICAL 8.2 KD PROTEIN IN MOBL 3'REGION (ORF 3).//0.85:27:37//THIOBACILLUS FERROOXIDANS.//P20087
- F-PLACE1006883//VITAMIN D3 RECEPTOR (VDR) (1,25-DIHYDROXYVITAMIN D3 RECEPTOR).//0.78:51:37//MUS MUSCULUS (MOUSE).//P48281
- F-PLACE1006901//HYPOTHETICAL 8.1 KD PROTEIN.//0.99:55:23//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20567
- 15 F-PLACE1006904//MATING-TYPE LOCUS ALLELE B1 PROTEIN.//0.95:86:26//USTILAGO MAYDIS (SMUT FUNGUS).//P22015
- F-PLACE1006917//HYPOTHETICAL 40.9 KD PROTEIN C08B11.5 IN CHROMOSOME II.//6.9e-15:101:45//CAENORHABDITIS ELEGANS.//Q09442
- 20 F-PLACE1006932//HISTIDINE-RICH, METAL BINDING POLYPEPTIDE.//0.089:28:39//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//Q48251
- F-PLACE1006935//HYPOTHETICAL 95.2 KD PROTEIN R144.6 IN CHROMOSOME III.//0.93:35:48//CAENORHABDITIS ELEGANS.//Q10000
- F-PLACE1006956//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).//0.00079:122:36//HOMO SAPIENS (HUMAN).//O00268
- 25 F-PLACE1006958//OSMOTIC STRESS PROTEIN 94 (HEAT SHOCK 70-RELATED PROTEIN APG-1).//8.8e-70:140:98//MUS MUSCULUS (MOUSE).//P48722
- F-PLACE1006961
- F-PLACE1006962//APOLIPOPROTEIN C-I PRECURSOR (APO-C1).//1.0:25:40//PAPIO HAMADRYAS (HAMADRYAS BABOON).//P34929
- 30 F-PLACE1006966//HYPOTHETICAL 49.1 KD PROTEIN IN SSB2-SPX18 INTERGENIC REGION.//1.6e-47:221:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40160
- F-PLACE1006989//HYPOTHETICAL 13.1 KD HIT-LIKE PROTEIN IN P37 5'REGION.//0.15:46:32//MYCOPLASMA HYORHINIS.//P32083
- 35 F-PLACE1007014//36 KD NUCLEOLAR PROTEIN HNP36 (DELAYED-EARLY RESPONSE PROTEIN 12) (DER12).//3.4e-09:120:29//HOMO SAPIENS (HUMAN).//Q14542
- F-PLACE1007021//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.00046:42:59//HOMO SAPIENS (HUMAN).//P39188
- F-PLACE1007045//HYPOTHETICAL PROTEIN ORF-1137.//8.1e-14:115:35//MUS MUSCULUS (MOUSE).//P11260
- 40 F-PLACE1007053//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.038:48:39//HOMO SAPIENS (HUMAN).//P22531
- F-PLACE1007068//PROTEIN-LYSINE 6-OXIDASE PRECURSOR (EC 1.4.3.13) (LYSYL OXIDASE).//0.0040:113:39//GALLUS GALLUS (CHICKEN).//Q05063
- 45 F-PLACE1007097//HYPOTHETICAL 6.8 KD PROTEIN IN HE65-PK2 INTERGENIC REGION.//0.97:47:29//AUTOGRAPHAL CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41663
- F-PLACE1007105//HYPOTHETICAL 83.6 KD PROTEIN C15A10.10 IN CHROMOSOME L.//2.9e-33:219:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O13730
- F-PLACE1007111
- 50 F-PLACE1007112//HYPOTHETICAL 9.2 KD PROTEIN.//0.47:75:28//ESCHERICHIA COLI.//P03853
- F-PLACE1007132//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.8e-11:56:57//HOMO SAPIENS (HUMAN).//P39188
- F-PLACE1007140//GAR2 PROTEIN.//0.72:185:24//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P41891
- 55 F-PLACE1007178//HYPOTHETICAL 8.5 KD PROTEIN CY274.40C.//0.97:79:30//MYCOBACTERIUM TUBERCULOSIS.//Q10826

401-00752

F-PLACE1007537//MYOTROPHIN (V-1 PROTEIN) (GRANULE CELL DIFFERENTIATION PROTEIN)//0.045:92:30//MUS MUSCULUS (MOUSE), AND RATTUS NORVEGICUS (RAT)//P80144
 F-PLACE1007544//IMMEDIATE-EARLY PROTEIN IE180//1.5e-07:59:50//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV)//P33479
 5 F-PLACE1007547//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III//2.5e-16:188:34//CAENORHABDITIS ELEGANS//P34537
 F-PLACE1007557
 F-PLACE1007583//PROLINE RICH 33 KD EXTENSIN-RELATED PROTEIN PRECURSOR (FRAGMENT)//0.98:72:33//DAUCUS CAROTA (CARROT) //P06600
 10 F-PLACE1007598//ZINC FINGER PROTEIN 92 (ZINC FINGER PROTEIN HTF12) (FRAGMENT)//1.7e-11:88:43//HOMO SAPIENS (HUMAN)//Q03936
 F-PLACE1007618//ANION EXCHANGE PROTEIN 2 (NON-ERYTHROID BAND 3-LIKE PROTEIN) (B3RP)//0.19:109:27//MUS MUSCULUS (MOUSE)//P13808
 F-PLACE1007621//PHOSPHATE REGULON SENSOR PROTEIN PHOR (EC 2.7.3.-) (FRAGMENT)//0.98:34:41//PSEUDOMONAS AERUGINOSA//P23621
 15 F-PLACE1007632//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENT)//0.70:110:34//BOS TAURUS (BOVINE)//P02465
 F-PLACE1007645//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//0.99:20:45//STRUTHIO CAMELUS (OSTRICH)//O21401
 20 F-PLACE1007649//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)//8.1e-06:197:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P08640
 F-PLACE1007677//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.0:47:46//HOMO SAPIENS (HUMAN)//P39192
 25 F-PLACE1007688//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)//2.7e-06:116:28//AEDES ALBOPICTUS (FOREST DAY MOSQUITO)//Q26457
 F-PLACE1007690//SPERM PROTAMINE P1//0.12:26:50//TACHYGLOSSUS ACULEATUS ACULEATUS (AUSTRALIAN ECHIDNA)//P35311
 F-PLACE1007697//SPERM PROTAMINE P1//0.19:34:52//DIDELPHIS MARSUPIALIS VIRGINIANA (NORTH AMERICAN OPOSSUM), AND MONODELPHIS DOMESTICA (SHORT-TAILED GREY OPOSSUM)//P35305
 30 F-PLACE1007705//BIOH PROTEIN//0.015:97:29//ESCHERICHIA COLI//P13001
 F-PLACE1007706//HYPOTHETICAL 112.2 KD PROTEIN IN TIF35-NPL3 INTERGENIC REGION (ORF1)//5.3e-55:190:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32898
 F-PLACE1007725
 35 F-PLACE1007729//PROTEASE (EC 3.4.23.-)//1.8e-21:136:42//MOUSE MAMMARY TUMOR VIRUS (STRAIN BR6)//P10271
 F-PLACE1007730//SALIVARY PROLINE-RICH PROTEIN II-1 (FRAGMENT)//0.0031:77:40//HOMO SAPIENS (HUMAN)//P81489
 F-PLACE1007737//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.78:39:56//HOMO SAPIENS (HUMAN)//P39195
 40 F-PLACE1007743
 F-PLACE1007746//RRP5 PROTEIN HOMOLOG (KIAA0185) (FRAGMENT)//0.0066:168:25//HOMO SAPIENS (HUMAN)//Q14690
 F-PLACE1007791//KRUEPPEL PROTEIN (FRAGMENT)//0.62:17:41//LITHOBIUS FORFICATUS//Q01872
 45 F-PLACE1007807//HYPOTHETICAL 6.4 KD PROTEIN IN BLTR-SPOIIC INTERGENIC REGION//1.0:40:30//BACILLUS SUBTILIS//P54446
 F-PLACE1007810//ANTHOPLEURIN A (TOXIN AP-A)//0.79:28:46//ANTHOPLEURA XANTHOGRAMMICA (GIANT GREEN SEA ANEMONE)//P01530
 F-PLACE1007829//SPORE COAT PROTEIN G//1.0:65:38//BACILLUS SUBTILIS//P39801
 50 F-PLACE1007843
 F-PLACE1007846//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//1.5e-32:37:94//HOMO SAPIENS (HUMAN)//P08547
 F-PLACE1007852//RHO-RELATED GTP-BINDING PROTEIN RHOH (GTP-BINDING PROTEIN TTF)//8.7e-05:138:30//HOMO SAPIENS (HUMAN)//Q15669
 55 F-PLACE1007858//ANAPHASE SPINDLE ELONGATION PROTEIN//0.0039:127:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) (P32898)

F-PLACE1007897//CD44 ANTIGEN PRECURSOR (PHAGOCYTTIC GLYCOPROTEIN I) (PGP-1) (HUTCH-I) (EX-
TRACELLULAR MATRIX RECEPTOR-III) (ECMR-III) (GP90 LYMPHOCYTE HOMING/ADHESION RECEPTOR)
(HERMES ANTIGEN) (HYALURONATE RECEPTOR) (HEPARAN SULFATE PROTEOGLYCAN) (HAM1 ANTI-
GEN)//0.44:128:28//MESOCRICETUS AURATUS (GOLDEN HAMSTER)//Q60522

5 F-PLACE1007908//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/5.5e-28:61:65//HOMO SAPIENS (HUMAN)//
P39192

F-PLACE1007946//HYPOTHETICAL MERCURIC RESISTANCE PROTEIN MERC//0.84:48:37//PSEU-
DOMONAS AERUGINOSA//P04139

10 F-PLACE1007954//HYPOTHETICAL 45.5 KD PROTEIN IN FIG1-GIP1 INTERGENIC REGION//0.00070:96:29//
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38226

F-PLACE1007955//HYPOTHETICAL 84.3 KD PROTEIN ZK945.10 IN CHROMOSOME II//0.00027:255:23//
CAENORHABDITIS ELEGANS//Q09625

F-PLACE1007958//HIGH-AFFINITY CAMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE (EC 3.1.4.17)//
1.7e-09:127:30//MUS MUSCULUS (MOUSE)//P70453

15 F-PLACE1007969//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION//2.4e-05:104:37//
AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMPNV)//P41479

F-PLACE1007990//SPERM PROTAMINE P1//0.78:36:47//ORNITHORHYNCHUS ANATINUS (DUCKBILL PLAT-
YPUS)//P35307

20 F-PLACE1008000//CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSIN-110) (SYNAPTIC DEN-
SITY PROTEIN PSD-93)//1.2e-16:128:39//RATTUS NORVEGICUS (RAT)//Q63622

F-PLACE1008002

F-PLACE1008044//NUCLEAR PORE COMPLEX PROTEIN NUP107 (NUCLEOPORIN NUP107) (107 KD NU-
CLEOPORIN) (P105)//3.9e-106:208:93//RATTUS NORVEGICUS (RAT)//P52590

25 F-PLACE1008045//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS)//3.9e-09:49:53//BOS TAURUS (BO-
VINE)//P25508

F-PLACE1008080//RNA REPLICASE POLYPROTEIN (EC 2.7.7.48)//0.00025:100:27//EGGPLANT MOSAIC VI-
RUS//P20126

F-PLACE1008095//PROTOPORPHYRINOGEN OXIDASE (EC 1.3.3.4) (PPO)//0.90:74:25//MYCOBACTERIUM
TUBERCULOSIS//O53230

30 F-PLACE1008111//HYPOTHETICAL PROTEIN MJEC512//0.30:38:42//METHANOCOCCUS JANNASCHII//
Q60311

F-PLACE1008122//PEA2 PROTEIN (PPF2 PROTEIN)//0.0085:117:34//SACCHAROMYCES CEREVISIAE
(BAKER'S YEAST)//P40091

35 F-PLACE1008129//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (FRAGMENTS)//1.8e-06:154:36//GAL-
LUS GALLUS (CHICKEN)//P02467

F-PLACE1008132//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III//1.4e-13:227:36//
CAENORHABDITIS ELEGANS//Q09531

F-PLACE1008177//TRICHOHYALIN//2.7e-10:230:26//OVIS ARIES (SHEEP)//P22793

F-PLACE1008181

40 F-PLACE1008198//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)//0.00044:121:34//
XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P17437

F-PLACE1008201//ZINC FINGER PROTEIN ZFMSA12A//3.0e-05:82:37//MICROPTERUS SALMOIDES
(LARGEMOUTH BASS)//P38621

45 F-PLACE1008209//METALLOTHIONEIN-I (MT-I)//0.95:39:35//CERCOPITHECUS AETHIOPS (GREEN MON-
KEY) (GRIVET)//P02797

F-PLACE1008231//PROCYCLIC FORM SPECIFIC POLYPEPTIDE B1-ALPHA PRECURSOR (PROCYCLIN)
(PARP)//0.028:23:52//TRYPANOSOMA BRUCEI BRUCEI//P08469

F-PLACE1008244//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1//2.2e-23:148:38//PODOSPORA AN-
SERINA//Q00808

50 F-PLACE1008273//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP)//1.1e-97:222:
81//BOS TAURUS (BOVINE)//P53620

F-PLACE1008275//DNA REPAIR PROTEIN REV1 (EC 2.7.7.-)//5.8e-20:161:37//SACCHAROMYCES CEREVI-
SIAE (BAKER'S YEAST)//P12689

55 F-PLACE1008280//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//6.1e-23:124:42//HOMO SAPIENS (HU-
MAN)//P08547

F-PLACE1008306//PROTEIN LAMBDA-1//0.0001:100:100//HOMO SAPIENS (HUMAN)//P08547

F-PLACE1008307//PROTEIN LAMBDA-2//0.0001:100:100//HOMO SAPIENS (HUMAN)//P08547

F-PLACE1008329//PROTEIN LAMBDA-3//0.0001:100:100//HOMO SAPIENS (HUMAN)//P08547

F-PLACE1008693//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR (MSTI)//1.0:36:38//MEDICAGO SCUTEL-
LATA (SNAIL MEDIC)//P80321

F-PLACE1008696//NADH-UBIQUINONE OXIDOREDUCTASE 23 KD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC
1.6.99.3) (COMPLEX I-23KD) (CI-23KD) (TYKY SUBUNIT)//4.8e-14:47:80//HOMO SAPIENS (HUMAN)//
O00217

F-PLACE1008715//HYPOTHETICAL 13.4 KD PROTEIN IN ACT5-YCK1 INTERGENIC REGION//0.66:105:24//
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38834

F-PLACE1008748//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION//0.10:178:
26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53214

F-PLACE1008757//HYPOTHETICAL 10.1 KD PROTEIN IN RHSD-GCL INTERGENIC REGION (ORFD3)//0.60:
44:34//ESCHERICHIA COLI//P33669

F-PLACE1008790//IMPORTIN ALPHA-6 SUBUNIT (KARYOPHERIN ALPHA-6 SUBUNIT) (IMPORTIN ALPHA
S2)//3.0e-69:191:80//MUS MUSCULUS (MOUSE)//O35345

F-PLACE1008798//BACTERIOCIN LACTOBIN A//1.0:34:41//LACTOBACILLUS AMYLOVORUS //P80696

F-PLACE1008807//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//0.91:77:36//HOMO SAPIENS (HU-
MAN)//P08547

F-PLACE1008808//REC1 PROTEIN//0.45:39:30//USTILAGO MAYDIS (SMUT FUNGUS)//P14746

F-PLACE1008813

F-PLACE1008851//VERY HYPOTHETICAL 11.8 KD PROTEIN IN KTR3-DUR1,2 INTERGENIC REGION//1.0:
62:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38309

F-PLACE1008854//HYPOTHETICAL 182.0 KD PROTEIN IN NMD5-HOM6 INTERGENIC REGION//1.0:82:26//
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P47170

F-PLACE1008867//PATATIN T5 PRECURSOR (POTATO TUBER PROTEIN)//0.65:61:36//SOLANUM TUBERO-
SUM (POTATO)//P15478

F-PLACE1008887//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//1.5e-56:180:54//NYCTICEBUS COU-
CANG (SLOW LORIS)//P08548

F-PLACE1008902

F-PLACE1008920

F-PLACE1008925//HYPOTHETICAL 41.2 KD PROTEIN IN GAPA-RND INTERGENIC REGION//0.90:77:33//ES-
CHERICHIA COLI//P76242

F-PLACE1008934//HYPOTHETICAL PROTEIN IN ADHS 5'REGION (ORF3) (FRAGMENT)//0.14:77:45//GLU-
CONOBACTER SUBOXDANS//O05543

F-PLACE1008941//ZINC FINGER PROTEIN 141//1.1e-17:45:95//HOMO SAPIENS (HUMAN)//Q15928

F-PLACE1008947//MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)//4.1e-
14:136:39//MUS MUSCULUS (MOUSE)//P27790

F-PLACE1009020//ANNEXIN VII (SYNEXIN) (FRAGMENT)//0.74:37:48//BOS TAURUS (BOVINE)//P20072

F-PLACE1009027//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3)//0.39:57:36//BALAENOP-
TERA MUSCULUS (BLUE WHALE)//P41301

F-PLACE1009039

F-PLACE1009045//HYPOTHETICAL 9.5 KD PROTEIN IN SPEA-METK INTERGENIC REGION (F83)//0.48:32:
43//ESCHERICHIA COLI//P46879

F-PLACE1009048

F-PLACE1009050

F-PLACE1009060//HYPOTHETICAL 98.3 KD PROTEIN R10E12.1 IN CHROMOSOME III//4.9e-23:244:31//
CAENORHABDITIS ELEGANS//P34552

F-PLACE1009090//50S RIBOSOMAL PROTEIN L35//1.0:27:51//MYCOPLASMA GENITALIUM//P47439

F-PLACE1009091

F-PLACE1009094//NEL-LIKE PROTEIN (FRAGMENT)//3.6e-15:180:30//HOMO SAPIENS (HUMAN)//Q92832

F-PLACE1009099//ZINC FINGER PROTEIN 27 (ZFP-27) (MKR4 PROTEIN) (FRAGMENT)//1.4e-94:228:71//
MUS MUSCULUS (MOUSE)//P10077

F-PLACE1009110//HIRUDIN HV1 (BUFRUDIN)//1.0:49:34//HIRUDINARIA MANILLENSIS (BUFFALO LEECH)//
P81492

F-PLACE1009111//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.4e-05:30:83//HOMO SAPIENS (HUMAN)//
P39195

F-PLACE1009113//ANNEXIN VII (SYNEXIN) (FRAGMENT)//0.032:40:52//BOS TAURUS (BOVINE)//P20072

F-PLACE1009130//HYPOTHETICAL PROTEIN IN CHROMOSOME III//4.9e-23:244:31//CAENORHABDITIS ELEGANS//P34552

3034

ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.4e-05:30:83//HOMO SAPIENS (HUMAN)

P39195

F-PLACE1009155/////ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.2e-17:101:57//HOMO SAPIENS (HUMAN)//P39194

F-PLACE1009158//HYPOTHETICAL PROTEIN HKRFX (J1I)//0.0058:73:42//HUMAN CYTOMEGALOVIRUS (STRAIN AD169)//P09711

F-PLACE1009166//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5)//0.0086:96:30//HOMO SAPIENS (HUMAN)//P49902

F-PLACE1009172//HYPOTHETICAL 8.7 KD PROTEIN IN GAPA-RND INTERGENIC REGION//1.0:19:52//ESCHERICHIA COLI//P76246

F-PLACE1009174/////ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.1e-17:47:82//HOMO SAPIENS (HUMAN)//P39194

F-PLACE1009183

F-PLACE1009186//HYPOTHETICAL 11.4 KD PROTEIN C13G6.04 IN CHROMOSOME I//0.019:62:24//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09783

F-PLACE1009190//PALMITOYL-COA HYDROLASE (EC 3.1.2.2) (LONG-CHAIN FATTY-ACYL-COA HYDROLASE) (FRAGMENT)//0.027:53:28//RATTUS NORVEGICUS (RAT)//P80250

F-PLACE1009200/////ALU SUBFAMILY SQ WARNING ENTRY !!!!!/5.4e-28:84:71//HOMO SAPIENS (HUMAN)//P39194

F-PLACE1009230/////ALU SUBFAMILY SB WARNING ENTRY !!!!!/2.8e-12:50:74//HOMO SAPIENS (HUMAN)//P39189

F-PLACE1009246//UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7.8 KD PROTEIN (EC 1.10.2.2) (MITOCHONDRIAL HINGE PROTEIN) (CR7)//1.0:17:52//SOLANUM TUBEROSUM (POTATO)//P48504

F-PLACE1009298//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35//6.6e-41:177:53//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P34110

F-PLACE1009308//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN)//0.00034:108:33//HOMO SAPIENS (HUMAN)//P26371

F-PLACE1009319//PRESYNAPTIC DENSITY PROTEIN 95 (PSD-95)//5.3e-16:84:50//HOMO SAPIENS (HUMAN)//P78352

F-PLACE1009328//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//6.9e-82:263:67//HOMO SAPIENS (HUMAN)//P08547

F-PLACE1009335//60S RIBOSOMAL PROTEIN L32//0.95:71:36//HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), AND RATTUS NORVEGICUS (RAT)//P02433

F-PLACE1009338//TRANSCRIPTION FACTOR HES-5 (HAIRY AND ENHANCER OF SPLIT 5)//0.90:42:40//MUS MUSCULUS (MOUSE)//P70120

F-PLACE1009368//BASIC PROLINE-RICH PEPTIDE IB-1//0.013:33:48//HOMO SAPIENS (HUMAN)//P04281

F-PLACE1009375//HYPOTHETICAL 88.1 KD PROTEIN K02D10.1 IN CHROMOSOME III//0.0022:135:21//CAENORHABDITIS ELEGANS//P34492

F-PLACE1009388/////ALU SUBFAMILY SX WARNING ENTRY !!!!!/4.8e-22:73:65//HOMO SAPIENS (HUMAN)//P39195

F-PLACE1009398//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)//8.1e-83:223:65//HOMO SAPIENS (HUMAN)//P51523

F-PLACE1009404//GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT PW212 PRECURSOR//0.047:145:29//TRITICUM AESTIVUM (WHEAT)//P08489

F-PLACE1009410//TOXIN C13S1C1 PRECURSOR//0.22:21:47//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAMBA)//P18329

F-PLACE1009434//NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT K (EC 1.6.5.3) (FRAGMENT)//0.81:61:29//ANTHOCEROS FORMOSAE//Q31791

F-PLACE1009443//SPLICIOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66)//9.1e-05:93:32//MUS MUSCULUS (MOUSE)//Q62203

F-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KINASE) (PI4K-ALPHA)//6.4e-15:41:97//HOMO SAPIENS (HUMAN)//P42356

F-PLACE1009459//HYPOTHETICAL 42.3 KD PROTEIN C12G12.11C IN CHROMOSOME I//0.0011:119:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09874

F-PLACE1009468//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP)//4.2e-34:101:75//RATTUS NORVEGICUS (RAT)//P54319

F-PLACE1009476//DNA BINDING

SAPIENS (HUMAN) P30810

ACE100947

- F-PLACE1009925//ATP SYNTHASE D CHAIN, MITOCHONDRIAL (EC 3.6.1.34)//0.99:111:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P30902
- F-PLACE1009935//HYPOTHETICAL PROTEIN MJ0258//0.063:75:32//METHANOCOCCUS JANNASCHII//Q57706
- 5 F-PLACE1009947//NEUROGRANIN (NG) (P17) (B-50 IMMUNOREACTIVE C-KINASE SUBSTRATE) (BICKS) (FRAGMENT)//0.33:51:45//BOS TAURUS (BOVINE)//P35722
- F-PLACE1009971//MIPP PROTEIN (MURINE IAP-PROMOTED PLACENTA-EXPRESSED PROTEIN)//0.022:84:27//MUS MUSCULUS (MOUSE)//P28575
- 10 F-PLACE1009992//BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BMP-1)//0.00011:35:51//HOMO SAPIENS (HUMAN)//P13497
- F-PLACE1009995//TROPOMYOSIN, SMOOTH MUSCLE/FIBROBLAST CTM1//0.052:185:22//CIONA INTESTINALIS//Q07068
- F-PLACE1009997//TRANSCRIPTION ELONGATION FACTOR S-II (RNA POLYMERASE II ELONGATION FACTOR DMS-II) (TFIIS)//0.68:98:28//DROSOPHILA MELANOGASTER (FRUIT FLY)//P20232
- 15 F-PLACE1010023//HYPOTHETICAL 83.8 KD PROTEIN C27F2.7 IN CHROMOSOME III//6.6e-06:111:32//CAENORHABDITIS ELEGANS//Q18262
- F-PLACE1010031//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION//0.0024:72:33//AUTOGRAPHAL CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV)//P41479
- F-PLACE1010053//HYPOTHETICAL PROTEIN HI0593//0.83:24:45//HAEMOPHILUS INFLUENZAE//P44022
- 20 F-PLACE1010069
- F-PLACE1010074//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS5//0.00027:192:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q92331
- F-PLACE1010076//HUNCHBACK PROTEIN (FRAGMENT)//0.80:39:30//SCIARA COPROPHILA (FUNGUS GNAT)//Q01790
- 25 F-PLACE1010083//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131)//2.7e-48:177:46//HOMO SAPIENS (HUMAN)//P98171
- F-PLACE1010089//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 11 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 11) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 13) (DEUBIQUITINATING ENZYME 11) (KIAA0055)//7.9e-07:55:43//HOMO SAPIENS (HUMAN)//P40818
- 30 F-PLACE1010096//100 KD PROTEIN (EC 6.3.2.-)//1.0e-107:232:90//RATTUS NORVEGICUS (RAT)//Q62671
- F-PLACE1010102//DNA-DIRECTED RNA POLYMERASE SUBUNIT N (EC 2.7.7.6)//1.0:33:45//METHANOCOCCUS JANNASCHII//Q57649
- F-PLACE1010105//RING CANAL PROTEIN (KELCH PROTEIN)//1.2e-47:200:46//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q04652
- 35 F-PLACE1010106//RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE]//1.2e-14:94:41//MUS MUSCULUS (MOUSE)//P11369
- F-PLACE1010134//HYPOTHETICAL 171.5 KD HELICASE IN NUT1-ARO2 INTERGENIC REGION//4.0e-28:78:76//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53115
- F-PLACE1010148//GAR2 PROTEIN//2.6e-05:180:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//P41891
- 40 F-PLACE1010152//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME 64E)//2.1e-59:227:54//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q24574
- F-PLACE1010181//MALE SPECIFIC SPERM PROTEIN MST87F//0.39:12:58//DROSOPHILA MELANOGASTER (FRUIT FLY)//P08175
- 45 F-PLACE1010194//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN)//1.4e-07:95:43//GALLUS GALLUS (CHICKEN)//P30352
- F-PLACE1010202//TRISTETRAPROLINE (TTP) (TIS11A) (TIS11) (ZFP-36)//0.094:109:29//RATTUS NORVEGICUS (RAT)//P47973
- 50 F-PLACE1010231//LANTIBIOTIC NISIN A PRECURSOR//0.99:42:35//LACTOCOCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS)//P13068
- F-PLACE1010261//SEGREGATION DISTORTER PROTEIN//6.0e-71:201:62//DROSOPHILA MELANOGASTER (FRUIT FLY)//P25722
- F-PLACE1010270
- 55 F-PLACE1010274//HYPOTHETICAL 16.2 KD PROTEIN C4F8.01 IN CHROMOSOME I//4.4e-08:100:26//SCHIZOSACCHAROMYCES POMBE FISSON YEAST//Q01477

F-PLACE1010310//SYNAPSINS IA AND IB//5.7e-09:89:37//RATTUS NORVEGICUS (RAT)//P09951
 F-PLACE1010321//IMMEDIATE-EARLY PROTEIN IE180//0.033:145:31//PSEUDORABIES VIRUS (STRAIN KA-
 PLAN) (PRV)//P33479
 5 F-PLACE1010324//MAST CELL DEGRANULATING PEPTIDE (MCDP) (MCD)//0.60:25:48//MEGABOMBUS
 PENNSYLVANICUS (AMERICAN COMMON BUMBLEBEE)//P04567
 F-PLACE1010329//TOXIN S5C10//1.0:39:33//DENDROASPIS JAMESONI KAIMOSAE (EASTERN JAMESON'S
 MAMBA)//P01419
 F-PLACE1010341//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/0.0049:49:55//HOMO SAPIENS (HUMAN)//
 P39189
 10 F-PLACE1010362//VARIANT-SURFACE-GLYCOPROTEIN PHOSPHOLIPASE C (EC 3.1.4.47) (VSG LIPASE)
 (GLYCOSYLPHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C) (GPI-PLC)//0.0034:89:30//
 TRYPANOSOMA CRUZI//015886
 F-PLACE1010364//NADH-UBIQUINONE OXIDOREDUCTASE B17 SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3) (COM-
 PLEX I-B17) (CI-B17)//1.0:40:35//SUS SCROFA (PIG)//Q29259
 15 F-PLACE1010383
 F-PLACE1010401//140 KD NUCLEOLAR PHOSPHOPROTEIN (NOPP140)//0.10:174:22//RATTUS NORVEGI-
 CUS (RAT)//P41777
 F-PLACE1010481//HYPOTHETICAL 71.9 KD PROTEIN B0285.5 IN CHROMOSOME III//1.5e-21:170:35//
 CAENORHABDITIS ELEGANS//P46555
 20 F-PLACE1010491//HYPOTHETICAL 13.5 KD PROTEIN IN MOB1-SGA1 INTERGENIC REGION//1.0:31:41//
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40490
 F-PLACE1010492//HYPOTHETICAL 42.3 KD PROTEIN C12G12.11C IN CHROMOSOME I//0.77:97:30//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q09874
 F-PLACE1010522//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930)//0.74:45:3//HOMO SAPIENS
 25 (HUMAN)//P22531
 F-PLACE1010529//DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE (P5CS) [CONTAINS: GLUTAMATE
 5-KINASE (EC 2.7.2.11) (GAMMA-GLUTAMYL KINASE) (GK); GAMMA-GLUTAMYL PHOSPHATE REDUCTASE
 (GPR) (EC 1.2.1.41) (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIAL-
 DEHYDE DEHYDROGENASE)]//0.70:58:39//VIGNA ACONITIFOLIA (MOTHBEAN)//P32296
 30 F-PLACE1010547//HYPOTHETICAL 31.0 KD PROTEIN IN BUD9-RME1 INTERGENIC REGION//0.17:68:39//
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53227
 F-PLACE1010562//CHLOROPLAST 50S RIBOSOMAL PROTEIN L33//0.50:48:29//PORPHYRA PURPUREA//
 P51255
 F-PLACE1010579//HYPOTHETICAL PROTEIN HI1571//0.29:37:43//HAEMOPHILUS INFLUENZAE//P44260
 35 F-PLACE1010580//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06//3.3e-38:178:48//SCHIZOSAC-
 CHAROMYCES POMBE (FISSION YEAST)//Q09747
 F-PLACE1010599//PEROXISOMAL MEMBRANE PROTEIN PER10 (PEROXIN-14)//4.6e-17:192:31//PICHIA
 ANGUSTA (YEAST) (HANSENULA POLYMORPHA)//P78723
 F-PLACE1010616//HYPOTHETICAL 9.2 KD PROTEIN IN RNPA 3'REGION//0.44:32:37//PSEUDOMONAS PUT-
 40 IDA//P25753
 F-PLACE1010622//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR//5.0e-06:102:42//SACCHAROMY-
 CES CEREVISIAE (BAKER'S YEAST)//P32323
 F-PLACE1010624//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAG-
 MENT)//0.00036:134:321//HOMO SAPIENS (HUMAN)//P10162
 45 F-PLACE1010628
 F-PLACE1010629//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.7e-12:37:81//HOMO SAPIENS (HUMAN)//
 P39194
 F-PLACE1010630
 F-PLACE1010631//WNT-5B PROTEIN (FRAGMENT)//0.49:62:30//EUMECES SKILTONIANUS (WESTERN
 50 SKINK)//P28118
 F-PLACE1010661//MATERNAL EXUPERANTIA 2 PROTEIN//1.0:95:30//DROSOPHILA PSEUDOOBSCURA
 (FRUIT FLY)//Q24617
 F-PLACE1010662//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-)
 (DUGT)//3.2e-05:117:24//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q09332
 55 F-PLACE1010702//ZINC FINGER PROTEIN 195//1.4e-62:117:62//HOMO SAPIENS (HUMAN)//O14628
 F-PLACE1010714

- F-PLACE1010739//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT)//0.97:31:41//
HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BH5 ISOLATE) (HIV-1)//P04612
- F-PLACE1010743//PROLINE-RICH PROTEIN MP-3 (FRAGMENT)//3.8e-05:253:30//MUS MUSCULUS
(MOUSE)//P05143
- 5 F-PLACE1010761//HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II//1.5e-14:175:25//
CAENORHABDITIS ELEGANS//Q09217
- F-PLACE1010771//TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP//1.3e-120:216:89//MUS MUSCULUS
(MOUSE)//Q02614
- F-PLACE1010786//CENTROSOMIN (ARROW PROTEIN)//0.97:133:24//DROSOPHILA MELANOGASTER
10 (FRUIT FLY)//P54623
- F-PLACE1010800//HYPOTHETICAL 31.7 KD PROTEIN IN TRAX-FINO INTERGENIC REGION (ORFC)//
0.0060:111:31//ESCHERICHIA COLI//Q99390
- F-PLACE1010802//UREASE ACCESSORY PROTEIN UREI//0.82:44:29//BACILLUS SP. (STRAIN TB-90)//
Q07415
- 15 F-PLACE1010811//CYTOCHROME C-551 (C551)//0.99:42:38//ECTOTHIORHODOSPIRA HALOCHLORIS//
P38587
- F-PLACE1010833//CALTRACTIN, ISOFORM 1 (CENTRIN)//2.8e-09:90:34//HOMO SAPIENS (HUMAN)//
P41208
- F-PLACE1010856//MOLT-INHIBITING HORMONE (MIH)//1.0:32:37//PROCAMBARUS CLARKII (RED SWAMP
20 CRAYFISH)//P55848
- F-PLACE1010857//IG ALPHA-1 CHAIN C REGION//0.49:73:34//GORILLA GORILLA GORILLA (LOWLAND GO-
RILLA)//P20758
- F-PLACE1010870//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7)//1.2e-56:173:58//HO-
MO SAPIENS (HUMAN)//Q05481
- 25 F-PLACE1010877//HEAT SHOCK PROTEIN 82//0.13:130:25//ZEA MAYS (MAIZE)//Q08277
- F-PLACE1010891//HYPOTHETICAL 8.2 KD PROTEIN IN BLTR-SPOIIC INTERGENIC REGION//0.95:51:27//
BACILLUS SUBTILIS//P54436
- F-PLACE1010896//SERINE/THREONINE-PROTEIN KINASE PTK1/STK1 (EC 2.7.1.)/0.98:71:30//SACCHA-
ROMYCES CEREVISIAE (BAKER'S YEAST)//P36002
- 30 F-PLACE1010900//HYPOTHETICAL PROTEIN HI0840//1.0:42:30//HAEMOPHILUS INFLUENZAE//P44897
- F-PLACE1010916//KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIB3//0.060:59:35//OVIS ARIES (SHEEP)//
P02444
- F-PLACE1010917//E2 GLYCOPROTEIN PRECURSOR (SPIKE GLYCOPROTEIN) (PEPLOMER PROTEIN)//
0.71:141:24//BOVINE CORONAVIRUS (STRAIN L9)//P25191
- 35 F-PLACE1010925//HYPOTHETICAL 8.1 KD PROTEIN//1.0:17:58//THERMOPROTEUS TENAX VIRUS 1
(STRAIN KRA1) (TTV1)//P19285
- F-PLACE1010926//HYPOTHETICAL PROLINE-RICH PROTEIN KIAA0269//0.011:51:45//HOMO SAPIENS (HU-
MAN)//Q92558
- F-PLACE1010942//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN
40 EPS15)//3.1e-09:64:37//MUS MUSCULUS (MOUSE)//P42567
- F-PLACE1010944//GAP JUNCTION ALPHA-3 PROTEIN (CONNEXIN 44) (CX44)//0.17:71:38//BOS TAURUS
(BOVINE)//P41987
- F-PLACE1010947
- F-PLACE1010954//TROPOMYOSIN ALPHA CHAIN, SKELETAL MUSCLE//0.011:144:26//HOMO SAPIENS
45 (HUMAN)//P09493
- F-PLACE1010960//ACTIN-LIKE PROTEIN 13E//1.1 e-60:136:52//DROSOPHILA MELANOGASTER (FRUIT
FLY)//P45890
- F-PLACE1010965
- F-PLACE1011026//PERIOD CLOCK PROTEIN (FRAGMENT)//1.0:64:31//DROSOPHILA ANANASSAE (FRUIT
50 FLY)//Q03293
- F-PLACE1011032//RIBONUCLEASE HI (EC 3.1.26.4) (RNASE HI) (RIBONUCLEASE H) (RNASE H)//1.0:32:37//
SALMONELLA TYPHIMURIUM//P23329
- F-PLACE1011041//HOMEBOX PROTEIN VAB-7//0.36:65:30//CAENORHABDITIS ELEGANS//Q93899
- F-PLACE1011046//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 1 (EC
55 3.1.4.11) (PLC-BETA-1) (PHOSPHOLIPASE C-BETA-1) (PLC-I) (PLC-154)//1.3e-22:58:93//RATTUS NORVEGI-
CUS (RAT) //P10687

F-PLACE1011057

F-PLACE1011109//ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G)//5.4e-25:63.88//RAT-TUS NORVEGICUS (RAT)//Q07803

F-PLACE1011133//SERUM AMYLOID P-COMPONENT PRECURSOR (SAP) (9.5S ALPHA-1-GLYCOPROTEIN)//0.92:58:31//HOMO SAPIENS (HUMAN)//P02743

F-PLACE1011160//EARLY NODULIN 55-2 PRECURSOR (N-55-2) (NODULIN-315)//0.88:98:27//GLYCINE MAX (SOYBEAN)//Q02917

F-PLACE1011185/////ALU SUBFAMILY J WARNING ENTRY !!!!!/1.4e-13:98:50//HOMO SAPIENS (HUMAN).//
P39188

F-PLACE1011214//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//1.0:48:27//EQUUS ASINUS (DONKEY)//P92479

F-PLACE1011221//ANTITHROMBIN-III HOMOLOG//0.84:74:33//FOWLPOX VIRUS (ISOLATE HP-438[MU-
NICH])//P14369

F-PLACE1011263//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT).//
3.0e-07:99:36//HOMO SAPIENS (HUMAN).//Q01485

F-PLACE1011291//PROTEIN KINASE C SUBSTRATE 80 KD PROTEIN (FRAGMENTS)//0.011:36:50//RATTUS NORVEGICUS (RAT)//P20468

F-PLACE1011310//ATP SYNTHASE PROTEIN 9, MITOCHONDRIAL (EC 3.6.1.34) (LIPID-BINDING PROTEIN).//
0.46:43:44//PETUNIA SP. (PETUNIA) //Q07060

F-PLACE1011332//DNA-DAMAGE-REPAIR/TOLERANCE PROTEIN DRT101 PRECURSOR.//7.3e-27:113:52//
ABRIDOPSIS THALIANA (MOUSE-EAR CRESS) //Q05211

F-PLACE1011340/////ALU SUBFAMILY J WARNING ENTRY !!!!!/2.6e-07:40:62//HOMO SAPIENS (HUMAN).//
 P39188

F-PLACE1011371//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2) //2 2e-54:227.44//MUS MUSCULUS (MOUSE) //Q61703

F-PLACE1011375//PROBABLE E5 PROTEIN//0.93:28:57//HUMAN PAPILLIOMAVIRUS TYPE 51 //P26553

F-PLACE1011399//HISTONE H2B-IV//0.19:129:27//VOLVOX CARTER||P16868

F-PLACE1011419

F-PLACE1011433//ZINC FINGER PROTEIN GLI3 (FRAGMENT)//3.4e-05:133:24//GALLUS GALLUS (CHICK-EN)//P55879

F-PLACE1011452//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//3.9e-25:76:63//HOMO SAPIENS (HUMAN)//P08547

F-PLACE1011465//ECTODERMAL DYSPLASIA PROTEIN (EDA PROTEIN).//0.97:36:41//HOMO SAPIENS (HUMAN)//Q92838

F-PLACE1011472//METALLOTHIONEIN-1 (CUMT-1)//0.084:55:30//HOMARUS AMERICANUS (AMERICAN LOBSTER)//P29499

5 PLACE(10,"477"(OE) = 6 REAGE(1,"CERCIEA" + CREFC(RSCR, 0) TEN(1,"M" + DREFE(1,"B" * 1000

1. The first step in the process is to identify the problem or issue that needs to be addressed. This involves gathering information and understanding the context of the problem.

- 2.9e-13:147:31//BRASSICA OLERACEA (CAULIFLOWER)//P52178
 F-PLACE1011503//PUTATIVE FERREDOXIN-LIKE PROTEIN IN PURL-DPJ INTERGENIC REGION (086)//0.66:
 32:40//ESCHERICHIA COLI//P52102
 F-PLACE1011520
 5 F-PLACE1011563//LORICRIN//0.00023:112:39//HOMO SAPIENS (HUMAN)//P23490
 F-PLACE1011567//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//9.2e-31:78:76//HOMO SAPIENS (HUMAN)//
 P39195
 F-PLACE1011576//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7)//1.5e-32:45:86//HO-
 MO SAPIENS (HUMAN)//Q05481
 10 F-PLACE1011586//N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (OMEGA-CONOTOXIN-SENSITIVE N-
 TYPE, BRAIN CALCIUM CHANNEL ALPHA-1 SUBUNIT)//0.26:81:37//HOMO SAPIENS (HUMAN)//Q00975
 F-PLACE1011635//IMMEDIATE-EARLY PROTEIN IE180//0.00045:170:30//PSEUDORABIES VIRUS (STRAIN
 INDIANA-FUNKHAUSER/BECKER) (PRV)//P11675
 F-PLACE1011641
 15 F-PLACE1011643//CUTICLE COLLAGEN 40//1.0:128:32//CAENORHABDITIS ELEGANS//P34804
 F-PLACE1011646//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.1e-15:44:63//HOMO SAPIENS (HUMAN)//
 P39188
 F-PLACE1011649//HYPOTHETICAL PROTEIN F-215//0.48:106:34//HUMAN ADENOVIRUS TYPE 2//P03291
 F-PLACE1011650
 20 F-PLACE1011664//CROOKED NECK PROTEIN//1.2e-79:201:68//DROSOPHILA MELANOGASTER (FRUIT
 FLY)//P17886
 F-PLACE1011675//FERREDOXIN//1.0:44:29//METHANOCOCCUS THERMOLITHOTROPHICUS//P21305
 F-PLACE1011682//HYPOTHETICAL 7.0 KD PROTEIN IN RPS26A-COX4 INTERGENIC REGION//1.0:40:22//
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53098
 25 F-PLACE1011719//NEUROTOXIN TX2-6//0.90:31:35//PHONEUTRIA NIGRIVENTER (BRAZILIAN ARMED SPI-
 DER)//P29425
 F-PLACE1011725//NUCLEOBINDIN PRECURSOR (NUCB1) (BONE 63 KD CALCIUM-BINDING PROTEIN)//
 0.0065:125:25//RATTUS NORVEGICUS (RAT)//Q63083
 F-PLACE1011729//SRY-RELATED PROTEIN LG27 (FRAGMENT)//0.97:48:39//EUBLEPHARIS MACULAR-
 IUS//P40654
 30 F-PLACE1011749
 F-PLACE1011762//D-BINDING PROTEIN (DBP) (ALBUMIN D BOX-BINDING PROTEIN)//0.028:91:39//MUS
 MUSCULUS (MOUSE)//Q60925
 F-PLACE1011778
 35 F-PLACE1011783//EMBRYONIC GROWTH/DIFFERENTIATION FACTOR 1 PRECURSOR (GDF-1)//0.97:48:
 43//MUS MUSCULUS (MOUSE)//P20863
 F-PLACE1011858//COLLAGEN 1(X) CHAIN PRECURSOR//0.0027:154:33//BOS TAURUS (BOVINE)//P23206
 F-PLACE1011874//BACTERIOCHLOROPHYLL A PROTEIN (BCHL A PROTEIN) (BCP)//1.0:60:26//PROSTHE-
 COCHLORIS AESTUARII//P11741
 40 F-PLACE1011875//HYPOTHETICAL 6.6 KD PROTEIN IN GP54-ALT INTERGENIC REGION//0.99:34:35//AC-
 TERIOPHAGE T4//P39495
 F-PLACE1011891//SMOOTHELIN//0.018:122:31//HOMO SAPIENS (HUMAN)//P53814
 F-PLACE1011896//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)//6.3e-09:203:35//
 XENOPUS LAEVIS (AFRICAN CLAWED FROG)//P17437
 45 F-PLACE1011922//CRYPTDIN-RELATED PROTEIN 4C-2 PRECURSOR (CRS4C)//0.067:37:48//MUS MUSCU-
 LUS (MOUSE)//P50715
 F-PLACE1011923//SERINE/THREONINE-PROTEIN KINASE SNK (EC 2.7.1.-) (SERUM INDUCIBLE KINASE)//
 1.5e-83:175:89//MUS MUSCULUS (MOUSE)//P53351
 F-PLACE1011962//MATING-TYPE PHEROMONE BAP1(2) PRECURSOR//0.50:46:41//SCHIZOPHYLLUM
 50 COMMUNE (BRACKET FUNGUS)//Q02593
 F-PLACE1011964//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//1.6e-05:47:51//NYCTICEBUS COU-
 CANG (SLOW LORIS)//P08548
 F-PLACE1011982//APICAL MEMBRANE ANTIGEN 1 PRECURSOR (MEROZOITE SURFACE ANTIGEN)//0.98:
 83:31//PLASMODIUM FRAGILE//P22622
 55 F-PLACE1011995
 F-PLACE1012031//ALU SUBFAMILY A WARNING ENTRY
 F-PLACE2000003//ALU SUBFAMILY J WARNING ENTRY//0.48:18:63//HOMO SAPIENS (HUMAN)
 P39190

F-PLACE2000067//ANNEXIN VII (SYNEXIN) (FRAGMENT)//0.14:20:50//BOS TAURUS (BOVINE).//P20072
F-PLACE2000007//PROLINE-RICH PROTEIN MP-3 (FRAGMENT)//0.0045:176:30//MUS MUSCULUS (MOUSE).//P05143
F-PLACE2000011/////ALU SUBFAMILY SQ WARNING ENTRY /////3.6e-25:57:78//HOMO SAPIENS (HUMAN).//P39194
F-PLACE2000014//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III//0.00013:237:27//CAENORHABDITIS ELEGANS//Q09475
F-PLACE2000015/////ALU SUBFAMILY SP WARNING ENTRY /////1.4e-33:60:80//HOMO SAPIENS (HUMAN).//P39193
F-PLACE2000017//FOLATE RECEPTOR BETA PRECURSOR (FR-BETA) (FOLATE RECEPTOR 2) (FOLATE RECEPTOR, FETAL/PLACENTAL) (PLACENTAL FOLATE-BINDING PROTEIN) (FBP)//1.0:83:31//HOMO SAPIENS (HUMAN).//P14207
F-PLACE2000021//EPHRIN TYPE-A RECEPTOR 4 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR CEK8)//0.99:103:26//GALLUS GALLUS (CHICKEN).//Q07496
F-PLACE2000030//MALE SPECIFIC SPERM PROTEIN MST84DA//0.69:29:44//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01642
F-PLACE2000036//PROBABLE OXIDOREDUCTASE (EC 1.-.-.)//1.1e-05:74:41//STREPTOMYCES ANTIBIOTICUS.//Q03326
F-PLACE2000034//AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1) (TRANSIENT AXONAL GLYCOPROTEIN 1)//6.7e-18:191:35//HOMO SAPIENS (HUMAN).//Q02246
F-PLACE2000039//DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) (MAP 1C)//4.7e-80:163:96//RATTUS NORVEGICUS (RAT).//P38650
F-PLACE2000047/////ALU SUBFAMILY SB2 WARNING ENTRY /////6.4e-06:63:49//HOMO SAPIENS (HUMAN).//P39191
F-PLACE2000050/////ALU SUBFAMILY SC WARNING ENTRY /////3.2e-22:74:64//HOMO SAPIENS (HUMAN).//P39192
F-PLACE2000061
F-PLACE2000062//GLUCOSE STARVATION-INDUCIBLE PROTEIN B (GENERAL STRESS PROTEIN B)//1.9e-06:108:37//BACILLUS SUBTILIS.//P26907
F-PLACE2000072//ZINC FINGER PROTEIN 165.//3.5e-34:175:49//HOMO SAPIENS (HUMAN).//P49910
F-PLACE2000097//RIBONUCLEASE PANCREATIC (EC 3.1.27.5) (RNASE 1) (RNASE A)//0.36:39:38//ONDATRA ZIBETHICUS (MUSKRAT).//P00681
F-PLACE2000100
F-PLACE2000103//TUBULIN ALPHA-4 CHAIN (FRAGMENTS)//0.18:32:37//ZEA MAYS (MAIZE).//P33626
F-PLACE2000111//CMRF35 ANTIGEN PRECURSOR.//0.056:107:27//HOMO SAPIENS (HUMAN).//Q08708
F-PLACE2000115//DIAMINOPIMELATE EPIMERASE (EC 5.1.1.7) (DAP EPIMERASE) (FRAGMENT)//1.0:21:52//CLOSTRIDIUM PERFRINGENS.//Q46185
F-PLACE2000124/////ALU SUBFAMILY SQ WARNING ENTRY /////3.4e-37:108:68//HOMO SAPIENS (HUMAN).//P39194
F-PLACE2000132//PROBABLE MEMBRANE ANTIGEN GP85//0.99:133:29//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03224
F-PLACE2000136//VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 2 PRECURSOR (VIP-R-2) (PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE III RECEPTOR) (PACAP TYPE III RECEPTOR) (PACAP-R-3)//0.83:65:32//MUS MUSCULUS (MOUSE).//P41588
F-PLACE2000140
F-PLACE2000164//TIPD PROTEIN//5.7e-12:190:28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//Q15736
F-PLACE2000170//BACTERIOCIN CARNOBACTERIOCIN BM1 PRECURSOR (CARNOBACTERIOCIN B1)//1.0:30:26//CARNOBACTERIUM PISCICOLA.//P38579
F-PLACE2000172
F-PLACE2000176//HYPOTHETICAL PROTEIN AF0526//0.76:44:43//ARCHAEOGLOBUS FULGIDUS//Q29724
F-PLACE2000187//EM-LIKE PROTEIN GE46//0.84:42:35//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q02973
F-PLACE2000216
F-PLACE2000223//NEUROTOXIN III (LQQ III)//0.99:38:34//LEIURUS QUINQUESTRIATUS QUINQUESTRIATUS (EGYPTIAN SCORPION).//Q020023
F-PLACE2000246//HYPOTHETICAL PROTEIN N15163//0.21:42//DROSOPHILA MELANOGASTER (FRUIT FLY).

NOGASTER (FRUIT FLY)//Q04652

F-PLACE2000264//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/2.4e-05:77:42//HOMO SAPIENS (HUMAN)//P39191

F-PLACE2000274//DYNEIN BETA CHAIN, CILIARY//5.3e-46:232:45//TRIPNEUSTES GRATILLA (HAWAIIAN SEA URCHIN)//P23098

F-PLACE2000302//TRICHOHYALIN//1.5e-06:215:29//ORYCTOLAGUS CUNICULUS (RABBIT)//P37709

F-PLACE2000305//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/5.3e-06:33:66//HOMO SAPIENS (HUMAN)//P39188

F-PLACE2000317//TOXIN C13S1C1 PRECURSOR//0.44:45:33//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAMBA)//P18329

F-PLACE2000335//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/7.9e-08:35:71//HOMO SAPIENS (HUMAN)//P39195

F-PLACE2000341//SODIUM/GLUCOSE COTRANSPORTER 1 (NA(+)/GLUCOSE COTRANSPORTER 1) (HIGH AFFINITY SODIUM-GLUCOSE COTRANSPORTER)//0.014:141:24//ORYCTOLAGUS CUNICULUS (RABBIT)//P11170

F-PLACE2000342//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION//5.7e-09:96:38//AUTOGRAPHICA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV)//P41479

F-PLACE2000347//ZINC FINGER PROTEIN 177//5.9e-05:49:53//HOMO SAPIENS (HUMAN)//Q13360

F-PLACE2000359//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/7.5e-10:69:52//HOMO SAPIENS (HUMAN)//P39194

F-PLACE2000366

F-PLACE2000371//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN)//1.5e-05:216:29//HOMO SAPIENS (HUMAN)//P54259

F-PLACE2000373//MAX BINDING PROTEIN MNT (ROX PROTEIN) (MYC ANTAGONIST MNT)//0.27:63:33//HOMO SAPIENS (HUMAN)//Q99583

F-PLACE2000379//HYPOTHETICAL GENE 1 PROTEIN//0.72:120:31//EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1)//P28978

F-PLACE2000394//BASIC PROLINE-RICH PEPTIDE P-E (IB-9)//0.95:40:42//HOMO SAPIENS (HUMAN)//P02811

F-PLACE2000398//RIBONUCLEASE PRECURSOR (EC 3.1.27.-)//0.88:88:31//AEROMONAS HYDROPHILA//Q07465

F-PLACE2000399//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PROTEIN) (12E7)//7.6e-16:180:39//HOMO SAPIENS (HUMAN)//P14209

F-PLACE2000404//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE-TRNA LIGASE) (LEURS)//1.7e-94:243:64//CAENORHABDITIS ELEGANS//Q09996

F-PLACE2000411//SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOSPHATASE T) (PPT) (FRAGMENT)//1.2e-09:78:39//MUS MUSCULUS (MOUSE)//Q60676

F-PLACE2000419//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.6e-20:61:62//HOMO SAPIENS (HUMAN)//P39188

F-PLACE2000425//HYPOTHETICAL 11.9 KD PROTEIN IN MSB2-UGA1 INTERGENIC REGION//0.98:75:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53211

F-PLACE2000427//INSULIN PRECURSOR//0.98:55:34//CERCOPITHECUS AETHIOPS (GREEN MONKEY) (GRIVET)//P30407

F-PLACE2000433//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/7.5e-07:65:50//HOMO SAPIENS (HUMAN)//P39188

F-PLACE2000435

F-PLACE2000438//HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III//4.7e-66:178:47//CAENORHABDITIS ELEGANS//P34678

F-PLACE2000450//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.1e-23:88:62//HOMO SAPIENS (HUMAN)//P39195

F-PLACE2000455//TOXIN II (TOXIN II.10.9.2) (FRAGMENT)//0.093:18:44//CENTRURIDES LIMPIDUS LIMPIDUS (MEXICAN SCORPION)//P45630

F-PLACE2000458//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN)//3.1e-23:165:40//DROSOPHILA MELANOGASTER (FRUIT FLY)//P33450

F-PLACE2000465//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.6e-23:73:63//HOMO SAPIENS (HUMAN)//P39188

1. PLACE2000465//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.6e-23:73:63//HOMO SAPIENS (HUMAN)//P39188

F-PLACE3000004//EYES ABSENT HOMOLOG 3.//1.1e-09:27:100//MUS MUSCULUS (MOUSE)//P97480
F-PLACE3000009//PUTATIVE CUTICLE COLLAGEN C09G5.6//0.0061:148:34//CAENORHABDITIS ELE-
GANS//Q09457
F-PLACE3000020//ADENYLATE CYCLASE, OLFACTIVE TYPE (EC 4.6.1.1) (TYPE III) (ATP PYROPHOS-
PHATE-LYASE) (ADENYL CYCLASE)//8.8e-93:193:92//RATTUS NORVEGICUS (RAT)//P21932
F-PLACE3000029//50S RIBOSOMAL PROTEIN L31E//0.15:50:38//METHANOCOCCUS JANNASCHII//P54009
F-PLACE3000059//TCP1-CHAPERONIN COFACTOR A//0.96:50:34//BOS TAURUS (BOVINE)//P48427
F-PLACE3000070//HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3'REGION//0.29:22:59//SACCHAROMYCES
CEREVISIAE (BAKER'S YEAST)//P38898
F-PLACE3000103//LYSIS PROTEIN (E PROTEIN) (GPE)//0.99:53:32//BACTERIOPHAGE ALPHA-3//P31280
F-PLACE3000119//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/5.4e-41:87:78//HOMO SAPIENS (HUMAN)//
P39189
F-PLACE3000121//VESICULAR TRAFFIC CONTROL PROTEIN SEC151/1.0e-07:269:22//SACCHAROMYCES
CEREVISIAE (BAKER'S YEAST)//P22224
F-PLACE3000124//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.2e-29:97:73//HOMO SAPIENS (HUMAN)//
P39188
F-PLACE3000136//PARS INTERCEREBRALIS MAJOR PEPTIDE D1 (PMP-D1)//0.77:26:42//LOCUSTA MIGRA-
TORIA (MIGRATORY LOCUST)//P80059
F-PLACE3000142//HYPOTHETICAL 7.1 KD PROTEIN IN NAD2 3'REGION (ORF 63)//0.82:34:41//MARCHAN-
TIA POLYMORPHA (LIVERWORT)//P38468
F-PLACE3000145//TENSIN//3.5e-91:238:74//GALLUS GALLUS (CHICKEN)//Q04205
F-PLACE3000147//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/4.4e-30:61:65//HOMO SAPIENS (HUMAN)//
P39194
F-PLACE3000148//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE
(EC 2.7.7.49); ENDONUCLEASE]//1.4e-18:226:34//GIBBON APE LEUKEMIA VIRUS//P21414
F-PLACE3000155//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN)//0.00014:107:33//ZEA MAYS
(MAIZE)//P14918
F-PLACE3000156//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE
(EC 2.7.7.49); ENDONUCLEASE]//2.7e-19:169:30//BABOON ENDOGENOUS VIRUS (STRAIN M7)//P10272
F-PLACE3000157//PROBABLE SERINE/THREONINE-PROTEIN KINASE CY50.16 (EC 2.7.1.-)//0.0061:92:30//
MYCOBACTERIUM TUBERCULOSIS//Q11053
F-PLACE3000158//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/5.7e-49:56:80//HOMO SAPIENS (HUMAN)//
P39189
F-PLACE3000160//DNA TRANSFORMATION PROTEIN TFOX (COMPETENCE ACTIVATOR) (PROTEIN SXY)//
0.39:94:34//HAEMOPHILUS INFLUENZAE//P43779
F-PLACE3000169//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/5.6e-28:99:59//HOMO SAPIENS (HUMAN)//
P39193
F-PLACE3000194//PROLINE-RICH PROTEIN LAS17//0.91:80:36//SACCHAROMYCES CEREVISIAE (BAK-
ER'S YEAST)//Q12446
F-PLACE3000197//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M)//
0.24:119:32//GALLUS GALLUS (CHICKEN)//P16053
F-PLACE3000199//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)//
0.76:87:37//NICOTIANA TABACUM (COMMON TOBACCO)//P13983
F-PLACE3000207//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.5e-09:32:78//HOMO SAPIENS (HUMAN)//
P39188
F-PLACE3000208
F-PLACE3000218//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/7.2e-34:96:70//HOMO SAPIENS (HUMAN)//
P39194
F-PLACE3000220//OSTEOCALCIN (GAMMA-CARBOXYGLUTAMIC ACID-CONTAINING PROTEIN) (BONE
GLA- PROTEIN) (BGP)//0.46:13:53//CANIS FAMILIARIS (DOG)//P81455
F-PLACE3000221//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.8e-24:178:45//HOMO SAPIENS (HUMAN)//
P39188
F-PLACE3000226//30S RIBOSOMAL PROTEIN S18//0.98:38:34//NEISSERIA GONORRHOEAE//O07815
F-PLACE3000230//METALLOTHIONEIN (MT)//0.97:25:48//OREOCHROMIS MOSSAMBICUS (MOZAMBIQUE
TILAPIA) (TILAPIA MOSSAMBICA)//P52726
F-PLACE3000240//MELANOMATIN-1 (MEL-1) (MEL-1)
F-PLACE3000244//PROTEIN 125 (P125) (P125)
F-PLACE3000245//PROTEIN 125 (P125) (P125)
F-PLACE3000246//PROTEIN 125 (P125) (P125)
F-PLACE3000247//PROTEIN 125 (P125) (P125)
F-PLACE3000248//PROTEIN 125 (P125) (P125)
F-PLACE3000249//PROTEIN 125 (P125) (P125)
F-PLACE3000250//PROTEIN 125 (P125) (P125)
F-PLACE3000251//PROTEIN 125 (P125) (P125)
F-PLACE3000252//PROTEIN 125 (P125) (P125)
F-PLACE3000253//PROTEIN 125 (P125) (P125)
F-PLACE3000254//PROTEIN 125 (P125) (P125)
F-PLACE3000255//PROTEIN 125 (P125) (P125)
F-PLACE3000256//PROTEIN 125 (P125) (P125)
F-PLACE3000257//PROTEIN 125 (P125) (P125)
F-PLACE3000258//PROTEIN 125 (P125) (P125)
F-PLACE3000259//PROTEIN 125 (P125) (P125)
F-PLACE3000260//PROTEIN 125 (P125) (P125)
F-PLACE3000261//PROTEIN 125 (P125) (P125)
F-PLACE3000262//PROTEIN 125 (P125) (P125)
F-PLACE3000263//PROTEIN 125 (P125) (P125)
F-PLACE3000264//PROTEIN 125 (P125) (P125)
F-PLACE3000265//PROTEIN 125 (P125) (P125)
F-PLACE3000266//PROTEIN 125 (P125) (P125)
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F-PLACE3000268//PROTEIN 125 (P125) (P125)
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F-PLACE3000273//PROTEIN 125 (P125) (P125)
F-PLACE3000274//PROTEIN 125 (P125) (P125)
F-PLACE3000275//PROTEIN 125 (P125) (P125)
F-PLACE3000276//PROTEIN 125 (P125) (P125)
F-PLACE3000277//PROTEIN 125 (P125) (P125)
F-PLACE3000278//PROTEIN 125 (P125) (P125)
F-PLACE3000279//PROTEIN 125 (P125) (P125)
F-PLACE3000280//PROTEIN 125 (P125) (P125)
F-PLACE3000281//PROTEIN 125 (P125) (P125)
F-PLACE3000282//PROTEIN 125 (P125) (P125)
F-PLACE3000283//PROTEIN 125 (P125) (P125)
F-PLACE3000284//PROTEIN 125 (P125) (P125)
F-PLACE3000285//PROTEIN 125 (P125) (P125)
F-PLACE3000286//PROTEIN 125 (P125) (P125)
F-PLACE3000287//PROTEIN 125 (P125) (P125)
F-PLACE3000288//PROTEIN 125 (P125) (P125)
F-PLACE3000289//PROTEIN 125 (P125) (P125)
F-PLACE3000290//PROTEIN 125 (P125) (P125)
F-PLACE3000291//PROTEIN 125 (P125) (P125)
F-PLACE3000292//PROTEIN 125 (P125) (P125)
F-PLACE3000293//PROTEIN 125 (P125) (P125)
F-PLACE3000294//PROTEIN 125 (P125) (P125)
F-PLACE3000295//PROTEIN 125 (P125) (P125)
F-PLACE3000296//PROTEIN 125 (P125) (P125)
F-PLACE3000297//PROTEIN 125 (P125) (P125)
F-PLACE3000298//PROTEIN 125 (P125) (P125)
F-PLACE3000299//PROTEIN 125 (P125) (P125)
F-PLACE3000300//PROTEIN 125 (P125) (P125)
F-PLACE3000301//PROTEIN 125 (P125) (P125)
F-PLACE3000302//PROTEIN 125 (P125) (P125)
F-PLACE3000303//PROTEIN 125 (P125) (P125)
F-PLACE3000304//PROTEIN 125 (P125) (P125)
F-PLACE3000305//PROTEIN 125 (P125) (P125)
F-PLACE3000306//PROTEIN 125 (P125) (P125)
F-PLACE3000307//PROTEIN 125 (P125) (P125)
F-PLACE

F-PLACE3000271//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.2e-12:63:53/HOMO SAPIENS (HUMAN)//
P39188

F-PLACE3000304//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)//0.0028:31:54//HOMO SAPIENS (HUMAN)//P30808

F-PLACE3000310//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN).//0.98:82:34//
RATTUS NORVEGICUS (RAT).//P54258

F-PLACE3000320

F-PLACE3000322//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1 PRECURSOR.//2.2e-22:61:52//
ORYZA SATIVA (RICE)//P25074

F-PLACE3000331//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N).//0.32:15:53//HOMO SAPIENS (HUMAN).//P22532

F-PLACE3000339//CHORION PROTEIN S19.//0.34:89:37//DROSOPHILA VIRILIS (FRUIT FLY).//P24516

F-PLACE3000341//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3) (FRAGMENT).//1.0:47:38//
COTURNIX COTURNIX JAPONICA (JAPANESE QUAIL).//P24968

F-PLACE3000350//SERINE/THREONINE-PROTEIN KINASE SULU (EC 2.7.1.-)//3.9e-50:168:60//CAENORHABDITIS ELEGANS .//P46549

F-PLACE3000352//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//7.8e-29:76:71//HOMO SAPIENS (HUMAN).//
P39194

F-PLACE3000353//POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T1)//3.0e-09:100:41//HOMO SAPIENS (HUMAN)//Q10472

F-PLACE3000362//HYPOTHETICAL PROTEIN TP0064//1.0:75:26//TREPONEMA PALLIDUM.//O83103

F-PLACE3000363//METALLOTHIONEIN (MT)//0.067:42:33//ASTACUS FLUVIATILIS (BROAD-FINGERED CRAYFISH) (ASTACUS ASTACUS)//P55951

F-PLACE3000365//LYSIS PROTEIN (E PROTEIN) (GPE)//1.0:65:27//BACTERIOPHAGE PHI-K//Q38040

F-PLACE3000373//RETROVIRUS-RELATED ENV POLYPROTEIN//1.5e-18:90:47//HOMO SAPIENS (HUMAN)//P10267

F-PLACE3000388

F-PLACE3000399//!!!!ALU SUBFAMILY SP WARNING ENTRY !!!!/6.3e-45:60:75//HOMO SAPIENS (HUMAN).//
P39193

F-PLACE3000400

F-PLACE3000401//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.6e-09:46:73//HOMO SAPIENS (HUMAN).//
P39188

F-PLACE3000402//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.036:43:44//HOMO SAPIENS (HUMAN).//
P39188

F-PLACE3000405//POSTERIOR PITUITARY PEPTIDE//0.70:25:40//BOS TAURUS (BOVINE).//P01154

F-PLACE3000406//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/4.3e-09:49:67//HOMO SAPIENS (HUMAN).//
P39195

F-PLACE3000413//MALE SPECIFIC SPERM PROTEIN MST87F.//0.12:42:40//DROSOPHILA MELANOGASTER (FRUIT FLY).//P08175

F-PLACE3000416//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I)//0.67:236:21//BOS TAURUS (BOVINE)//
P35662

F-PLACE3000425//PROLINE-RICH PEPTIDE P-B.//0.45:19:42//HOMO SAPIENS (HUMAN).//P02814

F-PLACE3000455//AMELOGENIN, CLASS I PRECURSOR.//0.0073:81:43//BOS TAURUS (BOVINE).//P02817

F-PLACE3000475//8.6 KD TRANSGLUTAMINASE SUBSTRATE.//1.0:53:32//TACHYPLEUS TRIDENTATUS (JAPANESE HORSESHOE CRAB).//P81281

F-PLACE3000477//MUSCARINIC TOXIN 7 (MT-7)//0.13:55:32//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAMBA)//P80970

F-PLACE4000009//MYOSIN HEAVY CHAIN, SMOOTH MUSCLE ISOFORM (SMMHC) (FRAGMENT)//7.0e-19:
180:27//HOMO SAPIENS (HUMAN)//P35749

PLACE4000014//X LINKED UP PAGE

• five HUMAN. 4th

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NOGASTER (FRUIT FLY)//P22815
 F-PLACE4000049//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.8e-32:79:75//HOMO SAPIENS (HUMAN)//
 P39194
 F-PLACE4000052//ATP-BINDING CASSETTE TRANSPORTER 1//2.2e-99:178:97//MUS MUSCULUS
 5 (MOUSE)//P41233
 F-PLACE4000063//IMMEDIATE-EARLY PROTEIN//0.0017:159:25//HERPESVIRUS SAIMIRI (STRAIN 11)//
 Q01042
 F-PLACE4000089
 F-PLACE4000093
 10 F-PLACE4000100//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.5e-14:68:60//HOMO SAPIENS (HUMAN)//
 P39188
 F-PLACE4000106//1A PROTEIN [CONTAINS: HELICASE; METHYLTRANSFERASE]//1.0:46:41//BROAD BEAN
 MOTTLE VIRUS//Q00020
 F-PLACE4000128//HYPOTHETICAL PROTEIN E-115//0.00020:101:30//HUMAN ADENOVIRUS TYPE 2//
 15 P03290
 F-PLACE4000129//CORNIFIN B (SMALL PROLINE-RICH PROTEIN IB) (SPR-IB) (14.9 KD PANCORNULIN)//
 0.15:57:31//HOMO SAPIENS (HUMAN)//P22528
 F-PLACE4000131
 F-PLACE4000147//COMPETENCE PHEROMONE PRECURSOR//1.0:45:24//BACILLUS SUBTILIS//P45453
 20 F-PLACE4000156//ZINC FINGER PROTEIN 136//2.1e-88:194:59//HOMO SAPIENS (HUMAN)//P52737
 F-PLACE4000192//ZINC FINGER PROTEIN 142 (KIAA0236) (HA4654)//0.083:148:26//HOMO SAPIENS (HU-
 MAN)//P52746
 F-PLACE4000211//CALPHOTIN//0.20:43:39//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q02910
 F-PLACE4000222//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.1e-05:20:85//HOMO SAPIENS (HUMAN)//
 25 P39188
 F-PLACE4000230//DIHYDROFOLATE REDUCTASE (EC 1.5.1.3) / THYMIDYLATE SYNTHASE (EC 2.1.1.45)
 (DHFR-TS)//1.0:96:28//TRYPANOSOMA BRUCEI BRUCEI//Q27783
 F-PLACE4000233
 F-PLACE4000247//METALLOTHIONEIN (MT)//1.0e-05:34:41//PLEURONECTES PLATESSA (PLAICE)//
 30 P07216
 F-PLACE4000250//VPU PROTEIN (ORF-X PROTEIN) (UPX PROTEIN)//0.99:33:42//CAPRINE ARTHRITIS EN-
 CEPHALITIS VIRUS (CAEV)//P31834
 F-PLACE4000252//MALE SPECIFIC SPERM PROTEIN MST84DB//0.42:24:45//DROSOPHILA MELA-
 NOGASTER (FRUIT FLY)//Q01643
 35 F-PLACE4000259//PRE-MRNA SPLICING HELICASE BRR2 (EC 3.6.1.-)//3.5e-09:189:32//SACCHAROMYCES
 CEREVISIAE (BAKER'S YEAST)//P32639
 F-PLACE4000261//PEREGRIN (BR140 PROTEIN)//5.0e-11:103:37//HOMO SAPIENS (HUMAN)//P55201
 F-PLACE4000269//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1//0.037:181:25//SACCHARO-
 MYCES CEREVISIAE (BAKER'S YEAST)//P25386
 40 F-PLACE4000270//COAGULATION FACTOR VII PRECURSOR (EC 3.4.21.21)//1.0:46:39//MUS MUSCULUS
 (MOUSE)//P70375
 F-PLACE4000300//50S RIBOSOMAL PROTEIN L32//0.81:28:46//THERMUS AQUATICUS (SUBSP. THER-
 MOPHILUS)//P80339
 F-PLACE4000320//FKBP-RAPAMYCIN ASSOCIATED PROTEIN (FRAP) (RAPAMYCIN TARGET PROTEIN)//
 45 1.6e-29:44:93//HOMO SAPIENS (HUMAN)//P42345
 F-PLACE4000323
 F-PLACE4000326//PARATHYMOSIN//0.0018:54:48//HOMO SAPIENS (HUMAN)//P20962
 F-PLACE4000344//EPIDERMAL GROWTH FACTOR (EGF) (FRAGMENT)//0.97:28:42//SUS SCROFA (PIG)//
 Q00968
 50 F-PLACE4000367//NEUROTOXIN 1 (TOXIN SHP-I) (SHNA) (NEUROTOXIN SHI)//1.0:33:36//STOICHACTIS
 HELIANTHUS (CARRIBEAN SEA ANEMONE) (STICHODACTYLA HELIANTHUS)//P19651
 F-PLACE4000369//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN)//0.071:42:42//SORGHUM
 VULGARE (SORGHUM)//P24152
 F-PLACE4000379//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.4e-16:54:77//HOMO SAPIENS (HUMAN)//
 55 P39193
 F-PLACE4000392//FERROCHELATASE (EC 4.99.1.1) (PROTOHEME FERRO-LYASE) (HEME SYNTHETASE)
 FROM VULGARE (BARLEY) AND SECAL CEREAL RYE//P2587

(FRAGMENT)//0.91:36:50//YERSINIA PSEUDOTUBERCULOSIS//Q05338
 F-PLACE4000401//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/4.4e-29:96:67//HOMO SAPIENS (HUMAN)//
 P39194
 F-PLACE4000411//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.3e-18:41:73//HOMO SAPIENS (HUMAN)//
 5 P39188
 F-PLACE4000431//PRE-MRNA SPLICING HELICASE BRR2 (EC 3.6.1.-)//5.4e-21:237:33//SACCHAROMYCES
 CEREVISIAE (BAKER'S YEAST)//P32639
 F-PLACE4000445//HYPOTHETICAL 99.7 KD PROTEIN IN SDL1 5'REGION PRECURSOR//0.00081:210:26//
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40442
 10 F-PLACE4000450//TRANSCRIPTION FACTOR HBP-1A (HISTONE-SPECIFIC TRANSCRIPTION FACTOR
 HBP1)//0.020:87:33//TRITICUM AESTIVUM (WHEAT)//P23922
 F-PLACE4000465//METALLOTHIONEIN-IL (MT-1L) (MT1X)//0.20:18:38//HOMO SAPIENS (HUMAN)//P80297
 F-PLACE4000487//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.5e-19:73:52//HOMO SAPIENS (HUMAN)//
 P39188
 15 F-PLACE4000489
 F-PLACE4000494//NPC DERIVED PROLINE RICH PROTEIN 1 (NDPP-1)//0.17:130:30//MUS MUSCULUS
 (MOUSE)//Q03173
 F-PLACE4000521//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS REVERSE TRANSCRIPTASE
 (EC 2.7.7.49); ENDONUCLEASE] (FRAGMENT)//3.0e-05:50:36//MUS MUSCULUS (MOUSE)//P10400
 20 F-PLACE4000522//NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1 PRECURSOR//1.8e-45:231:47//
 RATTUS NORVEGICUS (RAT)//Q07008
 F-PLACE4000548//CYTOCHROME C-551 (C551)//0.96:50:34//ECTOTHIORHODOSPIRA HALOPHILA//
 P00122
 F-PLACE4000558//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF (EC 3.1.2.15) (UBIQUI-
 25 TIN THIOLESTERASE FAF) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF) (DEUBIQUITINATING EN-
 ZYME FAF) (FAT FACETS PROTEIN)//1.6e-28:223:36//DROSOPHILA MELANOGASTER (FRUIT FLY)//P55824
 F-PLACE000581//P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM)
 (CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3)//9.7e-11:166:281/HOMO
 SAPIENS (HUMAN)//P16109
 30 F-PLACE4000590//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE
 (EC 2.7.7.49); ENDONUCLEASE)//1.6e-17:134:35//GIBBON APE LEUKEMIA VIRUS//P21414
 F-PLACE4000593//GONADOTROPIN-RELEASING HORMONE RECEPTOR (GNRH-R)//1.0:54:29//RATTUS
 NORVEGICUS (RAT)//P30969
 F-PLACE4000612//GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12;
 35 CORE SHELL PROTEIN P30]//2.6e-14:221:32//MOLONEY MURINE SARCOMA VIRUS (STRAIN TS110)//
 P32594
 F-PLACE4000638//HYPOTHETICAL 9.3 KD PROTEIN IN NRDB-INAA INTERGENIC REGION//0.65:37:40//ES-
 CHERICHIA COLI//P37910
 F-PLACE4000650//ZINC FINGER PROTEIN 16 (ZINC FINGER PROTEIN KOX9) (FRAGMENT)//1.0:33:33//HO-
 40 MO SAPIENS (HUMAN)//P17020
 F-PLACE4000654
 F-PLACE4000670//HYPOTHETICAL 44.1 KD PROTEIN IN RPB5-CDC28 INTERGENIC REGION//1.6e-07:161:
 25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P33313
 F-SKNMC1000011//PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUBUNIT)//7.4e-15:223:
 45 31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//O60100
 F-SKNMC1000013//TRANSCRIPTION FACTOR BF-2 (BRAIN FACTOR 2) (BF2) (CBF-2) (T-14-6)//0.0013:128:
 35//GALLUS GALLUS (CHICKEN)//Q98937
 F-SKNMC1000046//CUTICLE COLLAGEN 1//0.0010:154:33//CAENORHABDITIS ELEGANS//P08124
 F-SKNMC1000050//CALPAIN 2, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEU-
 50 TRAL PROTEINASE) (CANP) (M-TYPE)//3.2e-41:87:98//HOMO SAPIENS (HUMAN)//P17655
 F-SKNMC1000091//NTAK PROTEIN (NEURAL- AND THYMUS- DERIVED ACTIVATOR FOR ERBB KINASES)//
 0.0032:154:35//HOMO SAPIENS (HUMAN)//O14511
 F-THYRO1000017//PUTATIVE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (EC 1.4.3.5) (PNP/PMP OXI-
 DASE)//1.6e-23:124:37//CAENORHABDITIS ELEGANS//Q20939
 55 F-THYRO1000026//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/3.0e-13:54:66//HOMO SAPIENS (HUMAN) //

F-THYRO1000035//CAMPATH-1 ANTIGEN PRECURSOR (CD52 ANTIGEN) (CDW52) (CAMBRIDGE PATHOL-
OGY 1 ANTIGEN)//0.83:59:37//MACACA FASCICULARIS (CRAB EATING MACAQUE) (CYNOMOLGUS MON-
KEY)//P32763

F-THYRO1000040//60S RIBOSOMAL PROTEIN L37 (FRAGMENT)//0.25:23:39//BOS TAURUS (BOVINE)//
P79244

F-THYRO1000070//HYPOTHETICAL 29.3 KD PROTEIN (ORF92)//2.3e-11:133:36//ORGYIA PSEUDOTSUGA-
TA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV)//O10341

F-THYRO1000072//C-PROTEIN, SKELETAL MUSCLE SLOW-ISOFORM//1.5e-14:205:29//HOMO SAPIENS
(HUMAN)//Q00872

F-THYRO1000085

F-THYRO1000092//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS)//0.063:59:33//HOMO SA-
PIENS (HUMAN)//P49901

F-THYRO1000107

F-THYRO1000111//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG//5.0e-58:110:67//NYCTICEBUS COU-
CANG (SLOW LORIS)//P08548

F-THYRO1000121//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66)//2.6e-06:134:35//MUS
MUSCULUS (MOUSE)//Q62203

F-THYRO1000124//TENECIN 3 PRECURSOR//0.047:76:35//TENEbrio MOLITOR (YELLOW MEALWORM)//
Q27270

F-THYRO1000129//FBROSIN (FRAGMENT)//0.35:43:34//MUS MUSCULUS (MOUSE)//Q60791

F-THYRO1000132//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//8.7e-14:104:42//HOMO SAPIENS (HUMAN)//
P39188

F-THYRO1000156

F-THYRO1000163//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//3.7e-20:71:71//HOMO SAPIENS (HUMAN)//
P39189

F-THYRO1000173//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN
AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN
ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN)//6.7e-88:216:76//MUS MUSCULUS (MOUSE)//P35585

F-THYRO1000186//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//2.9e-24:72:77//HOMO SAPIENS (HUMAN)//
P39192

F-THYRO1000187

F-THYRO1000190//PROTEIN TRANSPORT PROTEIN SEC61 BETA 2 SUBUNIT//0.060:50:42//SACCHARO-
MYCES CEREVISIAE (BAKER'S YEAST)//P52871

F-THYRO1000197

F-THYRO1000199//HYPOTHETICAL 49.8 KD PROTEIN D2007.5 IN CHROMOSOME III//2.0e-06:88:35//
CAENORHABDITIS ELEGANS//34379

F-THYRO1000206

F-THYRO1000221

F-THYRO1000241//HYPOTHETICAL 11.8 KD PROTEIN IN HE65-PK2 INTERGENIC REGION//1.0:51:35//
AUTOGRAPH A CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV)//P41661

F-THYRO1000242//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)//7.4e-37:137:36//HOMO SA-
PIENS (HUMAN)//P51523

F-THYRO1000253//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)//0.11:21:52//HO-
MO SAPIENS (HUMAN)//P30808

F-THYRO1000270//WDNM1 PROTEIN PRECURSOR//0.40:52:32//MUS MUSCULUS (MOUSE)//Q62477

F-THYRO1000279//BETA CRYSTALLIN A4//0.97:64:26//BOS TAURUS (BOVINE)//P11842

F-THYRO1000288//POTENTIAL CAAX PRENYL PROTEASE 1 (EC 3.4.24.-) (PRENYL PROTEIN- SPECIFIC
ENDOPROTEASE 1) (PPSEP 1)//3.4e-48:142:42//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//
Q10071

F-THYRO1000320//ZINC FINGER PROTEIN 14 (ZFP-14) (KROX-9 PROTEIN) (FRAGMENT)//0.87:35:45//MUS
MUSCULUS (MOUSE)//P10755

F-THYRO1000327//HYPOTHETICAL 64.7 KD PROTEIN F26E4.11 IN CHROMOSOME I//0.00010:75:26//
CAENORHABDITIS ELEGANS//P90859

F-THYRO1000343//CHROMOGRANIN A PRECURSOR (CGA) [CONTAINS: PANCREASTATIN; BETA-GRANIN;
WE-14]//0.88:107:26//MUS MUSCULUS (MOUSE)//P26339

F-THYRO1000358//SELENIUM-BINDING LIVER PROTEIN (LIVER PROTEIN 13.8 KDa) (LIVER PROTEIN 13.8 KDa)

F-THYRO1000368//PROMOTION RELATED KINETIC PROTEIN (PRK) (PROMOTION RELATED KINETIC PROTEIN 13.8 KDa)

SOPHILA MELANOGASTER (FRUIT FLY)//Q09101

F-THYRO1000381//GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]//0.032:99:35//SIMIAN SARCOMA VIRUS//P03330

F-THYRO1000387//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//0.90:46:30//HALICHOERUS GRYPUS (GRAY SEAL)//P38592

F-THYRO1000394//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930)//0.00019:48:37//HOMO SAPIENS (HUMAN)//P22531

F-THYRO1000395//RING CANAL PROTEIN (KELCH PROTEIN)//1.2e-33:186:38//DROSOPHILA MELANOGASTER (FRUIT FLY)//Q04652

F-THYRO1000401//50S RIBOSOMAL PROTEIN L7/L12 (FRAGMENT)//0.57:67:31//STAPHYLOCOCCUS AUREUS//P48860

F-THYRO1000438//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L)//1.0:42:38//STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN)//P15997

F-THYRO1000452//BACTERIOCIN CARNOBACTERIOCIN A PRECURSOR (PISCICOLIN 61)//0.31:34:44//CARNOBACTERIUM PISCICOLA//P38578

F-THYRO1000471//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.1e-31:94:72//HOMO SAPIENS (HUMAN)//P39194

F-THYRO1000484//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/5.9e-08:30:86//HOMO SAPIENS (HUMAN)//P39195

F-THYRO1000488//EARLY NODULIN 55-2 PRECURSOR (N-55-2) (NODULIN-315)//0.93:98:27//GLYCINE MAX (SOYBEAN)//Q02917

F-THYRO1000501//DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR//2.4e-51:198:50//MUS MUSCULUS (MOUSE)//P15533

F-THYRO1000502//HUNCHBACK PROTEIN (FRAGMENT)//0.84:41:43//APIS MELLIFERA (HONEYBEE)//P31504

F-THYRO1000505//HYPOTHETICAL BHLF1 PROTEIN//0.99:231:33//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4)//P03181

F-THYRO1000558//ANTITHROMBIN-III PRECURSOR (ATIII) (FRAGMENT)//0.47:58:37//GALLUS GALLUS (CHICKEN)//Q03352

F-THYRO1000569//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS)//0.00048:64:42//RATTUS NORVEGICUS (RAT)//P02454

F-THYRO1000570//HYPOTHETICAL 11.6 KD PROTEIN IN ACS1-GCV3 INTERGENIC REGION//0.94:61:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P39725

F-THYRO1000585//SPLICING FACTOR, ARGININE/SERINE-RICH 6 (PRE-MRNA SPLICING FACTOR SRP55)//0.050:104:36//HOMO SAPIENS (HUMAN)//Q13247

F-THYRO1000596//INFECTED CELL PROTEIN ICP34.5 (NEUROVIRULENCE FACTOR ICP34.5)//0.99:37:40//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN MGH-10)//P37319

F-THYRO1000602//EAMZP30-47 PROTEIN (FRAGMENT)//0.88:61:34//EIMERIA ACERVULINA//P21959

F-THYRO1000605//SUPPRESSOR PROTEIN SRP40//0.0016:116:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32583

F-THYRO1000625//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.4e-33:88:78//HOMO SAPIENS (HUMAN)//P39194

F-THYRO1000637//METALLOTHIONEIN A (MT A)//1.0:23:43//SPARUS AURATA (GILTHEAD SEA BREAM)//P52727

F-THYRO1000641//PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN//0.99:26:46//CYANIDIUM CALDARIUM (GALDIERIA SULPHURARIA)//O19925

F-THYRO1000658//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.5e-49:116:69//HOMO SAPIENS (HUMAN)//P39189

F-THYRO1000662//DNA-DAMAGE-INDUCIBLE PROTEIN P//3.7e-15:119:43//ESCHERICHIA COLI//Q47155

F-THYRO1000666//KINESIN-LIKE PROTEIN KLP1//1.0e-44:232:41//CHLAMYDOMONAS REINHARDTII//P46870

F-THYRO1000676//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/2.1e-15:144:39//HOMO SAPIENS (HUMAN)//P39193

F-THYRO1000684//HYPOTHETICAL 73.5 KD PROTEIN IN SCS3-RPS2 INTERGENIC REGION//0.00033:84:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53129

F-THYRO1000699//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.8e-33:88:78//HOMO SAPIENS (HUMAN)//P39194

SPARUS AURATA (GILTHEAD SEA BREAM) CARNOBACTERIUM PISCICOLA (PISCICOLIN 61) EIMERIA ACERVULINA HOMO SAPIENS (HUMAN)

P39188

F-THYRO1000715//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H]//4.6e-10:204:32//HOMO SAPIENS (HUMAN)//P04280

F-THYRO1000734

5 F-THYRO1000748//HYPOTHETICAL PROTEIN KIAA0411 (FRAGMENT)//1.8e-46:130:70//HOMO SAPIENS (HUMAN)//O43295

F-THYRO1000756//ALPHA-N-ACETYL GALACTOSAMINIDE ALPHA-2,6-SIALYLTRANSFERASE (EC 2.4.99.-) (ST6GALNACIII) (STY)//1.1e-06:95:31//RATTUS NORVEGICUS (RAT)//Q64686

10 F-THYRO1000777//CUTICLE COLLAGEN 2C (FRAGMENT)//0.0031:119:34//HAEMONCHUS CONTORTUS//P16252

F-THYRO1000783//MYOSIN IC HEAVY CHAIN//0.0014:121:37//ACANTHAMOEBA CASTELLANII (AMOEBA)//P10569

F-THYRO1000787//HUNCHBACK PROTEIN (FRAGMENT)//0.54:25:52//PHOLCUS PHALANGIODES//Q02031

15 F-THYRO1000793//PRE-MRNA SPLICING FACTOR PRP9//0.91:3 0:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P19736

F-THYRO1000796

F-THYRO1000805//HYPOTHETICAL 7.3 KD PROTEIN IN 100 KD PROTEIN REGION//0.081:31:38//HUMAN ADENOVIRUS TYPE 41//P23691

20 F-THYRO1000815/////ALU SUBFAMILY SX WARNING ENTRY !!!!!/6.0e-30:81:70//HOMO SAPIENS (HUMAN)//P39195

F-THYRO1000829//NEUROTOXIN III (BOM III)//0.022:32:34//BUTHUS OCCITANUS MARDOCHEI (MOROCCAN SCORPION)//P13488

25 F-THYRO1000843//HYPOTHETICAL 7.7 KD PROTEIN IN GENES 5-4 INTERGENIC REGION (ORF 109)//0.98:25:44//BACTERIOPHAGE P22//P26750

F-THYRO1000852//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)//7.3e-09:83:42//VOLVOX CARTERI//P21997

F-THYRO1000855//ANTIFREEZE PEPTIDE 4 PRECURSOR//1.0:54:35//PSEUDOPLEURONECTA AMERICANUS (WINTER FLOUNDER)//P02734

30 F-THYRO1000865/////ALU SUBFAMILY J WARNING ENTRY !!!!!/5.2e-17:66:57//HOMO SAPIENS (HUMAN)//P39188

F-THYRO1000895/////ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.0e-12:58:62//HOMO SAPIENS (HUMAN)//P39189

35 F-THYRO1000916/////ALU SUBFAMILY SB WARNING ENTRY !!!!!/2.0e-32:101:69//HOMO SAPIENS (HUMAN)//P39189

F-THYRO1000926//NITROGEN FIXATION REGULATORY PROTEIN//5.5e-05:108:27//KLEBSIELLA OXYTOCA//P56267

F-THYRO1000934//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE)//3.9e-50:147:40//HOMO SAPIENS (HUMAN)//P32322

40 F-THYRO1000951//DIHYDROXYACETONE KINASE (EC 2.7.1.29) (GLYCERONE KINASE)//1.8e-31:136:56//CITROBACTER FREUNDII//P45510

F-THYRO1000952//HYPOTHETICAL 182.0 KD PROTEIN IN NMD5-HOM6 INTERGENIC REGION//2.4e-05:91:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P47170

45 F-THYRO1000974//MITOCHONDRIAL ATP-DEPENDENT RNA HELICASE SUV3 PRECURSOR//1.0:35:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32580

F-THYRO1000975

F-THYRO1000983//HYPOTHETICAL 48.1 KD PROTEIN B0403.2 IN CHROMOSOME X//1.3e-20:96:51//CAENORHABDITIS ELEGANS//Q11076

50 F-THYRO1000984//GTP-BINDING ADP-RIBOSYLATION FACTOR HOMOLOG 1 PROTEIN//0.011:76:34//DROSOPHILA MELANOGASTER (FRUIT FLY)//P25160

F-THYRO1000988

F-THYRO1001003//HYPOTHETICAL 8.1 KD PROTEIN IN MSCL-RPLQ INTERGENIC REGION//0.97:60:31//ESCHERICHIA COLI//P36675

55 F-THYRO1001031/////ALU SUBFAMILY SX WARNING ENTRY !!!!!/9.5e-18:56:66//HOMO SAPIENS (HUMAN)//P39195

F-THYRO1001033//TRANSEFORMATION SIGNALING PROTEIN

HOMO SAPIENS (HUMAN)

F-THYRO1001062//ALU SUBFAMILY SX WARNING ENTRY

HOMO SAPIENS (HUMAN)

P39194

F-THYRO1001093//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/6.4e-13:70:57//HOMO SAPIENS (HUMAN)//

P39194

F-THYRO1001100//ZINC FINGER X-LINKED PROTEIN ZXDA (FRAGMENT)//4.2e-63:219:63//HOMO SAPIENS (HUMAN)//P98168

F-THYRO1001120//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53)//0.00068:160:31//HOMO SAPIENS (HUMAN)//Q15427

F-THYRO1001121//VERY HYPOTHETICAL 20.6 KD PROTEIN C56F8.15 IN CHROMOSOME I//0.37:158:28//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10263

F-THYRO1001133//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/7.3e-15:59:66//HOMO SAPIENS (HUMAN)//P39188

F-THYRO1001134//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) [CONTAINS: PEPTIDE P-D] (FRAGMENT)//0.00088:159:29//HOMO SAPIENS (HUMAN)//P10161

F-THYRO1001142//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.0e-29:81:71//HOMO SAPIENS (HUMAN)//P39194

F-THYRO1001173//CYTOCHROME C OXIDASE POLYPEPTIDE VIIS (EC 1.9.3.1)//0.88:51:35//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD)//P20610

F-THYRO1001177//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/3.0e-24:91:68//HOMO SAPIENS (HUMAN)//P39192

F-THYRO1001189//MKR2 PROTEIN (ZINC FINGER PROTEIN 2)//7.3e-27:165:39//MUS MUSCULUS (MOUSE)//P08043

F-THYRO1001204//BASIC PROLINE-RICH PEPTIDE P-E (IB-9)//0.67:42:42//HOMO SAPIENS (HUMAN)//P02811

F-THYRO1001213//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.9e-16:61:68//HOMO SAPIENS (HUMAN)//P39194

F-THYRO1001262//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.4e-36:50:84//HOMO SAPIENS (HUMAN)//P39193

F-THYRO1001271//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556//0.62:126:30//STREPTOMYCES FRADIAE//P20186

F-THYRO1001287//HYPOTHETICAL 91.2 KD PROTEIN IN RPS4B-SCH9 INTERGENIC REGION//1.9e-26:208:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38888

F-THYRO1001290//GIANT HEMOGLOBIN AIV CHAIN (FRAGMENT)//1.0:31:38//LAMELLIBRACHIA SP. (DEEP-SEA GIANT TUBE WORM)//P20413

F-THYRO1001313//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS5//0.00042:105:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//Q92331

F-THYRO1001320//COLLAGEN ALPHA 1(III) CHAIN//0.27:57:38//BOS TAURUS (BOVINE)//P04258

F-THYRO1001321//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/5.5e-20:74:64//HOMO SAPIENS (HUMAN)//P39188

F-THYRO1001322//HYPOTHETICAL 7.2 KD PROTEIN//0.66:49:30//VACCINIA VIRUS (STRAIN COPENHAGEN)//P21123

F-THYRO1001347//TOXIN F-VIII PRECURSOR (TOXIN TA2) (TOXIN DAF8)//0.94:61:36//DENDROASPIS ANGSTICEPS (EASTERN GREEN MAMBA)//P01404

F-THYRO1001363//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.0025:23:73//HOMO SAPIENS (HUMAN)//P39188

F-THYRO1001365//MERSACIDIN PRECURSOR//0.35:38:42//BACILLUS SP. (STRAIN HIL-Y85/54728)//P43683

F-THYRO1001374//PROTEIN VDLD//1.6e-3:140:31//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI)//O05729

F-THYRO1001401//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/0.047:43:48//HOMO SAPIENS (HUMAN)//P39192

F-THYRO1001403

F-THYRO1001405//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930)//0.0068:26:42//HOMO SAPIENS (HUMAN)//P22531

F-THYRO1001406//PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-)//3.1e-81:97:83//MUS MUSCULUS (MOUSE)//O70503

F-THYRO1001411//HYPOTHETICAL 10.5 KD PROTEIN IN CHROMOSOME I//0.37:158:28//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10263

F-THYRO1001412//HYPOTHETICAL 10.5 KD PROTEIN IN CHROMOSOME I//0.37:158:28//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10263

F-THYRO1001413//HYPOTHETICAL 10.5 KD PROTEIN IN CHROMOSOME I//0.37:158:28//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10263

PAGE: DB-098768 RANA ROBOBATA - ALGHINGT ROG. MARS-FROG; P4588;

F-THYRO1001895//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//6.1e-09:72:47//HOMO SAPIENS (HUMAN)//
P39188
F-THYRO1001907//TRYPOMASTIGOTE DECAY-ACCELERATING FACTOR (T-DAF) (FRAGMENT)//0.79:36:
44//TRYPANOSOMA CRUZI//Q26327
5 F-VESEN1000122//HOMEBOX PROTEIN HB9//0.57:64:32//HOMO SAPIENS (HUMAN)//P50219
F-Y79AA1000013//METALLOTHIONEIN B (MT-B)//0.034:35:48//SALMO SALAR (ATLANTIC SALMON)//
P52720
F-Y79AA1000033//CHOLECYSTOKININ//0.97:49:30//PSEUDEMYN SCRIPTA (SLIDER TURTLE)//P80345
F-Y79AA1000037//DNA-BINDING PROTEIN BMI-1//1.4e-23:80:60//HOMO SAPIENS (HUMAN)//P35226
10 F-Y79AA1000059//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556//0.0075:127:36//STREPTO-
MYCES FRADIAE//P20186
F-Y79AA1000065//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAG-
MENT)//0.022:135:29//HOMO SAPIENS (HUMAN)//P10162
F-Y79AA1000131//REGULATORY PROTEIN E2//1.1e-05:175:26//HUMAN PAPILLOMAVIRUS TYPE 24//
15 P50770
F-Y79AA1000181//PROLINE-RICH PROTEIN MP-3 (FRAGMENT)//1.4e-06:187:29//MUS MUSCULUS
(MOUSE)//P05143
F-Y79AA1000202//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT)//6.2e-09:47:53//OWENIA FUSI-
FORMIS//P21260
20 F-Y79AA1000214//HISTONE H2A VARIANT//1.7e-50:107:100//GALLUS GALLUS (CHICKEN)//P02272
F-Y79AA1000230//GONADOLIBERIN I PRECURSOR (LHRH I) (LUTEINIZING HORMONE RELEASING HOR-
MONE I) (GONADOTROPIN RELEASING HORMONE I) (GNRH I) (LULIBERIN I)//0.27:64:34//HOMO SAPIENS
(HUMAN)//P01148
F-Y79AA1000231//HYPOTHETICAL 47.9 KD PROTEIN M021B04.12//2.5e-72:277:53//ARABIDOPSIS THAL-
25 IANA (MOUSE-EAR CRESS)//O04658
F-Y79AA1000258//PROLINE-RICH PROTEIN MP-2 PRECURSOR//2.8e-08:174:35//MUS MUSCULUS
(MOUSE)//P05142
F-Y79AA1000268//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENT)//0.00020:176:33//RATTUS NORVEGICUS
(RAT)//P13941
30 F-Y79AA1000313//HYPOTHETICAL 54.0 KD PROTEIN C32A3.1 IN CHROMOSOME III//0.092:127:21//
CAENORHABDITIS ELEGANS//Q09260
F-Y79AA1000328//SEL-10 PROTEIN//5.3e-05:129:28//CAENORHABDITIS ELEGANS//Q93794
F-Y79AA1000342//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN)//1.0:73:30//OVIS AR-
IES (SHEEP)//P26372
35 F-Y79AA1000346//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP)//1.8e-95:205:
83//BOS TAURUS (BOVINE)//P53620
F-Y79AA1000349//ANTIFREEZE PEPTIDE 4 PRECURSOR//0.036:37:54//PSEUDOPLEURONECTA AMERI-
CANUS (WINTER FLOUNDER)//P02734
F-Y79AA1000355//HYPOTHETICAL 18.2 KD PROTEIN ZK632.13 IN CHROMOSOME III//0.0031:106:28//
40 CAENORHABDITIS ELEGANS//Q10120
F-Y79AA1000368//REDUCED VIABILITY UPON STARVATION PROTEIN 161//1.4e-16:208:28//SACCHARO-
MYCES CEREVISIAE (BAKER'S YEAST)//P25343
F-Y79AA1000405//LIGHT-HARVESTING PROTEIN B-800-850, ALPHA CHAIN C (ANTENNA PIGMENT PRO-
TEIN, ALPHA CHAIN C) (LH II-C ALPHA)//0.98:50:30//RHODOPSEUDOMONAS PALUSTRIS//P35103
45 F-Y79AA1000410//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//7.9e-20:62:79//HOMO SAPIENS (HUMAN)//
P39194
F-Y79AA1000420//HYPOTHETICAL 27.7 KD PROTEIN IN UME3-HDA1 INTERGENIC REGION//1.4e-06:86:38//
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53970
F-Y79AA1000469//HYPOTHETICAL 48.4 KD PROTEIN F44B9.5 IN CHROMOSOME III//2.8e-34:211:40//
50 CAENORHABDITIS ELEGANS//P34426
F-Y79AA1000480//HYPOTHETICAL 63.2 KD PROTEIN C1F3.09 IN CHROMOSOME I//3.9e-15:90:32//
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10414
F-Y79AA1000538//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//0.37:41:48//HOMO SAPIENS (HUMAN)//
P39195
55 F-Y79AA1000539//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75) //
1.8e-21:190:37//HOMO SAPIENS (HUMAN)//Q08170

*** SEQUENCE DATA ***
F-Y79AA1000539: 186-211-90-37//HOMO SAPIENS (HUMAN) //Q08170
F-Y79AA1000539: 186-211-90-37//HOMO SAPIENS (HUMAN) //Q08170

F-Y79AA1000560//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT)//1.6e-79:186:87//MUS MUSCULUS (MOUSE)//P17427

F-Y79AA1000574//AKLAVINONE C-11 HYDROXYLASE (EC 1.-.-) (FRAGMENT)//0.010:35:60//STREPTOMYCES PEUCETIUS//P32009

F-Y79AA1000589//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION//4.5e-27:197:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P28320

F-Y79AA1000627//ZINC FINGER PROTEIN 134//1.6e-34:191:35//HOMO SAPIENS (HUMAN)//P52741

F-Y79AA1000705//HYPOTHETICAL 128.5 KD HELICASE IN ATS1-TPD3 INTERGENIC REGION//8.7e-36:250:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P31380

F-Y79AA1000734//PEROXISOMAL MEMBRANE PROTEIN PMP30A (PMP31) (PEROXIN-11A)//0.00037:108:27//CANDIDA BOIDINII (YEAST)//Q00316

F-Y79AA1000748//HYPOTHETICAL 61.3 KD PROTEIN F25B5.5 IN CHROMOSOME III//1.0e-23:210:34//CAENORHABDITIS ELEGANS//Q09316

F-Y79AA1000752//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP)//1.4e-53:156:68//MUS MUSCULUS (MOUSE)//Q61990

F-Y79AA1000774//HYPOTHETICAL 77.9 KD PROTEIN IN RRN10-MCM2 INTERGENIC REGION//1.2e-11:231:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38205

F-Y79AA1000782//CUTICLE COLLAGEN 2//0.012:56:35//CAENORHABDITIS ELEGANS//P17656

F-Y79AA1000784//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR//1.3e-08:82:39//PLASMODIUM LOPHURAE//P04929

F-Y79AA1000794//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS)//0.043:13:53//HOMO SAPIENS (HUMAN)//P30808

F-Y79AA1000800//PRIA PROTEIN PRECURSOR//0.031:94:34//LENTINULA EDODES (SHIITAKE MUSHROOM) (LENTINUS EDODES)//Q01200

F-Y79AA1000802//HYPOTHETICAL 67.4 KD PROTEIN IN RPS3-PSD1 INTERGENIC REGION//0.26:186:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53882

F-Y79AA1000805//AMP DEAMINASE (EC 3.5.4.6) (MYOADENYLATE DEAMINASE)//0.99:78:35//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//P50998

F-Y79AA1000824//HYPOTHETICAL 81.7 KD PROTEIN IN MOL1-NAT2 INTERGENIC REGION//3.4e-44:111:49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P48234

F-Y79AA1000827//HYPOTHETICAL BHLF1 PROTEIN//0.0046:187:33//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4)//P03181

F-Y79AA1000833//TUBULIN ALPHA-1 CHAIN//1.0e-75:239:66//CRICETULUS GRISEUS (CHINESE HAMSTER)//P05209

F-Y79AA1000850//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174N)//0.0078:57:31//HOMO SAPIENS (HUMAN)//P22532

F-Y79AA1000962//MYOSIN HEAVY CHAIN, GIZZARD SMOOTH MUSCLE//8.5e-11:241:26//GALLUS GALLUS (CHICKEN)//P10587

F-Y79AA1000966//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6)//0.69:122:31//TRYPANOSOMA BRUCEI BRUCEI//P24499

F-Y79AA1000968//TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR)//3.3e-102:211:93//RATTUS NORVEGICUS (RAT)//P70541

F-Y79AA1000969//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR//1.0:67:38//GALLUS GALLUS (CHICKEN)//P02457

F-Y79AA1000976//INVOLUCRIN//0.99:66:31//CEBUS ALBIFRONS (WHITE-FRONTED CAPUCHIN)//P24709

F-Y79AA1000985//PERICENTRIN//1.1e-24:116:59//MUS MUSCULUS (MOUSE)//P48725

F-Y79AA1001023//HYPOTHETICAL 105.9 KD PROTEIN IN AAC3-RFC5 INTERGENIC REGION//0.37:79:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P38250

F-Y79AA1001041//SPERMATID-SPECIFIC PROTEIN T1 [CONTAINS: SPERM PROTAMINE SP1]//0.93:43:39//SEPIA OFFICINALIS (COMMON CUTTLEFISH)//P80001

F-Y79AA1001048//ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD)//1.5e-51:211:52//BOS TAURUS (BOVINE)//P48818

F-Y79AA1001061//ALU SUBFAMILY SQ WARNING ENTRY II//3.8e-25:85:69//HOMO SAPIENS (HUMAN)//P39194

F-Y79AA1001068//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR

1.2e-102:211:93//MUS MUSCULUS (MOUSE)//P2848

F-Y79AA1001077//ADULT SPECIFIC RIGID CUTICULAR PROTEIN (RCP) (P10399:36:4)//ARANEUS DI

ADEMATUS (SPIDER).//P80515

F-Y79AA1001078//HYPOTHETICAL 88.1 KD PROTEIN K02D10.1 IN CHROMOSOME III.//1.0e-06:197:23//
CAENORHABDITIS ELEGANS //P34492

F-Y79AA1001105//HOMEBOX PROTEIN OTX2.//2.9e-62:163:79//MUS MUSCULUS (MOUSE).//P80206

5 F-Y79AA1001145//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//0.024:42:59//HOMO SAPIENS (HUMAN).//
P39195

F-Y79AA1001167//HYPOTHETICAL 7.1 KD PROTEIN IN IAP2-VLF1 INTERGENIC REGION.//0.96:20:50//
AUTOGRAPHAL CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41471

10 F-Y79AA1001177//HYPOTHETICAL BHLF1 PROTEIN.//3.9e-05:135:34//EPSTEIN-BARR VIRUS (STRAIN
B95-8) (HUMAN HERPESVIRUS 4).//P03181

F-Y79AA1001185//PUTATIVE CUTICLE COLLAGEN C09G5.5.//0.00017:93:38//CAENORHABDITIS ELE-
GANS.//Q09456

F-Y79AA1001211

F-Y79AA1001216//TENSIN.//0.012:134:32//GALLUS GALLUS (CHICKEN).//Q04205

15 F-Y79AA1001228//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).//0.088:75:34//HOMO SAPIENS (HUMAN).//
Q02817

F-Y79AA1001233//ESTRADIOL 17 BETA-DEHYDROGENASE 1 (EC 1.1.1.62) (17-BETA-HSD 1) (17-BETA-HY-
DROXYSTEROID DEHYDROGENASE 1).//1.1e-40:139:51//RATTUS NORVEGICUS (RAT).//P51657

20 F-Y79AA1001236//HYPOTHETICAL 34.7 KD PROTEIN IN ORC2-TIP1 INTERGENIC REGION.//2.0e-22:108:53//
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38238

F-Y79AA1001281

F-Y79AA1001299//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.0022:49:44//MUS MUSCULUS
(MOUSE).//P05143

25 F-Y79AA1001312//50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR.//0.98:117:25//ARABIDOP-
SIS THALIANA (MOUSE-EAR CRESS).//P92959

F-Y79AA1001323//CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUA-
MOUS CELL MARKER) (SPRP).//0.082:44:40//SUS SCROFA (PIG).//P35323

F-Y79AA1001384//APOLOPOPROTEIN C-III PRECURSOR (APO-CIII).//0.99:47:40//MUS MUSCULUS
(MOUSE).//P33622

30 F-Y79AA1001391//HOMEBOX PROTEIN HOX-A13 (HOX-1J).//9.8e-58:157:62//HOMO SAPIENS (HUMAN).//
P31271

F-Y79AA1001394//TRICHOHYALIN.//4.7e-08:121:36//HOMO SAPIENS (HUMAN).//Q07283

F-Y79AA1001402//ETS-DOMAIN TRANSCRIPTION FACTOR ERF.//0.0087:81:33//MUS MUSCULUS
(MOUSE).//P70459

35 F-Y79AA1001493//HYPOTHETICAL 48.1 KD PROTEIN B0403.2 IN CHROMOSOME X.//4.5e-21:125:44//
CAENORHABDITIS ELEGANS.//Q11076

F-Y79AA1001511//HYPOTHETICAL 86.6 KD PROTEIN IN PFK1-TDS4 INTERGENIC REGION.//2.3e-17:249:
31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53313

40 F-Y79AA1001533//DNA-DIRECTED RNA POLYMERASE I49 KD POLYPEPTIDE (EC 2.7.7.6) (A49).//0.0099:
155:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q01080

F-Y79AA1001541

F-Y79AA1001548//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.1e-17:53:83//HOMO SAPIENS (HUMAN).//
P39192

F-Y79AA1001555//MAJOR SURFACE ANTIGEN.//0.046:62:29//HEPATITIS B VIRUS.//P31873

45 F-Y79AA1001581//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- AC-
TIVATING ENZYME).//8.6e-11:144:31//ESCHERICHIA COLI.//P27550

F-Y79AA1001585//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//0.012:64:40//MUS MUS-
CULUS (MOUSE).//P15265

F-Y79AA1001594//CORNIFIN BETA.//0.61:88:31//MUS MUSCULUS (MOUSE).//O09116

50 F-Y79AA1001603//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135)
(TAFII-130) (TAFII130).//0.024:170:30//HOMO SAPIENS (HUMAN).//O00268

F-Y79AA1001613//ZINC FINGER PROTEIN 42 (MYELOID ZINC FINGER 1) (MZF-1).//4.5e-09:136:27//HOMO
SAPIENS (HUMAN).//P28698

55 F-Y79AA1001647//HYPOTHETICAL 23.1 KD PROTEIN CY277.20C.//0.093:94:26//MYCOBACTERIUM TUBER-
CULOSIS.//P71779

F-Y79AA1001665//HOMO

F-Y79AA1001665//HOMO

F-Y79AA1001665//HOMO SAPIENS (HUMAN).//0.024:170:30//HOMO SAPIENS (HUMAN).//P14755

- F-Y79AA1002258//HYPOTHETICAL 103.9 KD PROTEIN ZK370.3 IN CHROMOSOME III//4.3e-45:164:48//CAENORHABDITIS ELEGANS//Q02328
- F-Y79AA1002298//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) [CONTAINS: PEPTIDE P-D] (FRAGMENT)//0.0063:99:31//HOMO SAPIENS (HUMAN)//P10161
- 5 F-Y79AA1002307
- F-Y79AA1002311//HYPOTHETICAL 105.3 KD PROTEIN C01G6.5 IN CHROMOSOME III//0.75:198:24//CAENORHABDITIS ELEGANS//P46012
- F-Y79AA1002351//CUTICLE COLLAGEN 34//0.74:128:35//CAENORHABDITIS ELEGANS//P34687
- 10 F-Y79AA1002361//GLC7-INTERACTING PROTEIN 2//0.050:71:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40036
- F-Y79AA1002399//NEUROMODULIN (AXONAL MEMBRANE PROTEIN GAP-43) (PP46) (B-50) (PROTEIN F1) (CALMODULIN-BINDING PROTEIN P-57)//1.0:89:30//CARASSIUS AURATUS (GOLDFISH)//P17691
- F-Y79AA1002407//HYPOTHETICAL 31.5 KD PROTEIN IN YGP1-YCK2 INTERGENIC REGION//3.7e-16:232:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P53899
- 15 F-Y79AA1002416//CTP SYNTHASE (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (CTP SYNTHETASE)//6.7e-72:162:84//HOMO SAPIENS (HUMAN)//P17812
- F-Y79AA1002431//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930)//0.81:34:41//HOMO SAPIENS (HUMAN)//P22531
- F-Y79AA1002433//CELL DIVISION CONTROL PROTEIN 68//0.00024:85:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P32558
- 20 F-Y79AA1002472//ZINC FINGER PROTEIN 35 (ZFP-35)//2.3e-60:217:44//MUS MUSCULUS (MOUSE)//P15620
- F-Y79AA1002482//ZINC FINGER PROTEIN 141//2.0e-31:90:55//HOMO SAPIENS (HUMAN)//Q15928
- F-Y79AA1002487//HYPOTHETICAL 67.1 KD TRP-ASP REPEATS CONTAINING PROTEIN C57A10.05C IN CHROMOSOME I//0.18:41:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//P87053
- 25

Homology Search Result Data 2.

- [0300] The result of the homology search of the GenBank using the clone sequence of 5'-end except EST and STS.
- 30 [0301] Data include

the name of clone,
 definition of the top hit data,
 the P-value: the length of the compared sequence: identity (%), and
 the Accession No. of the top hit data, as in the order separated by //.

- 35 [0302] Data are not shown for the clones in which the P-value was higher than 1.

- F-HEMBA1000005//Mouse tumor cell dnaJ-like protein 1 mRNA, complete cds//3.4e-106:695:86//L16953
- 40 F-HEMBA1000012//Caenorhabditis-elegans cosmid C16C10, complete sequence//1.5e-24:374:66//Z46787
- F-HEMBA1000020//Homo sapiens beta 2 gene//3.5e-112:529:90//X02344
- F-HEMBA1000030//Rattus norvegicus G protein-coupled receptor kinase-associated ADP ribosylation factor GT-Pase-activating protein (GIT1) mRNA, complete cds//5.6e-124:743:88//AF085693
- F-HEMBA1000042//Human Chromosome 15q26.1 PAC clone pDJ460g16, WORKING DRAFT SEQUENCE, 3 unordered pieces//1.1e-25:529:65//AC004581
- 45 F-HEMBA1000046//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 125I3, WORKING DRAFT SEQUENCE//3.2e-11:330:63//AL033528
- F-HEMBA1000050//Homo sapiens DNA sequence from PAC 172K10 on chromosome 6q24. Contains STS, GSS and chromosome 6 fragment, complete sequence//0.32:407:59//AL022477
- F-HEMBA1000076//Homo sapiens full-length insert cDNA clone ZB97G06//6.2e-135:594:98//AF086182
- 50 F-HEMBA1000111//CIT-HSP-2291M18.TF CIT-HSP Homo sapiens genomic clone 2291M18 genomic survey sequence//2.8e-16:132:79//AQ004134
- F-HEMBA1000129//Homo sapiens chromosome 17, clone HCIT48C15, complete sequence//8.6e-98:230:93//AC003104
- F-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds//2.1e-167:791:98//AB018340
- 55 F-HEMBA1000150//Homo sapiens mRNA for KIAA0788 protein, partial cds//2.2e-44:242:96//AB018331
- F-HEMBA1000156//Rattus norvegicus G protein-coupled receptor kinase-associated ADP ribosylation factor GT-Pase-activating protein (GIT1) mRNA, complete cds//5.6e-124:743:88//AF085693

F-HEMBA1000168//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 321D2, WORKING DRAFT SEQUENCE.//0.99:290:61//AL031033

F-HEMBA1000180//rat u2 small nuclear rna gene and flanks.//3.7e-18:112:98//K00034

F-HEMBA1000185

5 F-HEMBA1000193//Human FMR1 gene, 5' end.//0.0012:191:67//L19476

F-HEMBA1000201//Human Ini1 mRNA, complete cds.//2.0e-73:440:92//U04847

F-HEMBA1000213//Plasmodium falciparum MAL3P7, complete sequence.//0.90:332:59//AL034559

F-HEMBA1000216//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds.//4.8e-117:585:83//AF060194

10 F-HEMBA1000227//H.sapiens CpG island DNA genomic Mse1 fragment, clone 179h6, reverse read cpg179h6.rt1a.//1.9e-14:95:98//Z64921

F-HEMBA1000231//H.sapiens CpG island DNA genomic Mse1 fragment, clone 90a5, reverse read cpg90a5.rt1a.//5.1e-34:186:97//Z56144

15 F-HEMBA1000243//Human DNA sequence from PAC 440O21 on chromosome X contains ESTs and STS.//4.1e-67:291:82//Z84481

F-HEMBA1000244//M.musculus Ank-1 mRNA for erythroid ankydn.//0.029:316:59//X69065

F-HEMBA1000251//Homo sapiens PAC clone DJ0988L12 from 7q11.23-q21.1, complete sequence.//0.35:467:60//AC004454

F-HEMBA1000264

20 F-HEMBA1000280//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces.//8.9e-20:218:78//AC004825

F-HEMBA1000282//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//4.2e-08:134:77//AC004617

25 F-HEMBA1000288//345L5.TPB CIT978SKA1 Homo sapiens genomic clone A-345L05, genomic survey sequence.//1.1e-06:152:73//B17459

F-HEMBA1000290//Human ornithine decarboxylase gene, complete cds.//3.2e-11:507:62//M33764

F-HEMBA1000302//CIT-HSP-2169N13.TF CIT-HSP Homo sapiens genomic clone 2169N13, genomic survey sequence.//5.4e-06:86:88//B90730

F-HEMBA1000303//Mus musculus Plenty of SH3s (POSH) mRNA, complete cds.//7.9e-111:701:86//AF030131

30 F-HEMBA1000304//HS_3006_A1_A09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3006 Col=17 Row=A, genomic survey sequence.//5.2e-40:240:92//AQ118226

F-HEMBA1000307//Mus musculus mRNA for CDV-1R protein.//7.9e-127:815:84//Y10495

F-HEMBA1000327//HS_3124_B2_H08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3124 Col=16 Row=P, genomic survey sequence.//1.4e-11:87:96//AQ187492

35 F-HEMBA1000333

F-HEMBA1000338//Homo sapiens chromosome X, PAC 671D9, complete sequence.//4.0e-66:271:84//AF031078

F-HEMBA1000351//Homo sapiens PAC clone DJ0649P17 from 7q11.23-q21, complete sequence.//0.64:334:60//AC004848

40 F-HEMBA1000355//Pseudorabies virus serine/threonine kinase (ULPK) gene, partial cds and alkaline nuclease (AN) gene, complete cds.//0.017:313:63//U25056

F-HEMBA1000356//Oryctolagus cuniculus troponin T cardiac isoform mRNA, 3' end of cds.//0.87:198:61//L40178

F-HEMBA1000357//HS_3194_A1_D05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3194 Col=9 Row=G, genomic survey sequence.//6.5e-90:436:98//AQ173748

45 F-HEMBA1000366//HS_3027_B2_G06_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3027 Col=12 Row=N, genomic survey sequence.//0.0074:192:64//AQ128843

F-HEMBA1000369//Human DNA sequence from clone 1039K5 on chromosome 22q12.3-13.2 Contains gene similar to PICK1 perinuclear binding protein, gene similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS and a CpG island, complete sequence.//4.2e-106:133:99//AL031587

50 F-HEMBA1000376//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//1.6e-22:659:63//AC006116

F-HEMBA1000387//Homo sapiens chromosome 12p13.3 clone RPC111-264F23, WORKING DRAFT SEQUENCE, 90 unordered pieces.//3.2e-06:136:75//AC006122

F-HEMBA1000390//Homo sapiens BAC clone RG119C02 from 7p15, complete sequence.//3.5e-111:284:95//AC004520

55 F-HEMBA1000392//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 173D1, WORKING DRAFT SEQUENCE.//1.8e-39:332:80//AL021084

1. M33764 (1990) Human ornithine decarboxylase gene, complete cds. 2. Y10495 (1990) Mus musculus mRNA for CDV-1R protein. 3. AF030131 (1990) Mus musculus Plenty of SH3s (POSH) mRNA, complete cds. 4. B17459 (1990) CIT978SKA1 Homo sapiens genomic clone A-345L05, genomic survey sequence. 5. M33764 (1990) Human ornithine decarboxylase gene, complete cds. 6. B90730 (1990) CIT-HSP Homo sapiens genomic clone 2169N13, genomic survey sequence. 7. AF030131 (1990) Mus musculus Plenty of SH3s (POSH) mRNA, complete cds. 8. Y10495 (1990) Mus musculus mRNA for CDV-1R protein. 9. AQ118226 (1990) HS_3006_A1_A09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3006 Col=17 Row=A, genomic survey sequence. 10. Y10495 (1990) Mus musculus mRNA for CDV-1R protein. 11. AQ187492 (1990) HS_3124_B2_H08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3124 Col=16 Row=P, genomic survey sequence. 12. AF031078 (1990) Homo sapiens chromosome X, PAC 671D9, complete sequence. 13. AC004848 (1990) Homo sapiens PAC clone DJ0649P17 from 7q11.23-q21, complete sequence. 14. U25056 (1990) Pseudorabies virus serine/threonine kinase (ULPK) gene, partial cds and alkaline nuclease (AN) gene, complete cds. 15. L40178 (1990) Oryctolagus cuniculus troponin T cardiac isoform mRNA, 3' end of cds. 16. AQ173748 (1990) HS_3194_A1_D05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3194 Col=9 Row=G, genomic survey sequence. 17. AQ128843 (1990) HS_3027_B2_G06_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3027 Col=12 Row=N, genomic survey sequence. 18. AL031587 (1990) Human DNA sequence from clone 1039K5 on chromosome 22q12.3-13.2 Contains gene similar to PICK1 perinuclear binding protein, gene similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS and a CpG island, complete sequence. 19. AC006116 (1990) Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence. 20. AC006122 (1990) Homo sapiens chromosome 12p13.3 clone RPC111-264F23, WORKING DRAFT SEQUENCE, 90 unordered pieces. 21. AC004520 (1990) Homo sapiens BAC clone RG119C02 from 7p15, complete sequence. 22. AL021084 (1990) Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 173D1, WORKING DRAFT SEQUENCE.

F-HEMBA1000411//Human Xp22 contig of 3 PACS (R7-39D12, R7-134G1, R7-185L21) from the Roswell Park Cancer Institute, complete sequence.//8.1e-18:424:64//U96409

F-HEMBA1000418//Drosophila melanogaster Oregon-R mitochondrial A+T region.//0.0026:564:59//U11584

F-HEMBA1000422//Human DNA from chromosome 19 specific cosmid R30292, genomic sequence, complete sequence.//9.2e-14:232:70//AC003112

F-HEMBA1000428//Homo sapiens Xp22 BAC GSHB-590J6 (Genome Systems Human BAC library) complete sequence.//3.8e-37:408:69//AC004554

F-HEMBA1000434//Caenorhabditis elegans cosmid Y48E1B, complete sequence.//0.73:454:57//Z93393

F-HEMBA1000442

F-HEMBA1000456//RPCI11-30J5.TV RPCI-11 Homo sapiens genomic clone RPCI-11-30J5, genomic survey sequence.//6.3e-06:62:96//B85188

F-HEMBA1000459//Mus musculus hemin-sensitive initiation factor 2 alpha kinase mRNA, complete cds.//6.8e-70:580:79//AF028808

F-HEMBA1000460//Homo sapiens PAC clone DJ0593H12 from 7p31, complete sequence.//2.8e-154:746:98//AC004839

F-HEMBA1000464//Homo sapiens, clone hRPK.15_A_1, complete sequence.//4.8e-25:397:72//AC006213

F-HEMBA1000469//CIT-HSP-2167P21.TF CIT-HSP Homo sapiens genomic clone 2167P21, genomic survey sequence.//4.0e-83:406:99//B94160

F-HEMBA1000488//Homo sapiens Chromosome 22q11.2 PAC Clone p_m11 In BCRL2-GGT Region, complete sequence.//4.2e-53:312:93//AC004033

F-HEMBA1000490//Campylobacter jejuni groES, groEL genes.//0.59:451:62//Y13334

F-HEMBA1000491//Murine sarcoma virus (Harvey-strain) H-ras transforming p21 gene.//8.6e-06:338:58//X00740

F-HEMBA1000501//Homo sapiens chromosome 17, clone hRPK.264_B_14, complete sequence.//9.4e-41:591:69//AC005864

F-HEMBA1000504//Homo sapiens mRNA for osteoblast specific factor 2 (OSF-2os).//4.0e-07:57:100//D13666

F-HEMBA1000505

F-HEMBA1000508//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0135005; HTGS phase 1, WORKING DRAFT SEQUENCE, 23 unordered pieces.//0.035:329:61//AC004661

F-HEMBA1000518//Caenorhabditis elegans cosmid C17H12.//0.96:425:58//AF045642

F-HEMBA1000519//Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence.//1.6e-53:300:89//AC004616

F-HEMBA1000520//Homo sapiens clone DJ0813F11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.7e-10:117:86//AC006006

F-HEMBA1000523

F-HEMBA1000531//Mus musculus Hsp70-related NST-1 (hsr.1) mRNA, complete cds.//3.9e-35:290:80//U08215

F-HEMBA1000534//Homo sapiens chromosome 17, clone hRPK.177_H_5, WORKING DRAFT SEQUENCE, 2 ordered pieces.//1.7e-36:328:77//AC005973

F-HEMBA1000540//Arabidopsis thaliana DNA chromosome 4, BAC clone F7K2 (ESSAII project).//0.057:265:63//AL033545

F-HEMBA1000542//Rattus norvegicus mRNA for dipeptidyl peptidase III, complete cds.//1.2e-110:572:88//D89340

F-HEMBA1000545//Human DNA from cosmid L27h9, Huntington's Disease Region, chromosome 4p16.3 contains CpG island.//7.5e-130:780:89//Z49237

F-HEMBA1000555//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 134O19, WORKING DRAFT SEQUENCE.//3.2e-175:838:98//AL034555

F-HEMBA1000557//CIT-HSP-2369F15.TF CIT-HSP Homo sapiens genomic clone 2369F15, genomic survey sequence.//2.8e-32:315:78//AQ074611

F-HEMBA1000561//Rattus norvegicus Olf-1/EBF associated Zn finger protein Roaz mRNA, alternatively spliced form, complete cds.//3.4e-69:665:72//U92564

F-HEMBA1000563//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.59:261:61//AC005504

F-HEMBA1000568//HS_3243_B2_A12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3243 Col=24 Row=B, genomic survey sequence.//3.1e-54:323:91//AQ219628

F-HEMBA1000569//M.musculus mRNA for GPI-anchored protein.//1.4e-19:440:61//X89571

F-HEMBA1000575//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.0016:557:57//AC005506

F-HEMBA1000588//M.musculus mRNA for EBF associated protein.//1.4e-19:440:61//X89571

400

F-HEMBA1000589//M.musculus mRNA for EBF associated protein.//1.4e-19:440:61//X89571

F-HEMBA1000592//Mus musculus clone OST7314, genomic survey sequence.//7.3e-07:68:94//AF046733
 F-HEMBA1000594//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.//8.7e-71:553:79//Z83822
 F-HEMBA1000604//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 237J2, WORKING DRAFT SEQUENCE.//2.9e-21:158:75//AL021394
 F-HEMBA1000608//Homo sapiens mRNA for KIAA0456 protein, partial cds.//1.1e-118:561:99//AB007925
 F-HEMBA1000622//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence.//2.2e-28:426:70//AC004382
 F-HEMBA1000636//Human CpG island sequence, clone Q28B8.//1.0e-15:274:68//D85773
 F-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds.//6.7e-137:639:99//AB014590
 F-HEMBA1000655//, complete sequence.//5.1e-83:685:80//AC005815
 F-HEMBA1000657//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//1.1e-91:597:84//U35776
 F-HEMBA1000662//Homo sapiens clone DJ0853H20, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.019:695:57//AC004907
 F-HEMBA1000673//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 229A8, WORKING DRAFT SEQUENCE.//1.5e-48:325:85//Z86090
 F-HEMBA1000682//Homo sapiens (subclone 5_g5 from P1 H25) DNA sequence.//7.7e-61:615:74//L43411
 F-HEMBA1000686
 F-HEMBA1000702
 F-HEMBA1000705//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0037:569:57//AC005507
 F-HEMBA1000719//Streptomyces coelicolor cosmid 1C2.//2.0e-09:483:62//AL031124
 F-HEMBA1000722//Toxoplasma gondii chloroplast, complete genome.//0.00058:762:57//U87145
 F-HEMBA1000726//H.sapiens HLA-DRB1*15 gene.//9.8e-49:189:89//X88791
 F-HEMBA1000727//CIT-HSP-387P22.TRB CIT-HSP Homo sapiens genomic clone 387P22, genomic survey sequence.//0.0054:206:67//B60158
 F-HEMBA1000747
 F-HEMBA1000749//Human DNA sequence from clone 522P13 on chromosome 6p21.31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous Nuclear Riboprotein A3, FBRNP) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//3.3e-05:124:75//AL024509
 F-HEMBA1000752//Human Chromosome X, complete sequence.//5.9e-48:502:75//AC004073
 F-HEMBA1000769//Homo sapiens clone NH0576N21, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.011:179:67//AC005043
 F-HEMBA1000773//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y59A8, WORKING DRAFT SEQUENCE.//0.070:231:63//Z98870
 F-HEMBA1000774//Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete sequence.//6.2e-40:385:75//AC004953
 F-HEMBA1000791
 F-HEMBA1000817//Myrmecia pilosula HI87-135 mitochondrion cytochrome b gene, partial cds.//0.99:244:58//U15678
 F-HEMBA1000822//Human DNA sequence from PAC 179D3, between markers DXS6791 and DXS8038 on chromosome X contains S10 GTP-binding protein, ESTs and CpG island.//0.033:294:62//Z81370
 F-HEMBA1000827//Borrelia burgdorferi (section 50 of 70) of the complete genome.//9.7e-05:463:58//AE001164
 F-HEMBA1000843//Homo sapiens DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 PLC-II, PLC-148), the KIAA0395 gene for a probable Zinc Finger Homeobox protein and a 60S Ribosomal Protein L23 LIKE pseudogene. Contains a predicted CpG island, ESTs, STSs and GSSs, complete sequence.//3.0e-153:732:98//AL022394
 F-HEMBA1000851//Rattus norvegicus glucocorticoid modulatory element binding protein 2 mRNA, complete cds.//1.6e-31:386:72//AF059273
 F-HEMBA1000852//Homo sapiens Xp22 bins 3-5 PAC RPC14-617A9 (Roswell Park Cancer Institute Human PAC Library) containing Arylsulfatase D and E genes, complete sequence.//8.5e-115:455:98//AC005295
 F-HEMBA1000867
 F-HEMBA1000869//Human DNA sequence from cosmid J138O17, between markers DXS6791 and DXS8038 on chromosome X contains EST, CA repeat and a pseudogene (retroviral-like element).//6.6e-41:157:75//Z73511
 F-HEMBA1000870//Caenorhabditis elegans cytochrome oxidase II gene, partial cds. and tRNA-ASP, tRNA-His, tRNA-Phe, tRNA-Tyr genes, complete sequence. mitochondrial genes for mitochondrial products.//0.0049:211:66//AF034596

F-HEMBA1000872//CIT-HSP-2355D20.TF CIT-HSP Homo sapiens genomic clone 2355D20, genomic survey sequence.//3.7e-33:180:98//AQ059583

F-HEMBA1000876//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 473B4, WORKING DRAFT SEQUENCE.//5.6e-37:262:72//Z83826

5 F-HEMBA1000908//Triticum aestivum low-affinity cation transporter (LCT1) mRNA, complete cds.//1.0:304:59//AF015523

F-HEMBA1000910//M.musculus necdin mRNA, complete cds.//6.1e-08:256:61//M80840

F-HEMBA1000918//Tetrahymena thermophila micronuclear developmentally eliminated sequence region.//0.13:232:63//U88158

10 F-HEMBA1000919//Gallus domesticus filamin mRNA, complete cds.//1.0:213:65//U00147

F-HEMBA1000934//CIT-HSP-2053H24.TR CIT-HSP Homo sapiens genomic clone 2053H24, genomic survey sequence.//5.5e-11:275:64//B69224

F-HEMBA1000942//Homo sapiens clone DJ0754G14, WORKING DRAFT SEQUENCE, 15 unordered pieces.//9.7e-05:78:83//AC004878

15 F-HEMBA1000943//Homo sapiens chromosome 17, clone hRPK.640_I_15, complete sequence.//5.8e-140:661:99//AC005324

F-HEMBA1000946

F-HEMBA1000960//Homo sapiens clone DJ1111F22, WORKING DRAFT SEQUENCE, 12 unordered pieces.//8.3e-16:181:75//AC004967

20 F-HEMBA1000968//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 69M21, WORKING DRAFT SEQUENCE.//4.4e-117:398:86//AL031735

F-HEMBA1000971//H.sapiens CpG island DNA genomic Mse1 fragment, clone 182f4, forward read cpg182f4 ft1a.//1.5e-20:126:96//Z57528

25 F-HEMBA1000972//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 1/11.//0.34:642:59//AB020858

F-HEMBA1000974//Homo sapiens clone DA0091H08, complete sequence.//5.1e-183:865:98//AC004817

F-HEMBA1000975//Orf virus homologue of retroviral pseudoprotease gene, complete cds.//0.00065:391:62//M30023

30 F-HEMBA10009851//Human DNA sequence from clone 272E8 on chromosome Xp22.13-22.31. Contains a pseudogene similar to MDM2-Like P53-binding protein gene. Contains STSs, GSSs and a CA repeat polymorphism, complete sequence.//3.4e-05:243:65//Z93929

F-HEMBA1000986//Homo sapiens DNA from chromosome 19-cosmid R31491, genomic sequence.//6.6e-06:508:61//AD000813

F-HEMBA1000991//Homo sapiens mRNA for Hrs, complete cds.//1.2e-22:193:84//D84064 F-HEMBA1001007

35 F-HEMBA1001008//Human DNA sequence from clone 391O22 on chromosome 6p21.2-21.31 Contains pseudogenes similar to ribosomal protein, ESTs, GSSs, complete sequence.//7.8e-46:532:73//AL031577

F-HEMBA1001009//Human mRNA for IgM heavy chain complete sequence.//0.97:369:59//X17115

F-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds.//4.4e-139:661:98//AB007937

F-HEMBA1001019//Homo sapiens, clone hRPK.15_A_1, complete sequence.//1.6e-16:521:64//AC006213

40 F-HEMBA1001020//Homo sapiens chromosome 17, clone hRPK.178_C_3, complete sequence.//3.8e-50:367:72//AC005702

F-HEMBA1001022

F-HEMBA1001024//Homo sapiens T-cell receptor alpha delta locus from bases 1 to 250529 (section 1 of 5) of the Complete Nucleotide Sequence.//5.0e-23:378:69//AE000658

45 F-HEMBA1001026//Homo sapiens DNA sequence from PAC 435D1 on chromosome Xq25. Contains ESTs and STS.//7.6e-19:867:60//Z86064

F-HEMBA1001043//HS_2219_B1_A10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2219 Col=19 Row=B, genomic survey sequence.//3.0e-15:124:88//AQ301521

F-HEMBA1001051//Human Chromosome X clone bWDX342, complete sequence.//4.8e-79:308:84//AC004072

50 F-HEMBA1001052//Homo sapiens chromosome 17, clone hRPK.146_P_2, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.53:384:61//AC005341

F-HEMBA1001059//Human N-acetylgalactosamine 6-sulphatase (GALNS) gene, exon 10.//2.8e-26:397:71//U06084

55 F-HEMBA1001060//Homo sapiens chromosome 17, clone hRPK.855_D_21 complete sequence.//0.98:280:62//AC006079

F-HEMBA1001061//Homo sapiens DNA sequence from clone 272E8 on chromosome Xp22.13-22.31

F-HEMBA1001062//Human nuclear protein, complete cds.//3.6e-13:338:65//S7821

F-HEMBA1001080//Streptomyces coelicolor cosmid XA1000012.364.63//AL034446

F-HEMBA1001085//Human Chromosome 15q26.1 PAC clone pDJ290i21 containing fur, fes, and alpha mannosidase IIx genes, WORKING DRAFT SEQUENCE, 9 unordered pieces.//8.5e-134:476:96//AC004586

F-HEMBA1001088//Sequence 1 from patent US 5552529.//2.2e-71:303:78//I25863

F-HEMBA1001094//Homo sapiens clone RG491N20, complete sequence.//8.9e-119:609:96//AC005105

5 F-HEMBA1001099

F-HEMBA1001109//Homo sapiens BAC clone RG318M05 from 7q22-q31.1, complete sequence.//2.4e-58:347:87//AC005250

F-HEMBA1001121//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 90G24, WORKING DRAFT SEQUENCE.//3.4e-21:226:65//AL008723

10 F-HEMBA1001122//Plasmodium falciparum chromosome 2, section 20 of 73 of the complete sequence.//9.2e-07:732:57//AE001383

F-HEMBA1001123//Homo sapiens full-length insert cDNA clone ZD38E12.//1.1e-11:231:68//AF086247

F-HEMBA1001133//Homo sapiens clone DJ0856O24, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.011:163:69//AC004909

15 F-HEMBA1001137//Homo sapiens mRNA for KIAA0798 protein, complete cds.//6.9e-72:527:77//AB018341

F-HEMBA1001140//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.3e-120:578:98//AC005077

F-HEMBA1001172//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.010:520:59//AC005507

20 F-HEMBA1001174//R.norvegicus (Sprague Dawley) ARL5 mRNA for ARF-like protein 5.//1.0e-59:565:73//X78604

F-HEMBA1001197//Homo sapiens clone 82F9, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.0037:151:70//AC004815

F-HEMBA1001208//Human BAC clone RG264L19 from 7p15-p21, complete sequence.//7.4e-35:195:81//AC002410

25 F-HEMBA1001213//Homo sapiens clone DJ0892G19, complete sequence.//1.9e-171:826:98//AC004917

F-HEMBA1001226//Homo sapiens clone DJ0850101, WORKING DRAFT SEQUENCE, 1 unordered pieces.//0.00010:557:57//AC006009

F-HEMBA1001235//Homo sapiens chromosome 17, clone hRPK.601_N_13, complete sequence.//0.0086:372:58//AC005389

30 F-HEMBA1001247//H.sapiens CpG island DNA genomic MseI fragment, clone 11b11, reverse read cpg11b11.rt1a.//2.0e-24:154:93//Z64441

F-HEMBA1001257//Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds.//1.9e-88:659:81//AF047020

F-HEMBA1001265//Human 18S ribosomal RNA.//1.0e-32:180:97//X03205

35 F-HEMBA1001281

F-HEMBA1001286//B.taurus mRNA for RF-36-DNA-binding protein.//7.7e-26:236:81//X15543

F-HEMBA1001289//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12, complete sequence.//5.5e-28:530:64//AC004131

F-HEMBA1001294//Yeast mitochondrial aapl gene for ATPase subunit 8.//2.8e-15:722:60//X00960

40 F-HEMBA1001299//Human DNA sequence from clone 422G23 on chromosome 6q24 Contains EST, STS, GSS, CpG island, complete sequence.//4.2e-24:288:76//AL031003

F-HEMBA1001302//cDNA encoding a human homologue of a mouse novel polypeptide derived from stromal cell.//7.2e-121:439:96//E12260

45 F-HEMBA1001303//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.011:637:56//AC005505

F-HEMBA1001310//HS_3252_B2_B12_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=24 Row=D, genomic survey sequence.//1.2e-16:166:82//AQ217054

F-HEMBA1001319//CIT-HSP-2034J6.TF CIT-HSP Homo sapiens genomic clone 2034J6, genomic survey sequence.//0.33:256:59//B79408

50 F-HEMBA1001323//Homo sapiens proto-oncogene (Wnt-5a) mRNA, complete cds.//7.8e-30:165:99//L20861

F-HEMBA1001326//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs(BAC end sequences) and a CA repeat polymorphism, complete sequence.//5.4e-19:347:68//AL021368

55 F-HEMBA1001327//CIT-HSP-2354F1.CIT-HSP Homo sapiens genomic clone 2354F1, genomic survey sequence.//0.12:659:82//AF047020

F-HEMBA1001330//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.011:637:56//AC005505

plete sequence.//0.0037:254:62//AL010208

F-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds //1.1e-103:
516:97//AF057358

F-HEMBA1001361//Homo sapiens chromosome 9, clone hRPK.202_H_3, complete sequence.//1.7e-150:706:99//AC006241

F-HEMBA1001375//*Streptomyces coelicolor* cosmid 1E6.//1.0:375:59//AL033505

F-HEMBA1001377//HS_2020_B1_D12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3020 Col=23 Row=H, genomic survey sequence//0.00022:63:77//AQ105297

F-HEMBA1001383//Plasmodium falciparum chromosome 2, section 68 of 73 of the complete sequence//0.00035:317:60//AE001431

F-HEMBA1001387//HS_3039_B1_D01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3039 Col=1 Row=H, genomic survey sequence.//5.0e-90:437:98//AQ155035

F-HEMBA1001388//Homo sapiens clone RG189J21, WORKING DRAFT SEQUENCE, 15 unordered pieces.//
4.2e-47:159:89//AC005073

F-HEMBA1001391//Human DNA sequence from clone 409O10 on chromosome 20q12 Contains CA repeat, GSS, STS, complete sequence//2.0e-06:495:60//AL031256

F-HEMBA1001398//H.sapiens CpG island DNA genomic Mse1 fragment, clone 70d11, forward read
cpg70d11.ft1b//0.018:46:97//Z62591

F-HEMBA1001405//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50024, WORKING DRAFT SEQUENCE.//2.3e-74:623:71//AL034380

F-HEMBA1001407//Mus musculus domesticus Torino (Sry) gene, complete cds.//0.36:363:57//U03645

F-HEMBA1001411//Homo sapiens genomic DNA, 21q region, clone: S39BG29, genomic survey sequence.//8.4e-12:516:60//AG001050

F HEMBA1001413

F-HEMBA1001415//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 410I8, WORKING
DRAFT SEQUENCE.//0.98:177:64//AL031732

F-HEMBA1001432//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces//
8.0e-177:859:97//AC006146

F-HEMBA1001433//Homo sapiens clone DJ0892G19, complete sequence.//2.0e-35:376:64//AC004917

F-HEMBA1001435//Homo sapiens chromosome 17, clone hRPK.63_A_1, complete sequence.//1.2e-74:284:84//AC005670

F-HEMBA1001442//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-66, complete sequence.//0.056:194:63//AL010138

F-HEMBA1001446//Homo sapiens chromosome 4 clone B150J4 map 4q25, complete sequence.//0.96:328:61//AC004047

F-HEMBA1001450

F-HEMBA1001454//Human DNA sequence from clone 598A24 on chromosome Xp11.1-11.23 Contains zinc finger X-linked proteins ZXDA, ZXDB, ESTs and STS, complete sequence//2.0e-47:468:73//AL031115

F-HEMBA1001455//CIT978SK-32J2.TV CIT978SK Homo sapiens genomic clone 32J2, genomic survey sequence.//1.5e-05:223:65//B78859

F-HEMBA1001463//cSRL-69d1-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone
cSRL-69d1, genomic survey sequence.//5.1e-66:564:77//B05652

F-HEMBA1001476//Homo sapiens mRNA for KIAA0572 protein, partial cds.//1.9e-102:489:99//AB011144

F-HEMBA1001478//HS_2228_A2_B03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=6 Row=C, genomic survey sequence.//4.5e-40:275:88//AQ032041

F-HEMBA1001497//Human DNA sequence from clone 281H8 on chromosome 6q25.1-25.3. Contains up to four novel genes, one with similarity to KIAA0323 and worm C30F12.1 and another with Ubiquitin-Like protein gene SMT3 (the latter in an intron of a novel gene). Contains ESTs, STSs, GSSs, a putative CpG island and genomic marker D6S1553, complete sequence.//7.7e-47;311:85//AL031133

F-HEMBA1001510//Human HLA class III region containing cAMP response element binding protein-related protein (CREB-RP) and tenascin X (tenascin-X) genes, complete cds, complete sequence.//2.0e-130:699:93/U89337

F-HEMBA1001515//Homo sapiens chromosome 19, cosmid F24866, complete sequence.//4.1e-114:711:85//
AC005794

F-HEMBA1001517//Homo sapiens BAC clone RG459N13 from 7p15, complete sequence.//5.7e-162:769:98//AC004549

F. HEMBA1001522⁴Campylobacteritis elegans DSM 2428 (8.6) 1.7 1.0 0.5 1.4

* MBA (20 kb) map. The sequence from cosmid 444G8 (the contig from the 12 Mb array) contains the promoter, Mr. 1 (567 bp), and open reading frame. It also contains 5' and 3' UTR regions.

F-HEMBA1001533

F-HEMBA1001557//*Chionoecetes opilio* (clone COP41) DNA microsatellite repeat regions.//7.0e-25:303:72//L49136

F-HEMBA1001566//Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethylaniline Monooxygenase (N-Oxide 3, EC1.14.13.8, Dimethylaniline Oxidase 3, FMO II, FMO 3), and a gene for another, unknown, Flavin-containing Monooxygenase family protein. Contains ESTs and GSSs, complete sequence.//7.2e-18:805:60//AL021026

F-HEMBA1001569//Homo sapiens mRNA for vesicle associated membrane protein 2 (VAMP2).//1.1e-64:338:95//AJ225044

F-HEMBA1001570//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence.//2.1e-148:698:99//AC004453

F-HEMBA1001579//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//2.2e-173:678:99//AJ012449

F-HEMBA1001581//Homo sapiens clone DJ1158B01, WORKING DRAFT SEQUENCE, 23 unordered pieces.//0.30:484:59//AC004980

F-HEMBA1001585

F-HEMBA1001589//Human BAC clone RG317G18 from 7q31, complete sequence.//0.98:197:63//AC002432

F-HEMBA1001595//Human mRNA for KIAA0128 gene, partial cds.//8.2e-109:855:78//D50918

F-HEMBA1001608//RPCI11-72E2.TJ RPCI11 Homo sapiens genomic clone R-72E2, genomic survey sequence.//3.8e-05:235:64//AQ267131

F-HEMBA1001620//*Oryza sativa* RINO1 mRNA for myo-inositol phosphate synthase, complete cds.//3.8e-40:719:64//AB012107

F-HEMBA1001635//HS_3208_A1_D07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3208 Col=13 Row=G, genomic survey sequence.//1.4e-15:120:90//AQ176944

F-HEMBA1001636//Homo sapiens 12q24 PAC RPCI1-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//0.15:221:64//AC004216

F-HEMBA1001640//HS_3253_B2_D03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3253 Col=6 Row=H, genomic survey sequence.//9.1e-52:278:95//AQ216058

F-HEMBA1001647//H.sapiens gene for plectin.//0.00052:629:61//Z54367

F-HEMBA1001651//*Salmo salar* DNA for a cryptic repeat.//7.9e-08:270:64//AJ012206

F-HEMBA1001655//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.//5.9e-164:802:97//AC005368

F-HEMBA1001658//*M.musculus* COL3A1 gene for collagen alpha-I.//2.4e-30:742:62//X52046

F-HEMBA1001661//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//2.2e-144:682:99//AC005740

F-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds.//6.1e-152:725:98//AF072247

F-HEMBA1001675//RPCI11-54F8.TV RPCI11 Homo sapiens genomic clone R-54F8, genomic survey sequence.//5.3e-75:341:85//AQ082126

F-HEMBA1001678//Homo sapiens Xp22 PAC RPCI1-167A22 (from Roswell Park Cancer Center) complete sequence.//8.4e-54:551:74//AC002349

F-HEMBA1001681

F-HEMBA1001702//*Plasmodium falciparum* chromosome 2, section 35 of 73 of the complete sequence.//0.94:676:54//AE001398

F-HEMBA1001709//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 702J19, WORKING DRAFT SEQUENCE.//0.74:659:58//AL033531

F-HEMBA1001711//*Lysiphlebus melandriicola* NADH dehydrogenase 1 gene, mitochondrial gene encoding mitochondrial protein, partial cds.//3.0e-07:413:60//AF069178

F-HEMBA1001712//Homo sapiens BAC clone RG041H04 from 7q21-q22, complete sequence.//0.091:315:61//AC004519

F-HEMBA1001714//*Rattus norvegicus* mitochondrial ATPase inhibitor gene, complete cds.//1.6e-28:218:75//U12250

F-HEMBA1001718//HS_3056_A2_H08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3056 Col=16 Row=O, genomic survey sequence.//2.0e-79:383:99//AQ106367

F-HEMBA1001723//HS_2188_A2_D02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2188 Col=4 Row=G, genomic survey sequence.//3.8e-28:174:94//AQ116795

F-HEMBA1001724//HS_2188_A2_D02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2188 Col=4 Row=G, genomic survey sequence.//2.5e-15:420:62//AQ154658

F-HEMBA1001734//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//0.00060:392:60//AC004617

F-HEMBA1001744//HS_3194_A1_D05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3194 Col=9 Row=G, genomic survey sequence.//5.8e-29:163:97//AQ252295

F-HEMBA1001745//Homo sapiens chromosome 9q34, clone 280C11, complete sequence.//0.66:627:59//AC002102

F-HEMBA1001746//HS_2163_B1_F04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2163 Col=7 Row=L, genomic survey sequence.//1.4e-16:238:70//AQ085995

F-HEMBA1001761//Genomic sequence from Mouse 9, complete sequence.//3.5e-52:198:86//AC002109

F-HEMBA1001781

F-HEMBA1001784//Genomic sequence from Human 9q34, WORKING DRAFT SEQUENCE, 2 unordered-pieces.//5.5e-13:296:65//AC002099

F-HEMBA1001791//Homo sapiens DNA from chromosome 19-cosmids R31158, R31874, and R28125, genomic sequence, complete sequence.//0.18:534:59//AF038458

F-HEMBA1001800//CrT-HFP-2049N5.TF CIT-HSP Homo sapiens genomic clone 2049N5, genomic survey sequence.//2.2e-40:335:80//AQ009222

F-HEMBA1001803//M.musculus (Ba1b/C) P/L01 mRNA.//1.7e-25:286:74//Z31360

F-HEMBA1001804//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//1.9e-58:358:89//M21977

F-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500.//7.8e-174:809:98//AB007969

F-HEMBA1001809//Bovine herpesvirus 1 complete genome.//9.0e-09:639:57//AJ004801

F-HEMBA1001815

F-HEMBA1001819//HS_3079_B1_E04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3079 Col=7 Row=J, genomic survey sequence.//1.4e-79:396:97//AQ186616

F-HEMBA1001820//Homo sapiens BAC clone GS165L15 from 7p15, complete sequence.//0.00026:436:60//AC005013

F-HEMBA1001822//Homo sapiens intersectin short form mRNA, complete cds.//1.2e-40:510:65//AF064243

F-HEMBA1001824//Homo sapiens expanded SCA7 CAG repeat.//6.1e-20:344:68//AF020275

F-HEMBA1001835//Homo sapiens BAC clone RG017K18 from 7q31, complete sequence.//0.0094:553:58//AC005161

F-HEMBA1001844//Homo sapiens chromosome Xp22-135-136 clone GSHB-56711, WORKING DRAFT SEQUENCE, 35 unordered pieces.//1.2e-22:316:70//AC005867

F-HEMBA1001847//M.musculus Zfp-29 gene for zinc finger protein.//5.3e-27:397:69//X55126

F-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds.//8.8e-184:865:98//AB014517

F-HEMBA1001864//Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence.//0.38:337:62//AC005395

F-HEMBA1001866//Caenorhabditis elegans cosmid F48E3.//1.4e-10:224:63//U28735

F-HEMBA1001869//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//6.7e-98:288:91//AC005065

F-HEMBA1001888//Human Chromosome 11p15.5 PAC clone pDJ915f1 containing KvLQT1 gene, complete sequence.//4.9e-114:476:84//AC003693

F-HEMBA1001896//Bos taurus pyruvate dehydrogenase phosphatase regulatory subunit precursor, mRNA, complete cds.//2.2e-137:839:86//AF026954

F-HEMBA1001910//Homo sapiens Chromosome 2p13 BAC Clone h173, complete sequence.//0.90:221:63//AC003065

F-HEMBA1001912//HS_2237_A1_C10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=19 Row=E, genomic survey sequence.//9.7e-76:364:100//AQ033732

F-HEMBA1001913//Leishmania major chromosome 3 clone L4625 strain Friedlin, WORKING DRAFT SEQUENCE, 6 unordered pieces.//0.00063:219:65//AC005766

F-HEMBA1001915//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 5/10.//0.00011:366:63//AB020873

F-HEMBA1001918//Pneumocystis carinii gene for major surface glycoprotein MSG105, exon1-2, complete cds.//0.00024:562:58//D82031

F-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds.//2.1e-184:855:99//AF000145

F-HEMBA1001922//Homo sapiens cDNA for tax-transcriptionally activated glycoprotein (34kDa) (CX40 ligand) (CX40L) and a GOT2 (Aspartate Aminotransferase) (mitochondrial precursor) (EC 2.6.1.1) (transaminase A) (Glutamate Oxaloacetate Transaminase-2)

pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//1.1e-42:380:80//AL022310
 F-HEMBA1001940//Homo sapiens clone DJ1093116, WORKING DRAFT SEQUENCE, 5 unordered pieces.//7.5e-175:861:97//AC005629
 F-HEMBA1001942//Homo sapiens chromosome 12p13.3 clone RPC11-96H9, WORKING DRAFT SEQUENCE, 66 unordered pieces.//0.097:107:71//AC006057
 F-HEMBA1001945//Drosophila F family transposable element F12 3' region.//0.94:140:65//X01934
 F-HEMBA1001950//H.sapiens CpG island DNA genomic Mse1 fragment, clone 15b5, forward read cpg15b5.ft1q.//1.4e-27:168:95//Z54728
 F-HEMBA1001960//Locusta migratoria mRNA for nAChR alpha1 subunit.//0.010:108:71//AJ000390
 F-HEMBA1001962//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//9.7e-05:494:60//AC005507
 F-HEMBA1001964
 F-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/Threonine Protein Kinase gene (presumptive isolog of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and GSSs, complete sequence.//9.6e-122:373:99//AL031178
 F-HEMBA1001979//HS_3067_B1_A06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3067 Col=11 Row=B, genomic survey sequence.//0.43:193:64//AQ143506
 F-HEMBA1001987//Plasmodium falciparum MAL3P6, complete sequence.//1.0:428:56//Z98551
 F-HEMBA1001991//HS_2237_A2_G09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=18 Row=M, genomic survey sequence.//4.3e-05:240:64//AQ067283
 F-HEMBA1002003//protein phosphatase 2C isoform [rats, liver, mRNA, 1950 nt].//2.7e-33:364:74//S90449
 F-HEMBA1002008//WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.00032:214:68//AC005948
 F-HEMBA1002018
 F-HEMBA10020227//Human p37NB mRNA, complete cds.//0.014:58:96//U32907
 F-HEMBA1002035//Mouse transcriptional control element.//7.8e-07:200:69//M17284
 F-HEMBA1002039//Human DNA sequence from clone 267M20 on chromosome Xq22.2-22.3. Contains part of the DIAPH2 gene and a pseudogene, ESTs, STSs and GSSs, complete sequence.//0.31:497:58//AL031053
 F-HEMBA1002049//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence.//4.5e-42:532:63//AC005216
 F-HEMBA1002084//Homo sapiens chromosome 19 cosmid F15386, genomic sequence, complete sequence.//0.81:435:59//AF025422
 F-HEMBA1002092//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//7.2e-130:769:87//U92703
 F-HEMBA1002100//Homo sapiens PAC clone DJ0991G20, complete sequence.//1.3e-47:124:96//AC004943
 F-HEMBA1002102//Xenopus laevis mRNA for xSox7 protein, complete cds.//2.7e-13:132:71//D83649
 F-HEMBA1002113//F.rubripes GSS sequence, clone 063K10bB4, genomic survey sequence.//0.029:142:66//Z88840
 F-HEMBA1002119//Human Chromosome 11 pac pDJ1173a5, complete sequence.//1.3e-14:515:62//AC000378
 F-HEMBA1002125//Homo sapiens calcium-activated potassium channel (KCNN3) mRNA, complete cds.//0.98:222:61//AF031815
 F-HEMBA1002139//Caenorhabditis elegans cosmid F55C9, complete sequence.//0.0081:371:60//Z81549
 F-HEMBA1002144//Saccharomyces cerevisiae mitochondrion transfer RNA-Met (tRNA-Met) gene, oxil gene, and ORF1.//4.9e-06:341:61//L36888
 F-HEMBA1002150//Homo sapiens mRNA for KIAA0720 protein, partial cds.//0.00017:353:62//AB018263
 F-HEMBA1002151
 F-HEMBA1002153//CITBI-E1-2519120.TR CITBI-E1 Homo sapiens genomic clone 2519120, genomic survey sequence.//8.5e-61:334:94//AQ277613
 F-HEMBA1002160//Homo sapiens clone DJ1189D06, complete sequence.//8.5e-44:385:77//AC005232
 F-HEMBA1002161//Coturnix coturnix slow myosin heavy chain 2 (qmyhc2) mRNA, partial cds.//2.1e-59:571:74//AF006829
 F-HEMBA1002162//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//5.3e-53:698:67//AC006210
 F-HEMBA1002166//Human DNA sequence from PAC 84F12 on chromosome Xq25-Xq26.3. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2), ESTs and CA repeat.//1.2e-50:319:78//AL008712
 F-HEMBA1002177//Homo sapiens BAC clone RG293F11 from 7q21-7q22, complete sequence.//2.5e-18:150:88//AC000066
 F-HEMBA1002200//Homo sapiens clone DJ1093116, WORKING DRAFT SEQUENCE, 5 unordered pieces.//7.5e-175:861:97//AC005629

F-HEMBA1002189//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces//3.3e-23:176:77//AC005015

F-HEMBA1002191//Homo sapiens mRNA for KIAA0689 protein, partial cds//1.0:382:59//AB014589

F-HEMBA1002199//Homo sapiens chromosome 4 clone B55B24 map 4q25, complete sequence//1.8e-20:368:66//AC005150

5 F-HEMBA1002204//HS_2055_A1_H09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2055 Col=17 Row=O, genomic survey sequence//1.2e-06:178:65//AQ235350

F-HEMBA1002212//S.cerevisiae chromosome IV reading frame ORF YDL101c//0.035:345:60//Z74149

F-HEMBA1002215//M.musculus mRNA for testin//4.6e-80:504:87//X78989

10 F-HEMBA1002226//Homo sapiens Xp22 bins 87-93 PAC RPC11-122K4 (Roswell Park Cancer Institute Human PAC Library) complete sequence//5.7e-63:336:74//AC003035

F-HEMBA1002229//Homo sapiens BAC clone NH0539B24 from 7p15.1-p14, complete sequence//2.6e-39:311:81//AC006044

F-HEMBA1002237//Homo sapiens PAC clone DJ0696N01 from 7p21-p22, complete sequence//1.6e-12:397:64//AC004861

15 F-HEMBA1002241

F-HEMBA1002253

F-HEMBA1002257//Homo sapiens diacylglycerol kinase iota (DGKi) mRNA, complete cds//3.5e-151:731:97//AF061936

20 F-HEMBA1002265//Human DNA sequence from cosmid N28H9 on chromosome 22q11.2-qter contains ESTs, STS and endogenous retrovirus//1.3e-09:313:62//Z71183

F-HEMBA1002267

F-HEMBA1002270//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence//0.069:495:58//AC006210

25 F-HEMBA1002321//Homo sapiens PAC clone DJ0991O23, complete sequence//0.019:564:58//AC004944

F-HEMBA1002328//CIT-HSP-2387N15.TF.1 CIT-HSP Homo sapiens genomic clone 2387N15, genomic survey sequence//1.8e-71:346:99//AQ240836

F-HEMBA1002337//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN8, complete sequence//0.84:547:57//AB020754

30 F-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds//2.4e-185:872:98//AB018314

F-HEMBA1002348//CIT-HSP-2372K24.TR CIT-HSP Homo sapiens genomic clone 2372K24, genomic survey sequence//9.1e-33:230:75//AQ110676

F-HEMBA1002349//Plasmodium falciparum histidine-rich protein II (HRP II) gene, complete cds//9.4e-06:504:57//U69551

35 F-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//7.3e-188:872:99//AF092563

F-HEMBA1002381//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 11/11//2.1e-20:262:72//AB020868

F-HEMBA1002389//D.discoideum spore coat 60 (sp60) gene, 5' flank//0.010:95:73//M34546

40 F-HEMBA1002417//Canis familiaris ZO-3 (zo-3) mRNA, complete cds//6.2e-120:767:85//AF023617

F-HEMBA1002419//HS-1047-A1-F01-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 830 Col=1 Row=K, genomic survey sequence//7.6e-06:111:76//B38165

F-HEMBA1002430//HS_3137_B2_F10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3137 Col=20 Row=L, genomic survey sequence//1.6e-56:367:88//AQ148697

45 F-HEMBA1002439//Dictyostelium discoideum actin 8 gene, 3' UTR//0.67:129:64//M25216

F-HEMBA1002458//Mus musculus REX-3 mRNA, complete cds//1.1e-30:274:72//AF051347

F-HEMBA1002460//Homo sapiens clone DJ1137M13, complete sequence//4.0e-173:822:98//AC005378

F-HEMBA1002462//Sequence 41 from patent US 5708157//9.8e-51:519:73//I80067

F-HEMBA1002469//Human mRNA for KIAA0122 gene, partial cds//4.0e-108:603:92//D50912

50 F-HEMBA1002475//Streptomyces coelicolor cosmid 2H4//0.0068:626:57//AL031514

F-HEMBA1002477//Homo sapiens BAC clone NH0342K06 from 2, complete sequence//1.5e-40:349:78//AC005034

F-HEMBA1002486

F-HEMBA1002495//HS_3218_B1_A12_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=23 Row=B, genomic survey sequence//1.0:179:67//AQ181410

55 F-HEMBA1002498//Homo sapiens full length insert cDNA clone ZD76801 from ZD76801-1

F-HEMBA1002503//Homo sapiens clone ZD742P04 WORKING DRAFT SEQUENCE, 3 unordered pieces//2.4:306:68//AC004877

F-HEMBA1002508//Homo sapiens chromosome 19, cosmid R33516, complete sequence.//2.9e-76:464:83//AC004799

F-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//2.8e-157:738:98//AJ011972

5 F-HEMBA1002515//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 407F11, WORKING DRAFT SEQUENCE.//2.6e-07:307:64//AL022329

F-HEMBA1002538//HS_2185_B2_B04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2185 Col=8 Row=D, genomic survey sequence.//4.7e-37:339:78//AQ298315

10 F-HEMBA1002542//HS_3197_B2_B10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3197 Col=20 Row=D, genomic survey sequence.//3.2e-70:372:95//AQ188792

F-HEMBA1002547//Homo sapiens agrin precursor mRNA, partial cds.//3.5e-137:655:98//AF016903

F-HEMBA1002552//Human Hep27 protein mRNA, complete cds.//8.8e-07:173:68//U31875

F-HEMBA1002555//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0190L06; HTGS phase 1, WORKING DRAFT SEQUENCE, 21 unordered pieces.//2.2e-15:628:60//AC004670

15 F-HEMBA1002558//Human Xp22 BAC CT-285I15 (from CalTech/Research Genetics), PAC RPC11-27C22 (from Roswell Park Cancer Center), and Cosmid U35B5 (from Lawrence Livermore), complete sequence.//2.3e-41:353:76//AC002366

F-HEMBA1002561//Homo sapiens chromosome 17, clone HRPC29G21, complete sequence.//1.1e-39:538:66//AC003687

20 F-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete cds.//1.3e-140:457:99//AF075587

F-HEMBA1002583//CIT-HSP-2321D3.TR CIT-HSP Homo sapiens genomic clone 2321D3, genomic survey sequence.//5.1e-79:385:99//AQ038102

25 F-HEMBA1002590//Homo sapiens chromosome 17, clone hRPK.167_N_20, complete sequence.//1.9e-35:430:70//AC005940

F-HEMBA1002592//Human genomic DNA sequence from clone 308O1 on chromosome Xp11.3-11.4. Contains EST, CA repeat, STS, GSS, CpG island.//4Ae-19:303:71//Z93403

F-HEMBA1002609//Homo sapiens mRNA for KIAA0597 protein, partial cds.//4.4e-175:820:99//AB011169

30 F-HEMBA1002621//Homo sapiens PAC clone DJ0650P09 from 7q21, complete sequence.//0.14:353:58//AC004413

F-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds.//2.9e-187:632:97//AB018351

F-HEMBA1002628//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.5e-05:792:58//AC004153

F-HEMBA1002629//Streptomyces coelicolor cosmid 1A9.//8.4e-08:576:58//AL034446

35 F-HEMBA1002645//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 153G14, WORKING DRAFT SEQUENCE.//5.6e-47:222:86//AL031118

F-HEMBA1002651//Homo sapiens PAC clone DJ0593H12 from 7p31, complete sequence.//3.8e-182:859:99//AC004839

F-HEMBA1002659//Z.mobilis alcohol dehydrogenase I (adhA) gene, complete cds.//0.97:144:66//M32100

40 F-HEMBA1002661//Homo sapiens PAC clone DJ0698G21 from 7p21-p22, complete sequence.//1.3e-116:774:84//AC004535

F-HEMBA1002666

F-HEMBA1002678//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1137F22, WORKING DRAFT SEQUENCE.//5.7e-156:750:98//AL034421

45 F-HEMBA1002679//nbxb0002cC12r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0002F23r, genomic survey sequence.//4.3e-09:517:58//AQ051621

F-HEMBA1002688//Herpes simplex virus type 2 (strain HG52), complete genome.//8.3e-20:651:61//Z86099

F-HEMBA1002696//Mus musculus proteasome regulator PA28 beta subunit gene, complete cds.//7.6e-62:306:81//AF060195

50 F-HEMBA1002703//Homo sapiens mRNA for KIAA0455 protein, complete cds.//1.9e-10:327:62//AB007924

F-HEMBA1002712

F-HEMBA1002716//HS_3064_A1_C10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=19 Row=E, genomic survey sequence.//8.4e-97:491:96//AQ142980

55 F-HEMBA1002728//Homo sapiens chromosome 5, BAC clone 205e20 (LBNL H170), complete sequence.//6.1e-21:217:77//AC004782

F-HEMBA1002730//Homo sapiens chromosome 19, cosmid R33516, complete sequence.//2.9e-76:464:83//AC004799

F-HEMBA1002742//RPC11-27C22 (from Roswell Park Cancer Center), and Cosmid U35B5 (from Lawrence Livermore), complete sequence.//2.3e-41:353:76//AC002366

F-HEMBA1002746//Mus musculus chromosome 19, clone CIT282B21, complete sequence.//7.1e-70:303:82//AC003694

F-HEMBA1002748//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 410I8, WORKING DRAFT SEQUENCE.//0.096:212:62//AL031732

5 F-HEMBA1002750//Homo sapiens chromosome 5, PAC clone 170m10 (LBNL H89), complete sequence.//6.7e-40:232:70//AC004622

F-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds.//9.0e-177:834:98//AB011126

F-HEMBA1002770//cDNA encoding novel rat protein TIP120 which is formed of complex with TBP (TATA binding protein).//1.3e-140:840:88//E12829

10 F-HEMBA1002777//F.rubripes GSS sequence, clone 189C06dB12, genomic survey sequence.//1.1e-28:263:77//AL007965

F-HEMBA1002779//CIT-HSP-2333I1.TF CIT-HSP Homo sapiens genomic clone 2333I1, genomic survey sequence.//1.8e-32:180:98//AQ036891

15 F-HEMBA1002780//Homo sapiens PAC clone DJ0244J05 from 5q31, complete sequence.//7.0e-06:199:67//AC004592

F-HEMBA1002794//H.sapiens mRNA for protein kinase C mu.//0.00015:244:67//X75756

F-HEMBA1002801//Plasmodium falciparum MAL3P2, complete sequence.//0.0010:534:57//AL034558

F-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds.//1.1e-167:820:97//AF071185

20 F-HEMBA1002816//Homo sapiens clone NH0576N21, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.1e-113:254:90//AC005043

F-HEMBA1002818//Cricetulus griseus H411 precursor (H411) mRNA, complete cds.//1.2e-122:760:86//AF046870

F-HEMBA1002826//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS, GSS, complete sequence.//0.0055:235:65//AL022153

25 F-HEMBA1002833//Homo sapiens chromosome 17, clone hRPC.117_B_12, complete sequence.//1.4e-170:744:99//AC004707

F-HEMBA1002850//Ephedrus persicae NADH dehydrogenase 1 gene, mitochondrial gene encoding mitochondrial protein, partial cds.//1.3e-05:334:59//AF069186

F-HEMBA1002863//CIT-HSP-2323A16.TF CIT-HSP Homo sapiens genomic clone 2323A16, genomic survey sequence.//2.9e-140:750:93//AQ028419

30 F-HEMBA1002876//HS_2270_B1_H03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2270 Col=5 Row=P, genomic survey sequence.//0.44:163:64//AQ164031

F-HEMBA1002886

F-HEMBA1002896//Homo sapiens chromosome 5, P1 clone 793C5 (LBNL H58), complete sequence.//0.00015:277:61//AC005195

35 F-HEMBA1002921

F-HEMBA1002924//CIT-HSP-2171H4.TR CIT-HSP Homo sapiens genomic clone 2171H4, genomic survey sequence.//0.0016:175:66//B89715

F-HEMBA1002934//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 862K6, WORKING DRAFT SEQUENCE.//1.2e-169:797:98//AL031681

40 F-HEMBA1002935//Homo sapiens mRNA for KIAA0576 protein, partial cds.//4.9e-173:803:99//AB011148

F-HEMBA1002937//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 702J19, WORKING DRAFT SEQUENCE.//1.2e-163:411:99//AL033531

F-HEMBA1002939//RPCI11-74O14.TJ RPCI11 Homo sapiens genomic clone R-74O14, genomic survey sequence.//1.7e-41:215:99//AQ266676

45 F-HEMBA1002944//RPCI11-55C2.TV RPCI11 Homo sapiens genomic clone R-55C2, genomic survey sequence.//1.7e-37:375:74//AQ082240

F-HEMBA1002951//Homo sapiens chromosome 19, cosmid F20887, complete sequence.//0.00074:683:58//AC005578

50 F-HEMBA1002954//RPCI11-79F7.TV RPCI11 Homo sapiens genomic clone R-79F7, genomic survey sequence.//6.1e-24:250:78//AQ284146

F-HEMBA1002968//HS_2262_B2_G04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2262 Col=8 Row=N, genomic survey sequence.//0.99:270:60//AQ217059

F-HEMBA1002970//RPCI11-5L24.TV RPCI11 Homo sapiens genomic clone RPCI11-5L24, genomic survey sequence.//1.4e-10:189:71//B49289

55 F-HEMBA1002971//CIT-HSP-2363L16.TF CIT-HSP Homo sapiens genomic clone 2363L16, genomic survey sequence.//4.3e-21:181:80//AQ085536

F-HEMBA1002973//Hattus medialis (Hattus medialis) 5'-phosphodiesterase 3B mRNA, partial cds.//1.4e-25:789:100//U0129

F-HEMBA1002997//CIT-HSP-2387H15.TF.1 CIT-HSP Homo sapiens genomic clone 2387H15, genomic survey sequence.//9.5e-17:128:92//AQ240797

F-HEMBA1002999//Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds.//3.1e-62:713:73//U20286

5 F-HEMBA1003021//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.5e-50:331:85//AC005484

F-HEMBA1003033//Drosophila melanogaster, chromosome 3L, region 62A10-62B5, P1 clones DS02777, DS03222, DS02345, and DS04808, complete sequence.//2.6e-20:357:66//AC005557

10 F-HEMBA1003034//Human DNA sequence from 4PTCL, Huntington's Disease Region, chromosome 4p16.3.//4.5e-60:415:73//Z95704

F-HEMBA1003035//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//2.3e-05:591:57//AC004617

F-HEMBA1003037//RPC11-88F2.TJ RPC11 Homo sapiens genomic clone R-88F2, genomic survey sequence.//0.68:230:60//AQ286677

15 F-HEMBA1003041//Homo sapiens PAC clone DJ1163J12 from 7q21.2-q31.1, complete sequence.//8.1e-128:550:94//AC004983

F-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, complete cds.//1.0e-164:777:98//AF054182

20 F-HEMBA1003064//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.5e-07:744:59//AC005505

F-HEMBA1003067//Rat dynorphin gene, exon 3.//1.0:140:63//M32783

F-HEMBA1003071//Homo sapiens alpha2-C4-adrenergic receptor gene, complete cds.//1.5e-20:595:65//U72648

F-HEMBA1003077//CIT-HSP-2366J21.TF CIT-HSP Homo sapiens genomic clone 2366J21, genomic survey sequence.//4.4e-33:176:99//AQ060257

25 F-HEMBA1003078//Homo sapiens DNA sequence from PAC 262D12 on chromosome 1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neuroneurin, Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30S ribosomal protein S14-LIKE gene preceded by a CpG island. Contains ESTs, genomic marker D1S2691 and STSs.//9.4e-43:478:70//Z99297

F-HEMBA1003079//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//0.96:57:85//AC004673

30 F-HEMBA1003083//Homo sapiens PAC clone DJ1182N03 from 7q11.23-q21.1, complete sequence.//8.0e-74:359:81//AC004548

F-HEMBA1003086//Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence.//3.6e-11:734:58//AF001550

35 F-HEMBA1003096//Sequence 4 from patent US 5440017.//5.7e-56:594:71//I13750

F-HEMBA1003098//Human DNA sequence from cosmid SRL11M20, chromosome region 11p13. Contains EST and STS.//1.9e-09:230:69//Z83308

F-HEMBA1003117//Mouse TIS11 primary response gene, complete cds.//0.00054:480:60//M58564

40 F-HEMBA1003129//HS_3139_B2_F05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3139 Col=10 Row=L, genomic survey sequence.//2.3e-100:510:97//AQ187635

F-HEMBA1003133//Mouse BAC CitbCJ7 219m7, genomic sequence, complete sequence.//1.3e-78:370:90//AC005259

F-HEMBA1003136

F-HEMBA1003142//Homo sapiens full-length insert cDNA clone ZC39B06.//6.9e-121:563:100//AF086197

45 F-HEMBA1003148//Homo sapiens mRNA for dachshund protein.//6.7e-183:850:99//AJ005670

F-HEMBA1003166//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-345G4 ~complete genomic sequence, complete sequence.//3.8e-27:229:76//AC002302

F-HEMBA1003175//Homo sapiens genomic DNA for centromeric end of MHC class I region on chromosome 6, WORKING DRAFT SEQUENCE.//9.4e-09:837:58//AB000882

50 F-HEMBA1003179//Homo sapiens DNA sequence from Fosmid 27C3 on chromosome 22q11.2-qter. Contains two possibly alternatively spliced unknown genes, one with homology to a worm protein. Contains ESTs, complete sequence.//5.4e-115:174:98//AL022325

F-HEMBA1003197//Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence.//1.1e-05:473:59//AC005824

55 F-HEMBA1003199//Rattus norvegicus Sprague-Dawley thyroid hormone receptor alpha gene, exon 1.//1.6e-05:267:61//U09302

F-HEMBA1003204//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 409J21, WORKING DRAFT SEQUENCE.//4.7e-26:141:83//Z83824

F-HEMBA1003212//Human Chromosome 11 Overlapping Cosmids cSRL72g7 and cSRL140b8, complete sequence.//1.9e-31:158:86//AC002037

F-HEMBA1003220//Homo sapiens chromosome 17, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//3.4e-24:284:75//AC004150

F-HEMBA1003222//RPC11-47P17.TJ RPC11 Homo sapiens genomic clone R-47P17, genomic survey sequence.//8.7e-39:202:99//AQ202885

F-HEMBA1003229//Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence.//0.86:227:62//AB019230

F-HEMBA1003235//Plasmodium falciparum chromosome 2, section 10 of 73 of the complete sequence.//8.6e-05:372:61//AE001373

F-HEMBA1003250//HS-1063-A1-H02-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 796 Col=3 Row=O, genomic survey sequence.//0.00032:57:96//B46142

F-HEMBA1003257//H.sapiens mRNA for RDC-1 POU domain containing protein.//2.2e-08:531:59//X64624

F-HEMBA1003273//H.sapiens flow-sorted chromosome 6 HindIII-fragment, SC6pA19H4.//0.070:267:64//Z78949

F-HEMBA1003276//CIT-HSP-2301B4.TF CIT-HSP Homo sapiens genomic clone 2301B4, genomic survey sequence.//5.2e-08:295:63//AQ015073

F-HEMBA1003278//HS_3075_A1_G09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=17 Row=M, genomic survey sequence.//0.98:399:58//AQ120599

F-HEMBA1003281//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//4.8e-101:277:97//AC005840

F-HEMBA1003286//Homo sapiens chromosome 3q13 beta-1,4-galactosyltransferase mRNA, complete cds.//9.0e-145:539:97//AF038662

F-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds.//5.0e-166:799:98//AB011109

F-HEMBA1003296//CITBI-E1-2507M8.TR CITBI-E1 Homo sapiens genomic clone 2507M8, genomic survey sequence.//1.9e-05:388:63//AQ262551

F-HEMBA1003304//Budworm mitochondrial partial transfer RNA-Met (tRNA-Met) gene, and partial 12S ribosomal RNA (12S rRNA) gene.//8.0e-05:388:62//L17343

F-HEMBA1003309//Crassostrea gigas clone CN20 microsatellite sequence.//0.0017:210:64//AF051177

F-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds.//4.6e-188:865:99//AB001872

F-HEMBA1003322//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 169I5, WORKING DRAFT SEQUENCE.//2.4e-54:316:87//Z93015

F-HEMBA1003327//CIT-HSP-2024C24.TRB CIT-HSP Homo sapiens genomic clone 2024C24, genomic survey sequence.//8.4e-12:166:76//B67147

F-HEMBA1003328//HS_2230_B2_H08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2230 Col=16 Row=P, genomic survey sequence.//0.026:128:71//AQ153313

F-HEMBA1003330//Homo sapiens wbscr1 (WBSR1) and replication factor C subunit 2 (RFC2) genes, complete cds.//4.0e-160:745:99//AF045555

F-HEMBA1003348//HS_3194_A1_G05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3194 Col=9 Row=M, genomic survey sequence.//5.0e-79:381:99//AQ173779

F-HEMBA1003369//H.vulgare GAA-satellite DNA.//0.12:89:71//Z50100

F-HEMBA1003370//Homo sapiens cosmid 123E15, complete sequence.//3.5e-32:199:80//AF024533

F-HEMBA1003373//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 537K23, WORKING DRAFT SEQUENCE.//0.019:117:71//AL034405

F-HEMBA1003376//Human clone HS4.66 Alu-Ya5 sequence.//4.2e-30:196:85//U67229

F-HEMBA1003380//Homo sapiens DNA sequence from clone 394P21 on chromosome 1p36.12-36.13. Contains the PAX7 gene, locus D1S2644, ESTs and STSs, complete sequence.//4.6e-22:206:81//AL021528

F-HEMBA1003384//Homo sapiens clone GS096J14, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.00094:72:90//AC006026

F-HEMBA1003395//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P1, WORKING DRAFT SEQUENCE.//0.00041:826:57//AL031744

F-HEMBA1003402//CIT-HSP-2339K16.TR CIT-HSP Homo sapiens genomic clone 2339K16, genomic survey sequence.//2.4e-05:265:64//AQ056234

F-HEMBA1003403//Homo sapiens clone

AC00406:

F-HEMBA10034

F-HEMBA1003417//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS, complete sequence//1.9e-41:239:95//AL031321

F-HEMBA1003418//Rattus norvegicus Wistar polymeric immunoglobulin receptor (PIGR) gene, 3'UTR and trinucleotide repeat microsatellites//2.2e-06:247:64//U08273

5 F-HEMBA1003433//Homo sapiens nibrin (NBS) mRNA, complete cds//1.4e-149:697:99//AF051334

F-HEMBA1003447//Homo sapiens chromosome 4 clone B353C18 map 4q25, complete sequence//1.7e-77:461:90//AC004066

F-HEMBA1003461//Rhodobacter sphaeroides FliH (fliH) gene, partial cds, FliI (fliI) and FliJ (fliJ) genes, complete cds//8.6e-08:752:58//U31090

10 F-HEMBA1003463//Homo sapiens chromosome 17, clone HCIT305D20, complete sequence//0.089:172:68//AC004098

F-HEMBA1003480//Homo sapiens clone NH0523H20, complete sequence//4.5e-150:562:97//AC005041

F-HEMBA1003528//Streptomyces fradiae gene for trypsinogen precursor, complete cds//4.7e-09:433:60//D16687

15 F-HEMBA1003531//Homo sapiens PAC clone DJ1185I07 from 7q11.23-q21, complete sequence//2.3e-48:297:90//AC004990

F-HEMBA1003538//Human complement C1r mRNA, complete cds//4.3e-22:474:63//M14058

F-HEMBA1003545//Rattus norvegicus (clone 1.6kb) islet-2 mRNA, complete cds//3.5e-143:805:91//L35571

F-HEMBA1003548

20 F-HEMBA1003555//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 447E6, WORKING DRAFT SEQUENCE//3.4e-58:331:83//AL031724

F-HEMBA1003556//Homo sapiens Xp22-175-176 BAC GSHB-484017 (Genome Systems Human BAC Library) complete sequence//6.0e-99:703:84//AC005913

F-HEMBA1003560//Bovine GTP-binding regulatory protein gamma-6 subunit mRNA, complete cds//1.3e-99:587:89//J05071

25 F-HEMBA1003568//HS_3149_A1_C04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3149 Col=7 Row=E, genomic survey sequence//4.1e-05:389:57//AQ166810

F-HEMBA1003569//Homo sapiens BAC clone NH0335J18 from 2, complete sequence//1.6e-102:669:85//AC005539

F-HEMBA1003571//Dictyostelium discoideum RegA (regA) gene, complete cds//0.00033:649:58//U60170

30 F-HEMBA1003579//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P1, WORKING DRAFT SEQUENCE//0.00034:623:56//AL031744

F-HEMBA1003581//Mouse mRNA for talin//3.3e-41:181:86//X56123

F-HEMBA1003591//Homo sapiens chromosome 16, BAC clone RPCI-11_192K18, complete sequence//4.4e-70:273:94//AC006075

35 F-HEMBA1003595//Plasmodium falciparum chromosome 2, section 32 of 73 of the complete sequence//6.0e-17:768:58//AE001395

F-HEMBA1003597//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence//4.0e-09:777:56//AE001398

40 F-HEMBA1003598//Homo sapiens PAC clone DJ0537P09 from 7p11.2-p12, complete sequence//1.3e-146:692:98//AC005153

F-HEMBA1003615//HS_2010_A2_A07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2010 Col=14 Row=A, genomic survey sequence//1.1e-22:137:97//AQ226592

F-HEMBA1003617//Homo sapiens HRIHFB2157 mRNA, partial cds//2.4e-169:501:97//AB015344

F-HEMBA1003621//Mus musculus PIAS3 mRNA, complete cds//4.7e-37:165:92//AF034080

45 F-HEMBA1003622//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces//0.0024:514:58//AC005139

F-HEMBA1003630//CIT-HSP-2168N15.TR CIT-HSP Homo sapiens genomic clone 2168N15, genomic survey sequence//6.5e-15:358:63//B92984

F-HEMBA1003637//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces//5.0e-21:238:76//AC005077

50 F-HEMBA1003640//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 112K5, WORKING DRAFT SEQUENCE//2.3e-15:371:63//Z85987

F-HEMBA1003645//A.thaliana 81kb genomic sequence//1.0:529:57//X98130

F-HEMBA1003646

55 F-HEMBA1003656

F-HEMBA1003660

AC00574r

F-HEMBA1003667//Homo sapiens chromosome 12p11.2 WORKING DRAFT SEQUENCE, 2 unordered pieces

es.//1.1e-24:190:87//AC004765

F-HEMBA1003679//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//1.7e-162:579:99//AC005065

F-HEMBA1003680//H.sapiens DNA sequence.//7.3e-22:172:87//Z22322

5 F-HEMBA1003684//H.sapiens mRNA for Miz-1 protein.//0.0054:146:70//Y09723

F-HEMBA1003690//Homo sapiens antigen NY-CO-9 (NY-CO-9) mRNA, partial cds.//2.9e-72:606:77//AF039691

F-HEMBA1003692

F-HEMBA1003711//Homo sapiens chromosome 17, clone HRPC41C23, complete sequence.//0.55:450:60//AC003101

10 F-HEMBA1003714

F-HEMBA1003715//Human DNA sequence from clone 931E15 on chromosome Xq25. Contains STSs, GSSs and genomic marker DXS8098, complete sequence.//3.0e-16:316:68//AL023575

F-HEMBA1003720//Homo sapiens chromosome 4 clone B227H22 map 4q25, complete sequence.//1.3e-41:483:73//AC004056

15 F-HEMBA1003725//CIT-HSP-2351H9.TF CIT-HSP Homo sapiens genomic clone 2351H9, genomic survey sequence.//1.1e-112:532:99//AQ079348

F-HEMBA1003729//HS_3043_A1_E07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3043 Col=13 Row=I, genomic survey sequence.//1.6e-12:87:98//AQ129345

F-HEMBA1003733//Homo sapiens, clone hRPK.15_A_1, complete sequence.//4.7e-104:761:82//AC006213

20 F-HEMBA1003742//HS_3027_A2_B02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3027 Col=4 Row=C, genomic survey sequence.//3.4e-08:67:97//AQ154731

F-HEMBA1003758//CIT-HSP-2379D18.TR CIT-HSP Homo sapiens genomic clone 2379D18, genomic survey sequence.//2.9e-10:310:63//AQ113513

F-HEMBA1003760//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds.//6.4e-114:714:86//AF060194

25 F-HEMBA1003773//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.078:378:58//AC005139

F-HEMBA1003783//Human DNA sequence from PAC 509L4 on chromosome 6q22.1-6q22.33. Contains SSX3 like pseudogene, EST, STS.//9.0e-135:804:89//Z99496

30 F-HEMBA1003784//Caenorhabditis elegans cosmid C55B6.//0.054:463:58//U88181

F-HEMBA1003799//Homo sapiens Chromosome 22q11.2 Cosmid Clone 105a In DGCR Region, complete sequence.//1.9e-44:425:76//AC000070

F-HEMBA1003803//Oryctolagus cuniculus troponin T cardiac isoform mRNA, 3' end of cds.//0.95:198:62//L40178

35 F-HEMBA1003804//Homo sapiens chromosome 17, clone hCIT.175_E_5, complete sequence.//1.2e-138:275:99//AC004596

F-HEMBA1003805//Mus musculus quaking type I (QKI) mRNA, complete cds.//6.6e-148:753:95//U44940

F-HEMBA1003807//HS-1068-B1-G06-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 278 Col=11 Row=N, genomic survey sequence.//6.7e-07:241:67//B47212

F-HEMBA1003827//Homo sapiens mRNA for KIAA0616 protein, partial cds.//1.0e-83:586:87//AB014516

40 F-HEMBA1003836//S.cerevisiae chromosome IX cosmid 9150.//5.1e-16:368:63//Z38125

F-HEMBA1003838//CIT-HSP-384J15.TR CIT-HSP Homo sapiens genomic clone 384J15, genomic survey sequence.//1.4e-45:180:90//B54810

F-HEMBA1003856//Homo sapiens chromosome 10 clone CIT9875K-1188B12 map 10p12.1, complete sequence.//0.0014:574:58//AC005875

45 F-HEMBA1003864//, complete sequence.//2.1e-91:234:95//AC005300

F-HEMBA1003866//Mus musculus semaphorin VIa mRNA, complete cds.//5.9e-81:853:71//AF030430

F-HEMBA1003879//H.sapiens CBP80 mRNA.//2.0e-08:87:95//X80030

F-HEMBA1003880//Homo sapiens genomic DNA, chromosome 21q11.1, segment 7/28, WORKING DRAFT SEQUENCE.//1.7e-180:853:98//AP000036

50 F-HEMBA1003885//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence.//4.5e-39:376:67//AC004079

F-HEMBA1003893//H.sapiens CpG island DNA genomic MseI fragment, clone 11b6, forward read cpg11b6.ft1a.//3.6e-32:173:99//Z59012

F-HEMBA1003902//RPCI11-26M20.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-26M20, genomic survey sequence.//8.2e-12:422:61//AQ003455

55 F-HEMBA1003908//H.sapiens DNA sequence

F-HEMBA1003908

F-HEMBA1003926//H.sapiens DNA sequence.//1.3e-104:761:82//AC006213, WORKING

DRAFT SEQUENCE.//3.6e-27:278:76//AL031658

F-HEMBA1003937//Homo sapiens chromosome 3 subtelomeric region.//1.4e-55:315:81//AF109718

F-HEMBA1003939//HS-1047-A1-G04-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 830 Col=7 Row=M, genomic survey sequence.//6.1e-09:413:63//B38195

5 F-HEMBA1003942//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.42:205:65//AC005140

F-HEMBA1003950//M.capricolum DNA for CONTIG MC072.//0.029:458:58//Z33058

F-HEMBA1003953//HS_2268_A1_B04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2268 Col=7 Row=C, genomic survey sequence.//9.0e-07:239:64//AQ085098

10 F-HEMBA1003958//Homo sapiens PAC clone DJ0808G16 from 7q11.23-q21, complete sequence.//2.8e-57:424:74//AC004894

F-HEMBA1003959//RPC111-78E8.TV RPC111 Homo sapiens genomic clone R-78E8, genomic survey sequence.//4.3e-86:441:9611AQ285498

15 F-HEMBA1003976//HS_3146_A1_H09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3146 Col=17 Row=O, genomic survey sequence.//6.3e-10:129:80//AQ141146

F-HEMBA1003978

F-HEMBA1003985//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y105C5, WORKING DRAFT SEQUENCE.//1.0:258:60//Z98855

F-HEMBA1003987

20 F-HEMBA1003989//Streptomyces coelicolor cosmid 1A9.//0.40:238:61//AL034446

F-HEMBA1004000//Rattus norvegicus satellite sequence d0Mco2.//2.0e-07:116:70//U19354

F-HEMBA1004011//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.098:286:60//AC004710

25 F-HEMBA1004012//Homo sapiens chromosome 17, clone hRPK.63_A_1, complete sequence.//2.8e-185:896:97//AC005670

F-HEMBA1004015//Homo sapiens chromosome 17, clone hRPK.721_K_1, complete sequence.//6.3e-68:417:80//AC005411

F-HEMBA1004024//Homo sapiens Xp22-83 BAC GSHB-324M7 (Genome Systems Human BAC Library) complete sequence.//2.0e-47:418:77//AC005859

30 F-HEMBA1004038//Homo sapiens genomic DNA, chromosome 21q11.1, segment 23/28, WORKING DRAFT SEQUENCE.//1.6e-51:564:74//AP000052

F-HEMBA1004042//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//1.2e-05:636:55//AE001398

35 F-HEMBA1004045//Homo sapiens (subclone 1_g7 from BAC H76) DNA sequence, complete sequence.//1.9e-31:373:76//AC002252

F-HEMBA1004048//Homo sapiens DNA for P35-related protein, exon 2.//0.039:234:63//D63393

F-HEMBA1004049//Homo sapiens Xp22 GS-52411 (Genome Systems Human BAC library), complete sequence.//4.8e-135:780:89//AC003106

F-HEMBA1004055//Human chromosome 3p21.1 gene sequence.//4.7e-09:457:58//L13435

40 F-HEMBA1004056//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 447C4, WORKING DRAFT SEQUENCE.//3.3e-25:246:77//AL021977

F-HEMBA1004074//CIT-HSP-2053J5.TF CIT-HSP Homo sapiens genomic clone 2053J5, genomic survey sequence.//7.8e-24:233:76//B68555

45 F-HEMBA1004086//Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.//4.5e-08:614:59//U49822

F-HEMBA1004097//Mus musculus putative transcription factor mRNA, complete cds.//5.9e-121:502:85//AF091234

50 F-HEMBA1004111//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0481P14; HTGS phase 1, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.0e-36:317:80//AC006160

F-HEMBA1004131//Mus musculus clone OST2067, genomic survey sequence.//8.7e-24:320:71//AF046393

F-HEMBA1004132//HS_3226_B1_D10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3226 Col=19 Row=H, genomic survey sequence.//9.7e-13:232:71//AQ182017

F-HEMBA1004133

55 F-HEMBA1004138//HS_3036_B1_G11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3036 Col=21 Row=M, genomic survey sequence.//9.7e-13:232:71//AQ182017

F-HEMBA1004141

F-HEMBA1004142

F-HEMBA1004150//Human DNA sequence from PAC 52D1 on chromosome Xq21. Contains CA repeats, STS.//0.00011:618:60//Z96811

F-HEMBA1004164//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library) complete sequence.//2.9e-30:454:68//AC005913

5 F-HEMBA1004168//Homo sapiens geminin mRNA, complete cds.//4.5e-133:649:97//AF067855

F-HEMBA1004199

F-HEMBA1004200//HS_2015_A1_B05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2015 Col=9 Row=C, genomic survey sequence.//8.5e-34:236:87//AQ247957

10 F-HEMBA1004202//Mus musculus chromosome 11, clone mCIT.268_P_23, complete sequence.//7.8e-59:216:83//AC004807

F-HEMBA1004203//Homo sapiens clone NH0313P13, WORKING DRAFT SEQUENCE, 15 unordered pieces.//6.3e-98:173:98//AC005488

F-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, complete cds.//3.2e-166:791:98//U50748

15 F-HEMBA1004225//Plasmodium falciparum chromosome 2, section 61 of 73 of the complete sequence.//6.5e-08:584:60//AE001424

F-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, complete cds.//8.0e-115:713:86//AF095927

F-HEMBA1004238

20 F-HEMBA1004241//CIC5B11.1 check: 4870 from: 1 to: 167234, complete sequence.//0.57:552:58//AC004708

F-HEMBA1004246//Human DNA sequence from clone 422F24 on chromosome 6q24.1-25.2. Contains a novel gene similar to C. elegans C02C2.5. Contains ESTs, STSs and GSSs, complete sequence.//6.1e-21:254:77//AL031010

25 F-HEMBA1004248//Rattus rattus insulin-induced growth-respons protein (CL-6) mRNA, complete cds.//1.7e-30:315:74//L13619

F-HEMBA1004264//Homo sapiens cosmid clone LUCA20 from 3p21.3, complete sequence.//4.4e-07:674:60//AC004693

F-HEMBA1004267//Homo sapiens chromosome 17, clone hRPC.117_B_12, complete sequence.//3.1e-78:335:87//AC004707

30 F-HEMBA1004272//Homo sapiens 12p13.3 PAC RPCI5-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.4e-176:856:97//AC005831

F-HEMBA1004274//HS_3064_B2_A04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, genomic survey sequence.//3.1e-28:153:100//AQ136993

35 F-HEMBA1004275//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 501A4, WORKING DRAFT SEQUENCE.//5.2e-17:109:99//Z98051

F-HEMBA1004276//CIT-HSP-2387K6.TF.1 CIT-HSP Homo sapiens genomic clone 2387K6, genomic survey sequence.//5.0e-07:63:98//AQ240477

F-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds.//2.1e-185:868:99//AF022795

40 F-HEMBA1004289//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQN23, complete sequence.//1.0:387:59//AB013395

F-HEMBA1004295//Homo sapiens DNA, anonymous heat-stable fragment RP11-3A.//7.8e-06:92:89//AB012254

F-HEMBA1004306//Homo sapiens clone DJ0811N16, complete sequence.//0.00037:413:59//AC004897

45 F-HEMBA1004312//Rickettsia prowazekii strain Madrid E, complete genome; segment 2/4.//0.28:522:57//AJ235271

F-HEMBA1004321//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//7.1e-136:548:92//AC006130

F-HEMBA1004323//Human DNA sequence from PAC 450C20 on chromosome X.//1.3e-32:320:65//Z84720

F-HEMBA1004327//Homo sapiens mRNA for KIAA0522 protein, partial cds.//0.93:222:62//AB011094

50 F-HEMBA1004330//Homo sapiens clone DJ1196H06, WORKING DRAFT SEQUENCE, 4 unordered pieces.//7.0e-168:895:93//AC004995

F-HEMBA1004334//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library) complete sequence.//4.6e-73:713:75//AC002980

55 F-HEMBA1004335//Human DNA-sequence *** SEQUENCING IN PROGRESS *** from clone 417M14, WORKING DRAFT SEQUENCE.//1.3e-25:121:85//AL024498

F-HEMBA1004337

F-HEMBA1004353//Homo sapiens mRNA for KIAA0522 protein, alternatively spliced, complete cds.//4.4e-06:278:85//AF022795

F-HEMBA1004354//Homo sapiens mRNA for KIAA0522 protein, alternatively spliced, complete cds.//4.1e-46:278:85//AF022795

190:92//U75968

F-HEMBA1004356

F-HEMBA1004366//*P.falciparum* complete gene map of plastid-like DNA (IR-A)//2.2e-07:736:57//X95275F-HEMBA1004372//*H.sapiens* dystrophin gene intron 44//1.0:129:62//X77644

5 F-HEMBA1004389//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end//4.7e-42:237:94//M21977

F-HEMBA1004394//*Plasmodium falciparum* chromosome 2, section 39 of 73 of the complete sequence//5.2e-05:519:59//AE001402

F-HEMBA1004396//Human BAC clone RG302F04 from 7q31, complete sequence//4.0e-32:261:76//AC002463

10 F-HEMBA1004405//*Plasmodium falciparum* 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces//1.4e-07:693:58//AC005507F-HEMBA1004408//*Homo sapiens* clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces//1.2e-69:195:100//AC005037F-HEMBA1004429//HS_3193_A1_B06_T7 CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3193 Col=11 Row=C, genomic survey sequence//5.1e-67:386:91//AQ172942

15 F-HEMBA1004433//Human Chromosome 11p11.2 PAC clone pDJ404m15, complete sequence//3.2e-27:242:82//AC002554

F-HEMBA1004460//*Homo sapiens* clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces//1.7e-75:590:81//AC004846

20 F-HEMBA1004461//Human DNA sequence from clone 657J8 on chromosome Xq26.1-26.3 Contains GSS, complete sequence//0.045:215:66//AL034407

F-HEMBA1004479//*Mus musculus* hypoxia inducible factor three alpha mRNA, complete cds//5.2e-43:364:79//AF060194F-HEMBA1004482//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces//6.8e-17:791:59//AC00550525 F-HEMBA1004499//*Homo sapiens* chromosome 17, clone hRPC.1073_F_15, complete sequence//4.4e-125:251:94//AC004686F-HEMBA1004502//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces//0.012:635:57//AC00470930 F-HEMBA1004506//*Homo sapiens* PAC clone DJ0844F09 from 7p12-p13, complete sequence//2.8e-127:766:88//AC004453

F-HEMBA1004507

F-HEMBA1004509//*Arabidopsis thaliana* DNA chromosome 4, BAC clone T10114 (ESSAll project)//1.0e-13:244:67//AL021712

F-HEMBA1004534//Human mRNA for actin-binding protein (filamin) (ABP-280)//1.6e-72:678:74//X53416

35 F-HEMBA1004538//Sequence 1 from patent US 5612190//0.00015:416:59//I36871

F-HEMBA1004542//*Homo sapiens* clone NH0486I22, WORKING DRAFT SEQUENCE, 5 unordered pieces//0.95:202:64//AC005038F-HEMBA1004554//*Arabidopsis thaliana* BAC T26D22//0.45:624:56//AFO58826

F-HEMBA1004560//Human mRNA for KIAA0281 gene, complete cds//9.1e-10:173:70//D87457

40 F-HEMBA1004573//Human BAC clone RG114A06 from 7q31, complete sequence//6.1e-23:134:73//AC002542

F-HEMBA1004577//*Homo sapiens* Chromosome 16 BAC clone CIT987SK-582J2, complete sequence//1.6e-15:190:77//AC004525F-HEMBA1004586//*Homo sapiens* clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces//3.1e-31:388:76//AC00489545 F-HEMBA1004596//RPC111-81O21.TJ RPC111 *Homo sapiens* genomic clone R-81O21, genomic survey sequence//2.2e-90:458:90//AQ285136F-HEMBA1004604//*Mus musculus* COP9 complex subunit 7a (COPS7a) mRNA, complete cds//8.6e-105:699:84//AF07131650 F-HEMBA1004610//*Homo sapiens* PAC clone DJ1163J12 from 7q21.2-q31.1, complete sequence//5.4e-20:267:72//AC004983F-HEMBA1004617//CIT-HSP-2319H15.TF CIT-HSP *Homo sapiens* genomic clone 2319H15, genomic survey sequence//6.2e-26:147:99//AQ034944F-HEMBA1004629//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces//5.6e-06:766:56//AC005504

55 F-HEMBA1004631//Human DNA sequence from PAC 368A4 on chromosome X. Contains ESTs. CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP) like gene and STSs 147c, 13, 11, 10, 28384

F-HEMBA1004632//*Canis familiaris* DNA 10 gene contig 10155, 10156, 10157, 10158, 10159, 10160, 10161, 10162, 10163, 10164, 10165, 10166, 10167, 10168, 10169, 10170, 10171, 10172, 10173, 10174, 10175, 10176, 10177, 10178, 10179, 10180, 10181, 10182, 10183, 10184, 10185, 10186, 10187, 10188, 10189, 10190, 10191, 10192, 10193, 10194, 10195, 10196, 10197, 10198, 10199, 10200, 10201, 10202, 10203, 10204, 10205, 10206, 10207, 10208, 10209, 10210, 10211, 10212, 10213, 10214, 10215, 10216, 10217, 10218, 10219, 10220, 10221, 10222, 10223, 10224, 10225, 10226, 10227, 10228, 10229, 10230, 10231, 10232, 10233, 10234, 10235, 10236, 10237, 10238, 10239, 10240, 10241, 10242, 10243, 10244, 10245, 10246, 10247, 10248, 10249, 10250, 10251, 10252, 10253, 10254, 10255, 10256, 10257, 10258, 10259, 10260, 10261, 10262, 10263, 10264, 10265, 10266, 10267, 10268, 10269, 10270, 10271, 10272, 10273, 10274, 10275, 10276, 10277, 10278, 10279, 10280, 10281, 10282, 10283, 10284, 10285, 10286, 10287, 10288, 10289, 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10433, 10434, 10435, 10436, 10437, 10438, 10439, 10440, 10441, 10442, 10443, 10444, 10445, 10446, 10447, 10448, 10449, 10450, 10451, 10452, 10453, 10454, 10455, 10456, 10457, 10458, 10459, 10460, 10461, 10462, 10463, 10464, 10465, 10466, 10467, 10468, 10469, 10470, 10471, 10472, 10473, 10474, 10475, 10476, 10477, 10478, 10479, 10480, 10481, 10482, 10483, 10484, 10485, 10486, 10487, 10488, 10489, 10490, 10491, 10492, 10493, 10494, 10495, 10496, 10497, 10498, 10499, 10500, 10501, 10502, 10503, 10504, 10505, 10506, 10507, 10508, 10509, 10510, 10511, 10512, 10513, 10514, 10515, 10516, 10517, 10518, 10519, 10520, 10521, 10522, 10523, 10524, 10525, 10526, 10527, 10528, 10529, 10530, 10531, 10532, 10533, 10534, 10535, 10536, 10537, 10538, 10539, 10540, 10541, 10542, 10543, 10544, 10545, 10546, 10547, 10548, 10549, 10550, 10551, 10552, 10553, 10554, 10555, 10556, 10557, 10558, 10559, 10560, 10561, 10562, 10563, 10564, 10565, 10566, 10567, 10568, 10569, 10570, 10571, 10572, 10573, 10574, 10575, 10576, 10577, 10578, 10579, 10580, 10581, 10582, 10583, 10584, 10585, 10586, 10587, 10588, 10589, 10590, 10591, 10592, 10593, 10594, 10595, 10596, 10597, 10598, 10599, 10600, 10601, 10602, 10603, 10604, 10605, 10606, 10607, 10608, 10609, 10610, 10611, 10612, 10613, 10614, 10615, 10616, 10617, 10618, 10619, 10620, 10621, 10622, 10623, 10624, 10625, 10626, 10627, 10628, 10629, 10630, 10631, 10632, 10633, 10634, 10635, 10636, 10637, 10638, 10639, 10640, 10641, 10642, 10643, 10644, 10645, 10646, 10647, 10648, 10649, 10650, 10651, 10652, 10653, 10654, 10655, 10656, 10657, 10658, 10659, 10660, 10661, 10662, 10663, 10664, 10665, 10666, 10667, 10668, 10669, 10670, 10671, 10672, 10673, 10674, 10675, 10676, 10677, 10678, 10679, 10680, 10681, 10682, 10683, 10684, 10685, 10686, 10687, 10688, 10689, 10690, 10691, 10692, 10693, 10694, 10695, 10696, 10697, 10698, 10699, 10700, 10701, 10702, 10703, 10704, 10705, 10706, 10707, 10708, 10709, 10710, 10711, 10712, 10713, 10714, 10715, 10716, 10717, 10718, 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11005, 11006, 11007, 11008, 11009, 11010, 11011, 11012, 11013, 11014, 11015, 11016, 11017, 11018, 11019, 11020, 11021, 11022, 11023, 11024, 11025, 11026, 11027, 11028, 11029, 11030, 11031, 11032, 11033, 11034, 11035, 11036, 11037, 11038, 11039, 11040, 11041, 11042, 11043, 11044, 11045, 11046, 11047, 11048, 11049, 11050, 11051, 11052, 11053, 11054, 11055, 11056, 11057, 11058, 11059, 11060, 11061, 11062, 11063, 11064, 11065, 11066, 11067, 11068, 11069, 11070, 11071, 11072, 11073, 11074, 11075, 11076, 11077, 11078, 11079, 11080, 11081, 11082, 11083, 11084, 11085, 11086, 11087, 11088, 11089, 11090, 11091, 11092, 11093, 11094, 11095, 11096, 11097, 11098, 11099, 11100, 11101, 11102, 11103, 11104, 11105, 11106, 11107, 11108, 11109, 11110, 11111, 11112, 11113, 11114, 11115, 11116, 11117, 11118, 11119, 11120, 11121, 11122, 11123, 11124, 11125, 11126, 11127, 11128, 11129, 11130, 11131, 11132, 11133, 11134, 11135, 11136, 11137, 11138, 11139, 11140, 11141, 11142, 11143, 11144, 11145, 11146, 11147, 11148, 11149, 11150, 11151, 11152, 11153, 11154, 11155, 11156, 11157, 11158, 11159, 11160, 11161, 11162, 11163, 11164, 11165, 11166, 11167, 11168, 11169, 11170, 11171, 11172, 11173, 11174, 11175, 11176, 11177, 11178, 11179, 11180, 11181, 11182, 11183, 11184, 11185, 11186, 11187, 11188, 11189, 11190, 11191, 11192, 11193, 11194, 11195, 11196, 11197, 11198, 11199, 11200, 11201, 11202, 11203, 11204, 11205, 11206, 11207, 11208, 11209, 11210, 11211, 11212, 11213, 11214, 11215, 11216, 11217, 11218, 11219, 11220, 11221, 11222, 11223, 11224, 11225, 11226, 11227, 11228, 11229, 11230, 11231, 11232, 11233, 11234, 11235, 11236, 11237, 11238, 11239, 11240, 11241, 11242, 11243, 11244, 11245, 11246, 11247, 11248, 11249, 11250, 11251, 11252, 11253, 11254, 11255, 11256, 11257, 11258, 11259, 11260, 11261, 11262, 11263, 11264, 11265, 11266, 11267, 11268, 11269, 11270, 11271, 11272, 11273, 11274, 11275, 11276, 11277, 11278, 11279, 11280, 11281, 11282, 11283, 11284, 11285, 11286, 11287, 11288, 11289, 11290, 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11434, 11435, 11436, 11437, 11438, 11439, 11440, 11441, 11442, 11443, 11444, 11445, 11446, 11447, 11448, 11449, 11450, 11451, 11452, 11453, 11454, 11455, 11456, 11457, 11458, 11459, 11460, 11461, 11462, 11463, 11464, 11465, 11466, 11467, 11468, 1

F-HEMBA1004637//G.gallus mRNA for LRP/alpha-2-macroglobulin receptor.//7.8e-47:784:65//X74904
 F-HEMBA1004638//Rattus norvegicus homeodomain protein Nkx6.1 (nkx6.1) mRNA, complete cds.//6.4e-06:458:61//AF004431
 F-HEMBA1004666//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y47D3, WORKING DRAFT SEQUENCE.//0.30:733:55//Z98865
 F-HEMBA1004669//Human DNA sequence from clone 465N24 on chromosome 1p35.1-36.13. Contains two novel genes, ESTs, GSSs and CpG islands, complete sequence.//7.5e-136:521:98//AL031432
 F-HEMBA1004670//Homo sapiens Chromosome 22q12 Cosmid Clone p90g5, complete sequence.//0.43:365:59//AC000045
 F-HEMBA1004672
 F-HEMBA1004693//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.096:651:54//AC005308
 F-HEMBA1004697//CIT-HSP-2326C13.TR CIT-HSP Homo sapiens genomic clone 2326C13, genomic survey sequence.//0.23:238:65//AQ040642
 F-HEMBA1004705//Homo sapiens Xp22 Cosmid U151G1 (from Lawrence Livermore X library) and PAC RPC11-93D11 (from Roswell Park Cancer Center) complete sequence.//2.1e-27:375:72//AC002357
 F-HEMBA1004709//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//1.6e-36:191:91//AC006210
 F-HEMBA1004711//Homo sapiens chromosome 17, clone hRPK.271_K_11, complete sequence.//1.1e-133:639:99//AC005562
 F-HEMBA1004725//RPC11-75013.TJ RPC11 Homo sapiens genomic clone R-75O13, genomic survey sequence.//6.2e-32:169:100//AQ266512
 F-HEMBA1004730//Human BAC clone RG035E18 from 7q31, complete sequence.//8.0e-68:732:72//AC004029
 F-HEMBA1004733//CIT-HSP-2305M23.TF CIT-HSP Homo sapiens genomic clone 2305M23, genomic survey sequence.//4.9e-18:209:69//AQ017556
 F-HEMBA1004734//Arabidopsis thaliana ubiquitin-conjugating enzyme 17 (UBC17) mRNA, complete cds.//1.8e-13:451:62//AF028340
 F-HEMBA1004736//Human DNA Sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinosischisis (X-linked, juvenile) 1 (XLRS1). Contains ESTs, an STS and GSSs, complete sequence.//5.0e-87:646:78//Z94056
 F-HEMBA1004748//Human BAC clone RG204I16 from 7q31, complete sequence.//0.24:526:57//AC002461
 F-HEMBA1004751//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.4e-25:268:76//AC004913
 F-HEMBA1004752//R.norvegicus mRNA for leucocyte common antigen-related protein (3941 bp).//1.1e-07:503:61//X83546
 F-HEMBA1004753//Homo sapiens Chromosome 12 Cosmid Clone 6e5, complete sequence.//4.5e-38:314:81//AC000028
 F-HEMBA1004756//Homo sapiens, complete sequence.//1.4e-111:326:84//AC005854
 F-HEMBA1004758//Sequence 29 from patent US 5534410.//3.9e-135:769:91//I23472
 F-HEMBA1004763//Homo sapiens apoptosis inhibitor survivin gene, complete cds.//3.6e-47:404:79//U75285
 F-HEMBA1004768//Homo sapiens PAC clone DJ0979P20 from 7q33-q35, complete sequence.//6.7e-107:890:78//AC004941
 F-HEMBA1004770//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.9e-09:806:59//AC004709
 F-HEMBA1004771//G.muris ribosomal RNA operon DNA encoding 16S, 23S and 5.8S ribosomal RNA.//0.69:239:61//X65063
 F-HEMBA1004776
 F-HEMBA1004778
 F-HEMBA1004795//Drosophila melanogaster A-kinase anchor protein DAKAP550 mRNA, partial cds.//3.4e-46:778:64//AF003622
 F-HEMBA1004803//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//4.3e-82:580:82//AC004617
 F-HEMBA1004806//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence.//5.4e-07:642:59//AC005083
 F-HEMBA1004807//Human HIV1 tata element modulatory factor mRNA sequence from chromosome 3.//1.4e-46:71:92//U01040
 F-HEMBA1004808//Homo sapiens DNA binding protein 1 (DBP1) mRNA, complete cds.//1.1e-104:661:66//M6621
 F-HEMBA1004829//Homo sapiens Progenitor cell complex genes.//0.0014:343:62//X87672

F-HEMBA1004847//Canine mRNA for 68kDA subunit of signal recognition particle (SRP68)//1.5e-85:512:88//X53744

F-HEMBA1004850//Homo sapiens TGF-beta type I receptor (TGFBRI) gene, exon 1//0.0065:284:61//AF054590

F-HEMBA1004863//Genomic sequence from Mouse 11, complete sequence//0.92:250:59//AC000400

5 F-HEMBA1004864

F-HEMBA1004865//Human DNA sequence from clone 459L4 on chromosome 6p22.3-24.1 Contains EST, STS, GSS, complete sequence//3.6e-12:214:72//AL031120

F-HEMBA1004880//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-319E8, complete sequence//1.1e-08:255:69//AC004020

10 F-HEMBA1004889//Schistocerca americana Antennapedia homeotic protein (Antp) mRNA, complete cds//0.062:155:69//U32943

F-HEMBA1004900//Plasmodium falciparum unidentified mRNA sequence//0.00055:323:60//L12043

F-HEMBA1004909//Homo sapiens chromosome 17, clone 289A8, complete sequence//9.6e-16:166:80//AC003051

15 F-HEMBA1004918//Turritella communis mitochondrial 16S ribosomal RNA gene, partial//0.81:146:65//M94003

F-HEMBA1004923//Human DNA from overlapping chromosome 19-specific cosmids R32543,, and F15613 containing ZNF gene family member, genomic sequence, complete sequence//1.4e-36:338:78//AC003006

F-HEMBA1004929//CIT-HSP-2373116.TR CIT-HSP Homo sapiens genomic clone 2373116, genomic survey sequence//2.4e-86:443:96//AQ108676

20 F-HEMBA1004930//Homo sapiens PAC clone DJ0608H12 from 7q21, complete sequence//4.6e-20:219:73//AC004109

F-HEMBA1004933//HS-1003-A1-E10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 497 Col=19 Row=I, genomic survey sequence//1.4e-28:216:85//B30726

F-HEMBA1004934//Homo sapiens chromosome 21q22.3 PAC 267O10, complete sequence//0.53:222:61//AF042091

25 F-HEMBA1004944//Homo sapiens clone DJ0736H05, WORKING DRAFT SEQUENCE, 5 unordered pieces//1.2e-58:509:78//AC005482

F-HEMBA1004954//HS_2033_A2_A08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2033 Col=16 Row=A, genomic survey sequence//3.7e-47:243:99//AQ229758

30 F-HEMBA1004956//P.falciparum complete gene map of plastid-like DNA (IR-B)//0.048:421:58//X95276

F-HEMBA1004960//Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 8//0.89:333:58//Z97343

F-HEMBA1004972

F-HEMBA1004973//RPC111-66P8.TK RPC111 Homo sapiens genomic clone R-66P8, genomic survey sequence//3.5e-22:245:77//AQ238471

35 F-HEMBA1004977//Homo sapiens full-length insert cDNA clone YZ83B08//9.0e-11:84:98//AF086080

F-HEMBA1004978//CIT-HSP-2354E10.TR CIT-HSP Homo sapiens genomic clone 2354E10, genomic survey sequence//0.0021:152:66//AQ075713

F-HEMBA1004980//HS_3018_A2_E04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=8 Row=I, genomic survey sequence//1.9e-77:392:97//AQ071873

40 F-HEMBA1004983//Albinaria corrugata isolate cor. Prn1.1 16S ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence//0.0030:276:61//AF031680

F-HEMBA1004995//Homo sapiens chromosome 16, cosmid bridge clone 306E6 (LANL), complete sequence//4.2e-138:640:99//AC005590

45 F-HEMBA1005008//Human mariner1 transposase gene, complete consensus sequence//6.8e-20:160:88//U52077

F-HEMBA1005009//Homo sapiens BAF53a (BAF53a) mRNA, complete cds//2.0e-144:668:99//AF041474

F-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds//1.4e-146:693:98//AB014548

F-HEMBA1005029//Homo sapiens DNA sequence from PAC 97D16 on chromosome 6p21.3-22.2. Contains an unknown pseudogene, a 60S Ribosomal protein L24 (L30) LIKE pseudogene and histone genes H2BFC (H2B/c), H4FFP (H4/f pseudogene), H2AFC (H2A/c), H3F1K (H3.1/k) and a tRNA-Val pseudogene and tRNA-Thr gene. Contains ESTs, STSs, GSSs and genomic marker D6S464, complete sequence//2.2e-115:668:90//AL009179

F-HEMBA1005035//Homo sapiens chromosome 17, clone hCIT.175_E_5, complete sequence//4.6e-138:591:98//AC004596

55 F-HEMBA1005039//CIT-HSP-2338L5.TR CIT-HSP Homo sapiens genomic clone 2338L5, genomic survey sequence//3.7e-61:271:88//AQ055486

F-HEMBA1005040//Homo sapiens chromosome 17, clone hCIT.175_E_5, complete sequence//4.6e-138:591:98//AC004596

F-HEMBA1005050//Homo sapiens chromosome 17, clone hCIT.175_E_5, complete cds//0.179:251:63//U07802

F-HEMBA1005062//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.018:560:56//AC004688

F-HEMBA1005066//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 774G10, WORKING DRAFT SEQUENCE.//3.4e-97:432:84//AL034410

5 F-HEMBA1005075//H.sapiens DNA 3' flanking simple sequence region clone wg2c3.//6.9e-07:176:68//X76589

F-HEMBA1005079//CIT-HSP-2325M21.TRB CIT-HSP Homo sapiens genomic clone 2325M21, genomic survey sequence.//2.1e-48:274:93//AQ038720

F-HEMBA1005083//HS_2248_B1_D05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2248 Col=9 Row=H, genomic survey sequence.//3.4e-06:230:64//AQ129575

10 F-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds.//1.3e-161:762:98//AF080561

F-HEMBA1005113//L.esculentum microsatellite repeat DNA region.//0.0038:742:57//X90770

F-HEMBA1005123//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//9.6e-83:479:78//AC004854

15 F-HEMBA1005133//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING DRAFT SEQUENCE.//3.9e-24:576:64//AL023808

F-HEMBA1005149//Homo sapiens PAC clone DJ430N08 from 22q12.1-qter, complete sequence.//4.7e-36:283:80//AC004542

20 F-HEMBA1005152//Homo sapiens chromosome Xp22-67-68, WORKING DRAFT SEQUENCE, 99 unordered pieces.//5.0e-10:332:64//AC004469

F-HEMBA1005159//Homo sapiens genomic DNA, chromosome 21q11.1, segment 1/5, WORKING DRAFT SEQUENCE.//4.0e-10:734:58//AP000023

F-HEMBA1005185//H.sapiens CpG island DNA genomic MseI fragment, clone 91b2, forward read cpg91b2.ft1a./12.2e-14:93:100//Z63847

25 F-HEMBA1005201//Drosophila melanogaster cosmid 152A3.//4.7e-35:679:64//AL009194

F-HEMBA1005202//Canine mRNA for 68kDA subunit of signal recognition particle (SRP68).//6.7e-138:778:90//X53744

F-HEMBA1005206//Drosophila melanogaster Su(P) and anon-73B1 genes and partial o25 gene and Pros26 gene.//7.1e-12:376:62//AJ011320

30 F-HEMBA1005219//Homo sapiens mRNA for KIAA0445 protein, complete cds.//7.1e-05:411:60//AB007914

F-HEMBA1005223//Homo sapiens PAC clone DJ430N08 from 22q12.1-qter, complete sequence.//3.5e-06:212:66//AC004542

F-HEMBA1005232//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.7e-07:625:57//AC005308

35 F-HEMBA1005241//Homo sapiens PAC clone DJ0777O23 from 7p14-p15, complete sequence.//8.7e-45:567:72//AC005154

F-HEMBA1005244//Homo sapiens chromosome X clone U177G4, U152H5, U168D5, 174A6, U172D6, and U186B3 from Xp22, complete sequence.//0.96:298:62//AC002365

F-HEMBA1005251

40 F-HEMBA1005252//Homo sapiens chromosome 17, clone hRPK.318_A_15, complete sequence.//4.5e-160:392:99//AC005837

F-HEMBA1005274//Homo sapiens BAC clone 255A7 from 8q21 containing NBS1 gene, complete sequence.//2.3e-05:496:60//AF069291

45 F-HEMBA1005275//Human DNA sequence from clone 444C7 on chromosome 6p22.3-23. Contains an EST, an STS and GSSs, complete sequence.//5.7e-05:220:64//AL033521

F-HEMBA1005293//Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA, complete cds.//2.4e-20:338:65//U97018

F-HEMBA1005296

50 F-HEMBA1005304//Human DNA sequence from clone 364I22 on chromosome Xq21.31-22.3. Contains an STS and GSSs, complete sequence.//1.6e-51:381:78//AL031012

F-HEMBA1005311

F-HEMBA1005314//Homo sapiens genomic DNA, chromosome 21q11.1, segment 2/28, WORKING DRAFT SEQUENCE.//0.94:226:63//AP000031

F-HEMBA1005315//Homo sapiens BAC810, complete sequence.//9.5e-15:684:62//U85198

55 F-HEMBA1005318//Human DNA sequence from PAC 394F12 on chromosome X contains EST STS CpG island

F-HEMBA1005319//Human DNA sequence from PAC 394F12 on chromosome X contains EST STS CpG island

F-HEMBA1005338//Homo sapiens mRNA for matrilin-4, partial//1.4e-151:740:97//AJ007581
F-HEMBA1005353//CIT-HSP-2310N10.TR CIT-HSP Homo sapiens genomic clone 2310N10, genomic survey sequence//2.1e-86:438:97//AQ016145
F-HEMBA1005359//Human zinc finger protein ZNF137 mRNA, complete cds//1.8e-98:500:88//U09414
F-HEMBA1005367//Mus musculus melastatin mRNA, complete cds//8.3e-72:577:73//AF047714
F-HEMBA1005372//Human DNA sequence from PAC 293E14 contains ESTs, STS//1.3e-07:274:66//Z82900
F-HEMBA1005374//Homo sapiens clone 277F10, WORKING DRAFT SEQUENCE, 5 unordered pieces//1.9e-48:611:69//AC004813
F-HEMBA1005382//HS_3063_B2_F11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3063 Col=22 Row=L, genomic survey sequence//1.6e-27:154:98//AQ103204
F-HEMBA1005389//Plasmodium falciparum telomere nucleotide sequence//4.0e-07:443:61//M23175
F-HEMBA1005394//CIT-HSP-2368B11.TR CIT-HSP Homo sapiens genomic clone 2368B11, genomic survey sequence//7.6e-17:225:71//AQ076749
F-HEMBA1005403//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE//4.5e-131:278:98//AL034379
F-HEMBA1005408//HS_3007_B2_G04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3007 Col=8 Row=N, genomic survey sequence//8.0e-06:218:66//AQ294366
F-HEMBA1005410//Human DNA sequence from cosmid cU120E2, on chromosome X contains Lowe oculocerebrorenal syndrome (OCRL) ESTs and STS//1.5e-41:432:76//Z73496
F-HEMBA1005411
F-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds//1.0e-169:537:99//AF041248
F-HEMBA1005426
F-HEMBA1005443//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence//7.1e-37:260:76//AC006130
F-HEMBA1005447//CIT-HSP-2173N7.TR CIT-HSP Homo sapiens genomic clone 2173N7, genomic survey sequence//5.0e-133:631:98//B93234
F-HEMBA1005468//Human DNA sequence from clone 20J23 on chromosome Xq26.2-27.2 Contains ras-related C3 botulinum toxin substrate 1 (P21-RAC1) (ras-like protein TC25) EST, CA repeat, STS, CpG island, complete sequence//1.5e-118:868:83//AL022576
F-HEMBA1005469//Homo sapiens chromosome 16, P1 clone 96-4B (LANL), complete sequence//1.2e-179:838:99//AC005212
F-HEMBA1005472//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 228H13, WORKING DRAFT SEQUENCE//3.4e-20:187:74//AL031985
F-HEMBA1005474//Homo sapiens genomic DNA, chromosome 21q11.1, segment 12/28, WORKING DRAFT SEQUENCE//4.1e-22:445:65//AP000041
F-HEMBA1005475//CIT-HSP-2322D14.TR CIT-HSP Homo sapiens genomic clone 2322D14, genomic survey sequence//6.7e-51:269:97//AQ026941
F-HEMBA1005497//HS_3097_A2_G05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3097 Col=10 Row=M, genomic survey sequence//1.4e-66:345:96//AQ103810
F-HEMBA1005500//Homo sapiens PAC clone DJ1093017 from 7q11.23-q21, complete sequence//5.4e-178:818:98//AC004957
F-HEMBA1005506//Mus musculus (clone 0EBF17) early B-cell factor (EBF) mRNA, complete cds//2.6e-06:73:98//L12147
F-HEMBA1005508//Homo sapiens clone hRPK.1_A_1, complete sequence//0.00012:455:60//AC006196
F-HEMBA1005511//Homo sapiens MHC class 1 region//3.3e-43:421:77//AF055066
F-HEMBA1005513//Drosophila melanogaster males-absent on the first (mof) gene, complete cds//2.3e-20:352:69//U71219
F-HEMBA1005517//Homo sapiens DNA for (CGG)n trinucleotide repeat region, isolate E7//2.5e-08:431:62//AJ001216
F-HEMBA1005518//M.musculus mRNA for paladin gene//8.2e-90:651:81//X99384
F-HEMBA1005520//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces//7.8e-167:755:99//AC004913
F-HEMBA1005526//Homo sapiens chromosome 9, clone hRPK.202_H_3, complete sequence//2.4e-42:475:73//AC006241
F-HEMBA1005528//Homo sapiens chromosome 9, clone hRPK.202_H_3, complete sequence//2.4e-42:475:73//AC006241

DRAFT SEQUENCE.//9.4e-87:422:99//AL034431

F-HEMBA1005552//Homo sapiens PAC clone DJ0807C15 from 7q34-q36, complete sequence.//6.1e-41:486:68//AC004743

F-HEMBA1005558//Drosophila melanogaster DNA sequence (P1 DS00837 (D87)), complete sequence.//2.9e-19:306:68//AC004377

F-HEMBA1005568//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0093:345:60//AC004153

F-HEMBA1005570//Plasmodium falciparum chromosome 2, section 44 of 73 of the complete sequence.//4.2e-09:592:59//AE001407

F-HEMBA1005576//Homo sapiens mRNA for KIAA0463 protein, partial cds.//5.9e-127:610:98//AB007932

F-HEMBA1005577//HS-1004-A1-E11 -MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 498 Col=21 Row=I, genomic survey sequence.//0.00034:254:64//B30971

F-HEMBA1005581//Rattus norvegicus mRNA for MEGF5, complete cds.//4.0e-57:826:65//AB011531

F-HEMBA1005582//HS_3242_A1_B07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3242 Col=13 Row=C, genomic survey sequence.//1.1e-13:91:98//AQ211275

F-HEMBA1005583

F-HEMBA1005588//Homo sapiens PAC clone DJ1188N21 from 7q11.23-q21.1, complete sequence.//8.7e-31:283:75//AC006025

F-HEMBA1005593//Homo sapiens chromosome 17, clone hRPK.332_H_18, complete sequence.//8.3e-158:748:99//AC005746

F-HEMBA1005595//CIT-HSP-2309F14.TF CIT-HSP Homo sapiens genomic clone 2309F14, genomic survey sequence.//6.4e-30:194:91//AQ016527

F-HEMBA1005606//CIT-HSP-2326I6.TR CIT-HSP Homo sapiens genomic clone 2326I6, genomic survey sequence.//0.0014:132:70//AQ041484

F-HEMBA1005609//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.9e-33:249:85//AC005089

F-HEMBA1005616//Homo sapiens DNA sequence from PAC 43C13 on chromosome Xq21.1-Xq21.3. rab proteins geranylgeranyltransferase component A 1 (rab escort protein 1) (REP-1) (choroideraemia protein) (TCD protein).//6.5e-29:279:69//AL009175

F-HEMBA1005621//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 330012, WORKING DRAFT SEQUENCE.//6.4e-90:158:87//AL031731

F-HEMBA1005627//RPCI11-34P9 TJ RPCI-11 Homo sapiens genomic clone RPCI-11-34P9, genomic survey sequence.//0.014:168:67//AQ045110

F-HEMBA1005631//Homo sapiens PAC clone DJ1086D14, complete sequence.//1.0e-149:736:93//AC004460

F-HEMBA1005632

F-HEMBA1005634//Human DNA sequence from PAC 187N21 on chromosome 6p21.2-6p21.33. Contains ESTs.//6.6e-38:452:67//Z98036

F-HEMBA1005666

F-HEMBA1005670//Homo sapiens PAC clone DJ0665C04 from 7p14-p13, complete sequence.//5.1e-59:687:74//AC004850

F-HEMBA1005679//Homo sapiens clone DJ0425I02, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.0e-47:357:85//AC005478

F-HEMBA1005680

F-HEMBA1005685//RPCI11-23D19.TKBR RPCI-11 Homo sapiens genomic clone RPCI-11-23D19, genomic survey sequence.//0.99:228:63//AQ013742

F-HEMBA1005699//Human ligand for eph-related receptor tyrosine kinases (EPLG8) mRNA, complete cds.//1.4e-72:406:92//U57001

F-HEMBA1005705//Human (D21S172) DNA segment containing (CA) repeat.//0.00040:190:66//X56513

F-HEMBA1005717//Plasmodium falciparum MAL3P1, complete sequence.//0.0099:260:63//Z97348

F-HEMBA1005732//Human mRNA for KIAA0003 gene, complete cds.//8.1e-19:151:88//D14697

F-HEMBA1005737//Homo sapiens PAC clone DJ1099C19 from 7q21-q22, complete sequence.//5.6e-15:157:79//AC005156

F-HEMBA1005746//RPCI11-63N8.TK RPCI11 Homo sapiens genomic clone R-63N8, genomic survey sequence.//1.3e-18:113:100//AQ238535

F-HEMBA1005755//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs and the DXS7 locus with GT and GTC repeats. GenBank accession number: U00001

F-HEMBA1005756//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs and the DXS7 locus with GT and GTC repeats. GenBank accession number: U00001

F-HEMBA1005757//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs and the DXS7 locus with GT and GTC repeats. GenBank accession number: U00001

F-HEMBA1005758//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs and the DXS7 locus with GT and GTC repeats. GenBank accession number: U00001

F-HEMBA1005780//RPCI11-74E19.TJ RPCI11 Homo sapiens genomic clone R-74E19, genomic survey sequence.//0.0011:283:62//AQ268432

F-HEMBA1005813//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence.//0.14:326:61//AC004079

5 F-HEMBA1005815//M.musculus mRNA for skeletal muscle-specific calpain.//6.3e-10:706:59//X92523

F-HEMBA1005822//Mouse Bac 291G16, WORKING DRAFT SEQUENCE, 19 unordered pieces.//0.87:417:56//AC003020

F-HEMBA1005829//Homo sapiens Chromosome 22q11.2 Fosmid Clone f39e1 In DGCR Region, complete sequence.//8.8e-42:370:79//AC000094

10 F-HEMBA1005834//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.1e-42:690:67//AL022577

F-HEMBA1005852//F.rubripes GSS sequence, clone 163A22aE9, genomic survey sequence.//4.3e-07:253:59//AL018749

15 F-HEMBA1005853//CIT-HSP-2289L23.TR CIT-HSP Homo sapiens genomic clone-2289L23, genomic survey sequence.//2.2e-68:333:99//B98952

F-HEMBA1005884//Homo sapiens chromosome 5, BAC clone 78c6 (LBNL H191), complete sequence.//1.9e-57:331:87//AC005351

20 F-HEMBA1005891//Homo sapiens PAC clone DJ0997N05 from 7q11.23-q21.1, complete sequence.//5.1e-182:864:98//AC004945

F-HEMBA1005894//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//3.0e-44:340:80//AC004086

F-HEMBA1005909//Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethylaniline Monooxygenase (N-Oxide 3, EC1.14.13.8, Dimethylaniline Oxidase 3, FMO II, FMO 3), and a gene for another, unknown, Flavin-containing Monooxygenase family protein. Contains ESTs and GSSs, complete sequence.//8.3e-12:828:57//AL021026

25 F-HEMBA1005911//Human DNA sequence from clone 1158E12 on chromosome Xp11.23-11.4 Contains EST, STS, GSS, CpG island, complete sequence.//1.0e-44:328:77//AL031584

30 F-HEMBA1005921//Homo sapiens chromosome 17, clone hRPK.112_H_10, complete sequence.//1.3e-41:431:77//AC005666

F-HEMBA1005931//Homo sapiens chromosome 12p13.3 clone RPCI4-761J14, WORKING DRAFT SEQUENCE, 60 unordered pieces.//1.1e-29:394:70//AC006086

35 F-HEMBA1005934//Homo sapiens PAC clone DJ1140G11 from 14q24.3, complete sequence.//8.1e-06:115:80//AC004974

F-HEMBA1005962//RPCI11-17O15.TV RPCI-11 Homo sapiens genomic clone RPCI-11-17015, genomic survey sequence.//9.5e-36:315:84//B82821

F-HEMBA1005963//HS_3055_A1_E08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=15 Row=I, genomic survey sequence.//9.3e-73:372:97//AQ147357

40 F-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//1.3e-149:697:99//AF082516

F-HEMBA1005991//Plasmodium falciparum chromosome 2, section 45 of 73 of the complete sequence.//6.3e-07:423:60//AE001408

45 F-HEMBA1005999//Homo sapiens chromosome 4 clone C0026P05 map 4P16, complete sequence.//3.8e-09:360:64//AC005599

F-HEMBA1006002

F-HEMBA1006005//Homo sapiens MLL (MLL) gene, exons 1-3, and partial cds.//4.5e-83:495:90//AF036405

F-HEMBA1006031

50 F-HEMBA1006035

F-HEMBA1006036//Human (lambda) DNA for immunoglobulin light chain.//2.4e-59:652:74//D87009

F-HEMBA1006042//Homo sapiens chromosome 10 clone CIT987SK-1057L21 map 10q25, complete sequence.//2.1e-43:330:7011AC005386

F-HEMBA1006067//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.11:433:59//AC004153

55 F-HEMBA1006081

F-HEMBA1006100//Homo sapiens chromosome 10 clone CIT987SK-1143A11 map 10q25, complete sequence.//2.8e-18:180:78//AC005880

F-HEMBA1006108//Human DNA sequence from clone 889N15 on chromosome Xq22.1-22.3. Contains part of the gene for a novel protein similar to X. laevis Cortical Thymocyte-Marker CTX, the possibly alternatively spliced gene for 26S Proteasome subunit p28 (Ankyrin repeat protein), a novel gene and exons 36 through 45 of the COL4A6 for Collagen Alpha 6(IV). Contains ESTs, STSs, GSSs and a putative CpG island, complete sequence.//0.26:84:71//AL031177

F-HEMBA1006121//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 691N24, WORKING DRAFT SEQUENCE.//5.2e-18:147:87//AL031672

F-HEMBA1006124//CIT-HSP-2355B17.TF CIT-HSP Homo sapiens genomic clone 2355B17, genomic survey sequence.//0.044:225:61//AQ058966

F-HEMBA1006130//CIT-HSP-386A20.TF CIT-HSP Homo sapiens genomic clone 386A20, genomic survey sequence.//8.8e-07:173:69//B55085

F-HEMBA1006138//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and GSSs, complete sequence.//7.5e-22:164:75//AL022162

F-HEMBA1006142//, complete sequence.//7.9e-125:586:99//AC005500

F-HEMBA1006155//H.sapiens CpG island DNA genomic MseI fragment, clone 119b6, forward read cpg119b6.ft1a.//1.0:85:72//Z64428

F-HEMBA1006158//Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds.//1.1e-185:852:99//AF048693

F-HEMBA1006173//striatum enriched phosphatase=protein-tyrosine-phosphatase [rat, striata, mRNA, 2815 nt].//8.4e-50:642:73//S49400

F-HEMBA1006182//Homo sapiens Chromosome 15q26.1 PAC clone pDJ105i19, complete sequence.//1.4e-22:194:74//AC005318

F-HEMBA1006198

F-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence.//2.6e-175:836:98//AF070557

F-HEMBA1006248//Pinctada fucata mRNA for insoluble protein, complete cds.//8.2e-05:359:61//D86074

F-HEMBA1006252//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 531H16, WORKING DRAFT SEQUENCE.//0.98:397:58//AL031664

F-HEMBA1006253

F-HEMBA1006259//HS_2231_A1_D10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2231 Col=19 Row=G, genomic survey sequence.//1.2e-11:233:68//AQ152722

F-HEMBA1006268//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//5.2e-27:156:85//AC004673

F-HEMBA1006272//Human endogenous retrovirus gag mRNA.//8.1e-115:847:80//X72791

F-HEMBA1006278//Mus musculus poly(A) polymerase VI mRNA, complete cds.//2.1e-57:665:70//U58134

F-HEMBA1006283

F-HEMBA1006284//Streptomyces fradiae ty lactone synthase, starter module and modules 1-7, (tylG) gene, complete cds.//9.6e-06:623:60//U78289

F-HEMBA1006291//HS_2208_A1_C03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2208 Col=5 Row=E, genomic survey sequence.//1.2e-13:105:92//AQ091804

F-HEMBA1006293//Sequence 8 from patent US 5721351.//5.6e-77:580:75//I89415

F-HEMBA1006309//Caenorhabditis elegans cosmid F01F1.//1.1e-21:420:63//U13070

F-HEMBA1006310//Rattus norvegicus cytosolic sorting protein PACS-1a (PACS-1) mRNA, complete cds.//6.8e-120:748:85//AF076183

F-HEMBA1006328//Homo sapiens fragile X mental retardation protein (FMR-1) gene (6 alternative splices), complete cds.//1.5e-46:485:73//L29074

F-HEMBA1006334//HS-1051-B2-F01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 773 Col=2 Row=L, genomic survey sequence.//0.0032:61:91//B40563

F-HEMBA1006344//HS-1009-A2-B02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 331 Col=4 Row=C, genomic survey sequence.//3.3e-09:218:66//B31420

F-HEMBA1006347//Drosophila melanogaster males-absent on the first (mof) gene, complete cds.//1.6e-31:484:68//U71219

F-HEMBA1006349//HS-1054-A1-G06-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 776 Col=1 Row=M, genomic survey sequence.//5.1e-15:115:91//B40563

F-HEMBA1006353//Human DNA sequence from clone 1020A1, AB0244

F-HEMBA1006364//Mouse mRNA for transforming growth factor beta2, 2.1 kb, 5' to 3' direction

F-HEMBA1006377//Mus musculus chromosome 7, clone 19K5, complete sequence //3.0e-57:401:81//AC002327
 F-HEMBA1006380//CIT-HSP-2172K18.TF CIT-HSP Homo sapiens genomic clone 2172K18, genomic survey sequence //1.3e-110:525:99//B92570

F-HEMBA1006381//HS-1045-B2-F10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 828 Col=20 Row=L, genomic survey sequence //4.4e-05:163:70//B37813

F-HEMBA1006398//Homo sapiens 12q24.2 BAC RPC111-360E11 (Roswell Park Cancer Institute Human BAC Library) complete sequence //3.8e-62:370:86//AC004806

F-HEMBA1006416//Homo sapiens chromosome 5, P1 clone 1041F10 (LBNL H88), complete sequence //3.7e-15:157:78//AC005179

F-HEMBA1006419//Human DNA sequence from clone 71L16 on chromosome Xp11. Contains a probable Zinc Finger protein (pseudo)gene, an unknown putative gene, a pseudogene with high similarity to part of antigen KI-67, a putative Chondroitin 6-Sulfotransferase LIKE gene and a KIAA0267 LIKE putative Na(+)/H(+) exchanger protein gene. Contains a predicted CpG island, ESTs, STSs and GSSs and genomic markers DXS1003 and DXS1055, complete sequence //1.2e-39:752:63//AL022165

F-HEMBA1006421//Homo sapiens chromosome 14q24.3 clone BAC270M14 transforming growth factor-beta 3 (TGF-beta 3) gene, complete cds; and unknown genes //2.4e-41:438:76//AF107885

F-HEMBA1006424//Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence //0.027:293:64//AL031781

F-HEMBA1006426//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 292E10, WORKING DRAFT SEQUENCE //1.7e-50:310:80//Z93930

F-HEMBA1006438//Liverwort Marchantia polymorpha chloroplast genome DNA //0.051:440:59//X04465

F-HEMBA1006445//Felis catus ras p21 (H-ras) mRNA, partial cds //1.0:238:59//U62088

F-HEMBA1006446//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P6, WORKING DRAFT SEQUENCE //2.4e-05:702:58//AL031749

F-HEMBA1006461//Homo sapiens chromosome 19, cosmid R30676, complete sequence //8.6e-55:409:83//AC004560

F-HEMBA1006467//Homo sapiens chromosome 17, clone hRPK.346_K_10, complete sequence //1.0:293:59//AC006120

F-HEMBA1006471//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces //1.4e-05:731:59//AC004709

F-HEMBA1006474//CIT-HSP-2017H3.TF CIT-HSP Homo sapiens genomic clone 2017H3, genomic survey sequence //5.2e-60:435:83//B54247

F-HEMBA1006483//Homo sapiens chromosome 5, BAC clone 8e5 (LBNL H167), complete sequence //2.9e-48:286:84//AC004752

F-HEMBA1006485//Homo sapiens BAC clone NH0044G14 from 7q11.23-21.1, complete sequence //0.96:283:59//AC006031

F-HEMBA1006486//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence //1.8e-14:259:67//AL022577

F-HEMBA1006489//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 467K16, WORKING DRAFT SEQUENCE //6.6e-11:595:61//AL031283

F-HEMBA1006492//Homo sapiens chromosome 17, clone hRPK.269_G_24, complete sequence //6.0e-122:337:100//AC005828

F-HEMBA1006494//Homo sapiens chromosome 7qtelo BAC E3, complete sequence //3.8e-23:459:68//AF093117

F-HEMBA1006497//HS_3023_B2_H03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3023 Col=6 Row=P, genomic survey sequence //2.3e-81:433:95//AQ093846

F-HEMBA1006502//H.sapiens 7SL repeat (clones 2-19b) //1.6e-13:86:87//X62364

F-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds //2.3e-139:470:98//AB014566

F-HEMBA1006521//Human BAC clone RG167B05 from 7q21, complete sequence //4.3e-27:406:71//AC003991

F-HEMBA1006530//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018D12, WORKING DRAFT SEQUENCE //2.9e-27:408:65//AL031650

F-HEMBA1006535//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE //6.0e-50:60:41//AL034557

F-HEMBA1006544//Homo sapiens chromosome 17, clone hRPK.269_G_24, complete sequence //6.0e-122:337:100//AC005828

F-HEMBA1006546//Human DNA sequence from cosmid 232L22, between markers DXS366 and DXS87 on chromosome X contains ESTs glycerol kinase pseudogene.//3.8e-104:811:80//Z73986

F-HEMBA1006559//Mus musculus PRAJA1 (Praja1) mRNA, complete cds.//4.8e-99:386:82//U06944

F-HEMBA1006562//Human fructose-1,6-biphosphatase (FBP1) gene, exon 1.//0.012:322:60//U21925

5 F-HEMBA1006566//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.0026:580:58//AC005504

F-HEMBA1006569//Ovis aries beta actin mRNA, complete cds.//6.3e-08:231:70//U39357

F-HEMBA1006579//CIT-HSP-2380A22.TR CIT-HSP Homo sapiens genomic clone 2380A22, genomic survey sequence.//0.036:250:62//AQ197107

10 F-HEMBA1006583//Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.//1.0:225:63//AL021841

F-HEMBA1006595//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 30A23, WORKING DRAFT SEQUENCE.//3.6e-50:689:69//AL022156

F-HEMBA1006597//Homo sapiens Chromosome 7 BAC Clone 239c10, WORKING DRAFT SEQUENCE, 9 unordered pieces.//1.9e-42:253:84//AC004166

15 F-HEMBA1006612//RPC11-88F20.TJ RPC11 Homo sapiens genomic clone R-88F20, genomic survey sequence.//1.1e-51:266:98//AQ286726

F-HEMBA1006617//HS_2193_B2_H07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2193 Col=14 Row=P, genomic survey sequence.//1.1e-59:413:85//AQ299685

20 F-HEMBA1006624//Human DNA sequence from clone 406A7 on chromosome 6q23-24. Contains three pseudogenes similar to Elongation Factor 1-Alpha (EF-1-ALPHA, Statin S1), 60S Acidic Ribosomal Protein P1 and NADH-Ubiquinone Oxidoreductase 15 kDa subunit, and part of the Microtubule Associated Protein E-MAP-115 gene. Contains ESTs, STSs and GSSs, complete sequence.//1.4e-35:257:89//AL023284

25 F-HEMBA1006631//Homo sapiens Chromosome 11q23 PAC clone pDJ356d6, complete sequence.//9.6e-112:800:83//AC002036

F-HEMBA1006635//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P2, WORKING DRAFT SEQUENCE.//0.15:393:58//AL031745

F-HEMBA1006639//Petromyzon marinus polyadenylate binding protein (PABP) mRNA, complete cds.//9.6e-15:318:68//AF032896

30 F-HEMBA1006643//Homo sapiens clone DJ0902E20, WORKING DRAFT SEQUENCE, 1 unordered pieces.//0.58:254:65//AC006148

F-HEMBA1006648//Mus musculus integrin binding protein kinase mRNA, complete cds.//1.5e-37:108:88//U94479

F-HEMBA1006652//Homo sapiens chromosome 5, BAC clone 343g16 (LBNL H180), complete sequence.//1.3e-154:671:96//AC005601

35 F-HEMBA1006653

F-HEMBA1006659//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//5.2e-110:254:93//AC005189

F-HEMBA1006665//Homo sapiens Xp22 BAC GSHB-590J6 (Genome Systems Human BAC library) complete sequence.//1.4e-14:177:76//AC004554

40 F-HEMBA1006674//Homo sapiens mRNA for nucleolar protein hNop56.//5.5e-15:122:90//Y12065

F-HEMBA1006676//Homo sapiens chromosome 19, fosmid 37502, complete sequence.//0.098:218:63//AC004755

F-HEMBA1006682//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 668J24, WORKING DRAFT SEQUENCE.//1.4e-05:719:57//AL034346

45 F-HEMBA1006695//Homo sapiens clone DJ0935K16, complete sequence.//3.1e-22:151:78//AC006011

F-HEMBA1006696//CITBI-E1-2522D16.TF CITBI-E1 Homo sapiens genomic clone 2522D16, genomic survey sequence.//5.6e-17:324:66//AQ280738

F-HEMBA1006708

F-HEMBA1006709

50 F-HEMBA1006717//Homo sapiens clone GS308H05, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.3e-08:136:79//AC005537

F-HEMBA1006737//Homo sapiens chromosome 17, clone hRPK.269_G_24, complete sequence.//5.8e-162:497:98//AC005828

55 F-HEMBA1006744//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g4, complete sequence.//7.4e-48:320:87//AC004796

F-HEMBA1006751

F-HEMBA1006754//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 30A23, WORKING DRAFT SEQUENCE.//3.6e-50:689:69//AL022156

F-HEMBA1006758//Homo sapiens chromosome 5, BAC clone 182a8 (LBNL H161), complete sequence//2.2e-162:766:99//AC005752

F-HEMBA1006767//Human Xq28 cosmid U247A3 from LLOXNC01 X chromosome library, complete sequence//1.2e-19:326:69//U73465

5 F-HEMBA1006779//Human DNA sequence from clone 80I19 on chromosome 6p21.31-22.2 Contains genes and pseudogenes for olfactory receptor-like proteins, STS, GSS, complete sequence//1.4e-103:355:87//AL022727

F-HEMBA1006780//CIT-HSP-2359P7.TR CIT-HSP Homo sapiens genomic clone 2359P7, genomic survey sequence//0.072:147:68//AQ077208

10 F-HEMBA1006789//nbxb0037113r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0037113r, genomic survey sequence//0.00011:288:63//AQ290474

F-HEMBA1006795//CIT-HSP-2307E3.TF CIT-HSP Homo sapiens genomic clone 2307E3, genomic survey sequence//5.1e-80:420:96//AQ020511

F-HEMBA1006796//Human clone 23803 mRNA, partial cds//4.5e-06:202:68//U79298

F-HEMBA1006807//Homo sapiens mRNA for SPOP//1.2e-66:651:73//AJ000644

15 F-HEMBA1006821//Homo sapiens chromosome 17, clone hRPC.62_O_9, complete sequence//6.0e-116:541:99//AC004797

F-HEMBA1006824//Homo sapiens chromosome 19, cosmid R29368, complete sequence//0.40:159:66//AC004262

20 F-HEMBA1006832//Homo sapiens (subclone 3_g8 from P1 H25) DNA sequence, complete sequence//1.8e-24:323:71//AC002196

F-HEMBA1006849//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 4/10//0.15:403:60//AB020872

F-HEMBA1006865//Plasmodium falciparum chromosome 2, section 6 of 73 of the complete sequence//0.20:472:57//AE001369

25 F-HEMBA1006877//Mus musculus clone OST9241, genomic survey sequence//3.4e-79:641:76//AF046757

F-HEMBA1006885//HS_2208_B2_G06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2208 Col=12 Row=N, genomic survey sequence//4.9e-18:206:76//AQ089246

F-HEMBA1006900//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS, complete sequence//5.4e-07:298:65//AL031321

30 F-HEMBA1006914//S.pombe chromosome II cosmid c16H5//0.00040:194:66//AL022104

F-HEMBA1006921//Homo sapiens BAC clone GS114I09 from 7p14-p15, complete sequence//1.1e-174:813:99//AC006027

F-HEMBA1006926//Caenorhabditis elegans cosmid ZK185//0.0075:183:65//AF036704

F-HEMBA1006929//P.falciparum complete gene map of plastid-like DNA (IR-A)//4.0e-06:739:57//X95275

35 F-HEMBA1006936

F-HEMBA1006938//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P4, WORKING DRAFT SEQUENCE//1.1e-05:733:57//AL031747

F-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein//1.3e-90:437:98//AJ010841

40 F-HEMBA1006949//Human DNA sequence from PAC 363L9 on chromosome X. contains STS and polymorphic CA repeat//0.67:217:62//Z82205

F-HEMBA1006973//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//5.6e-143:740:94//AF004828

F-HEMBA1006976//cDNA encoding alpha 2 to 3 sialyltransferase//2.8e-101:338:89//E06058

45 F-HEMBA1006993//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence//7.1e-31:536:66//AC003071

F-HEMBA1006996//Human DNA sequence from clone J428A131, WORKING DRAFT SEQUENCE//9.5e-07:285:60//Z82209

F-HEMBA1007002//Genomic sequence for Arabidopsis thaliana BAC F20N2, complete sequence//0.99:388:58//AC002328

50 F-HEMBA1007017//Sequence 3 from Patent WO9416067//0.96:220:62//A39358

F-HEMBA1007018//G.gallus mRNA for dynein light chain-A//1.3e-124:838:83//X79088

F-HEMBA1007045

F-HEMBA1007051//Caenorhabditis elegans cosmid Y57G11C, complete sequence//0.17:343:60//Z99281

F-HEMBA1007052//Homo sapiens FSHD-associated repeat DNA, proximal region//4.3e-67:659:74//U85056

55 F-HEMBA1007062//Tubulin gene//1.0:113:67//A18572

F-HEMBA1007066//Homo sapiens BAC clone 182a8 (LBNL H161), complete sequence//2.2e-162:766:99//AC005752

F-HEMBA1007067//Human Xq28 cosmid U247A3 from LLOXNC01 X chromosome library, complete sequence//1.2e-19:326:69//U73465

F-HEMBA1007068//Human DNA sequence from clone 80I19 on chromosome 6p21.31-22.2 Contains genes and pseudogenes for olfactory receptor-like proteins, STS, GSS, complete sequence//1.4e-103:355:87//AL022727

complete sequence//9.3e-54:519:68//AC004242

F-HEMBA1007078//CIT-HSP-2318N6.TF CIT-HSP Homo sapiens genomic clone 2318N6, genomic survey sequence//8.7e-80:387:98//AQ044076

F-HEMBA1007080

5 F-HEMBA1007085//Streptomyces coelicolor cosmid 7A1//3.5e-06:496:59//AL034447

F-HEMBA1007087//Plasmodium falciparum MAL3P6, complete sequence//7.4e-07:553:56//Z98551

F-HEMBA1007112//HS_2171_A1_B01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2171 Col=1 Row=C, genomic survey sequence//1.0:172:61//AQ091865

10 F-HEMBA1007113//Human DNA sequence from clone 1044O17 on chromosome Xp11.3-11.4 Contains GSS and STS, complete sequence//0.54:502:56//AL023875

F-HEMBA1007121//Caenorhabditis elegans cosmid ZK430//1.4e-08:265:64//U42833

F-HEMBA1007129//CITBI-E1-2504A5.TF CITBI-E1 Homo sapiens genomic clone 2504A5, genomic survey sequence//0.97:267:62//AQ264035

15 F-HEMBA1007147//HS_3208_A2_C04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3208 Col=8 Row=E, genomic survey sequence//9.1e-90:466:95//AQ176696

F-HEMBA1007149//Homo sapiens chromosome 19, cosmid F23149, complete sequence//6.0e-138:524:98//AC005239

F-HEMBA1007151//CITBI-E1-2522H6.TF CITBI-E1 Homo sapiens genomic clone 2522H6, genomic survey sequence//2.0e-20:157:87//AQ280780

20 F-HEMBA1007174//Homo sapiens epsin 2a mRNA, complete cds//2.0e-62:318:97//AF062085

F-HEMBA1007178//Homo sapiens chromosome 12p13.3 clone RPC11-372B4, WORKING DRAFT SEQUENCE, 129 ordered pieces//1.6e-21:205:80//AC005911

F-HEMBA1007194//HS_3124_B2_H08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3124 Col=16 Row=P, genomic survey sequence//1.3e-11:87:96//AQ187492

25 F-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.7e-156:478:98//D86987

F-HEMBA1007206//Homo sapiens chromosome 17, clone HRPC837J1, complete sequence//0.024:342:63//AC004223

F-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds//5.0e-176:839:98//AB018340

F-HEMBA1007243//Chinese hamster hprt mRNA, complete cds//4.3e-58:687:68//J00060

30 F-HEMBA1007251//Rabbit troponin T messenger fragment (aa 49 to 129)//0.084:177:62//V00899

F-HEMBA1007256//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 328E19, WORKING DRAFT SEQUENCE//1.3e-75:490:88//AL022240

F-HEMBA1007267//HS_3218_A1_F07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=13 Row=K, genomic survey sequence//2.9e-62:393:87//AQ181128

35 F-HEMBA1007273//CIT-HSP-2171B10.TF CIT-HSP Homo sapiens genomic clone 2171B10, genomic survey sequence//1.1e-63:314:99//B95401

F-HEMBA1007279//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-116A10, complete sequence//3.1e-31:401:72//AC004638

40 F-HEMBA1007281//HS_3115_A1_A11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3115 Col=21 Row=A, genomic survey sequence//5.0e-70:372:96//AQ186691

F-HEMBA1007288//Human DNA sequence from clone 422G23 on chromosome 6q24 Contains EST, STS, GSS, CpG island, complete sequence//1.2e-152:727:98//AL031003

F-HEMBA1007300//Canis familiaris PDE5 mRNA for 3',5'-Cyclic GMP Phosphodiesterase, complete cds//2.1e-21:542:63//AB008467

45 F-HEMBA1007301//COL1A1=type I collagen pro alpha 1(I) chain propeptide {3' region} [human, fetal cells 86-237, 86-146, 88-251, mRNA Partial Mutant, 855 nt]//1.7e-08:388:61//S64596

F-HEMBA1007319//Genomic sequence from Mouse 9, complete sequence//6.0e-84:390:75//AC000399

F-HEMBA1007320

50 F-HEMBA1007322//Homo sapiens BAC clone RG118E13 from 7p15-p21, complete sequence//0.091:260:64//AC004485

F-HEMBA1007327//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces//0.12:472:59//AC005140

F-HEMBA1007341//Homo sapiens chromosome 17, clone hRPK.346_K_10, complete sequence//1.5e-18:408:64//AC006120

55 F-HEMBA1007342//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE 4 unordered pieces // 1.7e-25:500:60//AF051001

F-HEMBA1007343//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE 4 unordered pieces // 1.7e-25:500:60//AF051001

F-HEM BB1000005//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//5.0e-05:441:60//AC004617

F-HEM BB1000008//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//1.0e-44:417:77//AC004491

5 F-HEM BB1000018//HS_2179_B2_E04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2179 Col=8 Row=J, genomic survey sequence.//0.012:87:77//AQ023250

F-HEM BB1000024//Human DNA sequence from PAC 106I20 on chromosome 22q12-qter contains NADH pseudogene, ESTs, STS.//8.1e-11:461:61//Z81369

10 F-HEM BB1000025//CIT-HSP-2348F3.TR CIT-HSP Homo sapiens genomic clone 2348F3, genomic survey sequence.//0.96:198:62//AQ062938

F-HEM BB1000030//Homo sapiens DNA sequence from PAC 32F7 on chromosome X. Contains NUCLEOSOME ASSEMBLY PROTEIN 1-LIKE 3, ESTs.//0.00049:276:64//AL009173

F-HEM BB1000036//H.sapiens chromosome 22 CpG island DNA genomic MseI fragment, clone 302e2, reverse read 302e2.r.//0.0057:66:81//Z79857

15 F-HEM BB1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//1.9e-100:450:98//AF084928

F-HEM BB1000039//HS_2167_B1_F12_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2167 Col=23 Row=L, genomic survey sequence.//0.022:108:69//AQ092404

F-HEM BB1000044//Borrelia burgdorferi (section 50 of 70) of the complete genome.//1.0e-07:486:61//AE001164

20 F-HEM BB1000048//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//5.3e-05:585:58//AC005507

F-HEM BB1000050//Homo sapiens DNA sequence from clone 501N12 on chromosome 6p22.1-22.3 Contains a gene almost identical to four genes of unknown function, a pseudogene, three (pseudo?) genes similar to genes of unknown function, an unknown gene similar to a rat EST, a PX19 LIKE pseudogene and another unknown gene. Contains ESTs, STSs and GSSs, complete sequence.//5.8e-38:549:67//AL022170

25 F-HEM BB1000054//Homo sapiens Xp22 PAC RPC11-167A22 (from Roswell Park Cancer Center) complete sequence.//7.0e-98:328:83//AC002349

F-HEM BB1000055//Homo sapiens genomic DNA for centromeric end of MHC class I region on chromosome 6, cosmid clone: TY2F10, WORKING DRAFT SEQUENCE.//3.7e-05:600:58//AB000880

30 F-HEM BB1000059//Homo sapiens clone RG339C12, WORKING DRAFT SEQUENCE, 10 unordered pieces.//1.3e-48:472:78//AC005096

F-HEM BB1000083

F-HEM BB1000089//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P1, WORKING DRAFT SEQUENCE.//0.0036:679:56//AL031744

35 F-HEM BB1000099//Homo sapiens chromosome 18 BAC RPC11-128D14 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//1.1e-15:312:68//AC005909

F-HEM BB1000103//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//1.0e-37:316:74//AC006210

40 F-HEM BB1000113//Homo sapiens chromosome 21q22.3 cosmid Q11M15, complete sequence.//3.1e-25:259:76//AF045450

F-HEM BB1000119//Homo sapiens ASMTL gene.//1.2e-137:654:98//Y15521

F-HEM BB1000136//Mycobacterium tuberculosis H37Rv complete genome; segment 127/162.//0.59:217:66//Z74697

45 F-HEM BB1000141//Homo sapiens DNA from chromosome 19q13.1 cosmid f14121 containing ATP4A and GADPH-2 genes, genomic sequence.//8.4e-31:113:88//AD000090

F-HEM BB1000144//Human BAC clone RG114A06 from 7q31, complete sequence.//4.4e-58:339:87//AC002542

F-HEM BB1000173//Homo sapiens 12q24 BAC RPC111-162P23 (Roswell Park Cancer Institute Human BAC library) complete sequence.//9.4e-160:562:93//AC002996

F-HEM BB1000175

50 F-HEM BB1000198//HS_3071_A2_A10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=20 Row=A, genomic survey sequence.//0.99:261:61//AQ137388

F-HEM BB1000215//Homo sapiens chromosome 17, clone hRPK.481_C_4, complete sequence.//6.7e-17:138:86//AC005839

55 F-HEM BB1000217//Arabidopsis thaliana ubiquitin activating enzyme (UBA1) gene, complete cds.//0.00083:287:60//U80808

F-HEM BB1000218//Homo sapiens chromosome 17, clone hRPK.481_C_4, complete sequence.//6.7e-17:138:86//AC005839

F-HEM BB1000219//Homo sapiens chromosome 17, clone hRPK.481_C_4, complete sequence.//6.7e-17:138:86//AC005839

F-HEMBB1000240//Human G-protein-coupled inwardly rectifying potassium channel (KCNJ3) gene, polymorphic repeat sequence//0.16:171:62//U07918

F-HEMBB1000244//Homo sapiens clone DJ1129E22, WORKING DRAFT SEQUENCE, 7 unordered pieces//4.8e-08:355:63//AC005522

5 F-HEMBB1000250//Homo sapiens protein associated with Myc mRNA, complete cds//6.6e-155:735:98//AF075587

F-HEMBB1000258//Human adenosine monophosphate deaminase 1 (AMPD1) gene, exons 1-16//0.58:396:59//M98818

10 F-HEMBB1000264//Human clone C3 CHL1 protein (CHLR1) mRNA, alternatively spliced, complete cds//4.4e-32:100:100//U75968

F-HEMBB1000266//Homo sapiens Xp22 BAC GSHB-433024 (Genome Systems Human BAC library) complete sequence//3.8e-16:176:78//AC004470

F-HEMBB1000272//Plasmodium falciparum chromosome 2, section 6 of 73 of the complete sequence//0.011:379:58//AE001369

15 F-HEMBB1000274//Arabidopsis thaliana DNA chromosome 4, BAC clone T5K18 (ESSAI project)//0.92:272:61//AL022580

F-HEMBB1000284//Human Xp22 BAC CT-285115 (from CalTech/Research Genetics), PAC RPC11-27C22 (from Roswell Park Cancer Center), and Cosmid U35B5 (from Lawrence Livermore), complete sequence//0.00071:568:57//AC002366

20 F-HEMBB1000307//Human DNA sequence from PAC 29K1 on chromosome 6p21.3-22.2. Contains glutathione peroxidase-like; zinc finger, ESTs, mRNA, STS, tRNAs, olfactory receptor pseudogene//3.0e-13:439:65//Z98745

F-HEMBB1000312//Homo sapiens clone GS051M12, complete sequence//0.031:252:65//AC005007

F-HEMBB1000317//Fugu rubripes GSS sequence, clone 060J22aE10, genomic survey sequence//0.00033:173:65//AL026242

25 F-HEMBB1000318//HS_3244_B2_H10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3244 Col=20 Row=P, genomic survey sequence//3.9e-85:438:95//AQ252951

F-HEMBB1000335//Homo sapiens chromosome 18, clone hRPK.24_A_23, complete sequence//0.63:285:61//AC005968

F-HEMBB1000336

30 F-HEMBB1000337//Homo sapiens chromosome 4 clone B208G5 map 4q25, complete sequence//0.0014:309:64//AC004051

F-HEMBB1000338//HS_3108_A2_F07_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3108 Col=14 Row=K, genomic survey sequence//3.8e-09:331:63//AQ140356

35 F-HEMBB1000339//Homo sapiens 12q24 PAC RPC11-46F2 (Roswell Park Cancer Institute Human PAC library) complete sequence//1.2e-52:295:77//AC002351

F-HEMBB1000341

F-HEMBB1000343//Plasmodium falciparum MAL3P3, complete sequence//0.00081:397:61//Z98547

F-HEMBB1000354//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudo-gene similar to rat Plasmolipin, ESTs and GSSs, complete sequence//9.1e-34:596:66//AL020989

40 F-HEMBB1000369//Genomic sequence from Human 17, complete sequence//0.012:298:60//AC002090

F-HEMBB1000374//Human Xp22 contig of 3 PACS (R7-39D12, R7-134G1, R7-185L21) from the Roswell Park Cancer Institute, complete sequence//9.3e-69:294:89//U96409

F-HEMBB1000376//Human DNA sequence from clone 751H9 on chromosome 6q13. Contains part of an unknown gene, ESTs, STSs and GSSs, complete sequence//3.5e-54:352:88//AL034377

45 F-HEMBB1000391//Trichothecium roseum internal transcribed spacer 1, 5.8S ribosomal RNA gene; and internal transcribed spacer 2, complete sequence//0.011:168:67//U51982

F-HEMBB1000399//Homo sapiens Rad17-like protein (RAD17) mRNA, complete cds//2.6e-163:762:98//AF076838

50 F-HEMBB1000402//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence//7.7e-15:466:63//AC002368

F-HEMBB1000404//Homo sapiens mRNA for myosin-IXA//3.5e-65:324:98//AJ001714

F-HEMBB1000420//244Kb Contig from Human Chromosome 11p15.5 spanning D11S1 through D11S25, complete sequence//0.013:399:62//AC001228

F-HEMBB1000434//Homo sapiens PAC clone 278C19 from 12q, complete sequence//6.1e-83:571:84//AC004263

55 F-HEMBB1000438//RPC11-21E14.TP RPCI-11 Homo sapiens genomic clone RPCI-11-21E14, genomic survey sequence//0.0030:295:63//BR311

F-HEMBB1000444//Homo sapiens clone 129E22, WORKING DRAFT SEQUENCE, 7 unordered pieces//4.8e-08:355:63//AC005522

AC000031

F-HEM BB1000449//Human DNA sequence from PAC 296K21 on chromosome X contains cytoke-
 ratin exon, delta-aminolevulinic acid synthase (erythroid); 5-aminolevulinic acid synthase (EC 2.3.1.37). 6-phosphofructo-2-kinase/
 fructose-2,6-bisphosphatase (EC 2.7.1.105, EC 3.1.3.46), ESTs and STS.//1.3e-51:534:72//Z83821

F-HEM BB1000455//*Saccharomyces cerevisiae* mitochondrion origin of replication (ori6) and oli1 gene, complete
 cds.//0.016:522:58//L36899

F-HEM BB1000472

F-HEM BB1000480

F-HEM BB1000487//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 128O3, WORKING
 DRAFT SEQUENCE.//0.00013:314:64//Z98742

F-HEM BB1000490//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1185N5, WORKING
 DRAFT SEQUENCE.//4.1e-110:529:98//AL034423

F-HEM BB1000491//*Plasmodium falciparum* chromosome 2, section 25 of 73 of the complete sequence.//0.10:
 187:65//AE001388

F-HEM BB1000493//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alterna-
 tively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin,
 subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs,
 complete sequence.//3.7e-06:637:58//AL022577

F-HEM BB1000510//Homo sapiens chromosome 17, clone hRPK.112_J_9, complete sequence.//3.1e-96:737:81//
 AC005553

F-HEM BB1000518//Homo Sapiens Chromosome X clone bWXD171, WORKING DRAFT SEQUENCE, 1 ordered
 pieces.//0.00014:163:68//AC004676

F-HEM BB1000523//*Plasmodium falciparum* DNA *** SEQUENCING IN PROGRESS *** from contig 3-105, com-
 plete sequence.//0.41:349:56//AL010212

F-HEM BB1000530//H.sapiens mRNA for extracellular matrix protein collagen type XIV, C-terminus.//6.6e-37:138:
 96//Y11710

F-HEM BB1000550//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and
 non-small cell lung cancer, segment 3/11.//3.9e-56:683:71//AB020860

F-HEM BB1000554//Homo sapiens *** SEQUENCING IN PROGRESS *** WORKING DRAFT SEQUENCE.//2.2e-
 51:282:84//AJ011929

F-HEM BB1000556//Homo sapiens mRNA for KIAA0750 protein, complete cds.//6.1e-32:537:65//AB018293

F-HEM BB1000564

F-HEM BB1000573//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//8.2e-
 33:268:73//AC005077

F-HEM BB1000575//Human DNA sequence from clone 323M22 on chromosome 22q13.1-13.2. Contains the 5'
 part of the human ortholog of chicken P52 and mouse H74, and a novel gene coding for a protein similar to
 KIAA0173 and worm Tubulin Tyrosine Ligase. Contains ESTs, STSs, GSSs, genomic marker D22S418 and puta-
 tive CpG islands, complete sequence.//5.8e-47:734:66//AL022476

F-HEM BB1000586//H.sapiens highly polymorphic microsatellite DNA.//0.030:147:67//X79883

F-HEM BB1000589//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//6.3e-
 41:278:83//AC002300

F-HEM BB1000591//Homo sapiens Xp22 bins 45-47 BAC GSHB-665N22 (Genome Systems Human BAC Library)
 complete sequence.//1.1e-182:871:98//AC005184

F-HEM BB1000592//Hepatitis C virus genomic RNA, 3' nontranslated region, partial sequence. clone #19.//0.012:
 185:64//AF009074

F-HEM BB1000593//Homo sapiens chromosome 7q22 sequence, complete sequence.//1.2e-131:353:93//
 AF053356

F-HEM BB1000598//Homo sapiens 12p13.3 BAC RPCI3-488H23 (Roswell Park Cancer Institute Human BAC Li-
 brary) complete sequence.//9.1e-58:600:72//AC006207

F-HEM BB1000623//cDNA encoding *Coliolum* manganese peroxidase.//0.89:284:62//E12284

F-HEM BB1000630//*Mus musculus* clone NSAT47 nonsatellite RNA sequence.//1.9e-15:129:87//U26231

F-HEM BB1000631//Sequence 26 from patent US 5708157.//3.2e-27:180:88//I80057

F-HEM BB1000632//Human mRNA for KIAA0351 gene, complete cds.//1.6e-48:811:65//AB002349

F-HEM BB1000637//Homo sapiens clone DJ0425102, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.1e-
 58:649:73//AC005478

F-HEM BB1000638//HS 3051 A1 G01 MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic DNA

F-HEM BB1000643//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//8.2e-
 33:268:73//AC005077

F-HEM BB1000649//Homo sapiens Chromosome 16 BAC clone CIT987-SK502C10, complete sequence//5.2e-64:775:69//AC003009

F-HEM BB1000652//Homo sapiens chromosome 10 clone CRI-JC2048 map 10q22.1, WORKING DRAFT SEQUENCE, 4 unordered pieces//2.7e-52:334:89//AC006186

5 F-HEM BB1000665//Human DNA sequence from clone 452M16 on chromosome Xq21.1-21.33 Contains capping protein alpha subunit isoform 1 pseudogene, STS, GSS, and CA repeat, complete sequence//0.0062:426:60//AL024493

F-HEM BB1000671//Human DNA sequence from PAC 93H18 on chromosome 6 contains ESTs heterochromatin protein HP1Hs-gamma pseudogene, STS and CpG island//9.6e-95:399:78//Z84488

10 F-HEM BB1000673//HS_3039_A2_C08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3039 Col=16 Row=E, genomic survey sequence//3.8e-50:293:92//AQ155121

F-HEM BB1000684//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 222E13, WORKING DRAFT SEQUENCE//8.0e-65 :282:83//Z93241

F-HEM BB1000693//Homo sapiens neuroan1 mRNA, complete cds//1.6e-118:575:97//AF040723

15 F-HEM BB1000705//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces//8.6e-07:251:61//AC005507

F-HEM BB1000706//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 153G14, WORKING DRAFT SEQUENCE//2.9e-20:434:64//AL031118

20 F-HEM BB1000709//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 994L9, WORKING DRAFT SEQUENCE//0.26:184:65//AL034554

F-HEM BB1000725//Rattus norvegicus GTPase Rab8b (Rab8b) mRNA, complete cds//1.8e-129:692:93//U53475

F-HEM BB1000726//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence//2.7e-40:304:80//U91321

25 F-HEM BB1000738//Human Xq28 cosmids U126G1, U142F2, U69B6, U145C10, U169A5, U84H1, U24D12, U80A7, U153E6, L35485, and R7-163A8 containing iduronate 2-sulfatase gene and pseudogene, complete sequence//8.9e-35:582:63//AF011889

F-HEM BB1000749//Homo sapiens chromosome 11 clone CIT-HSP-1337H24, WORKING DRAFT SEQUENCE, 9 unordered pieces//6.2e-46:262:89//AC005849

30 F-HEM BB1000763//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 537K23, WORKING DRAFT SEQUENCE//1.6e-99:316:98//AL034405

F-HEM BB1000770//Human DNA sequence from clone 80I19 on chromosome 6p21.31-22.2 Contains genes and pseudogenes for olfactory receptor-like proteins, STS, GSS, complete sequence//0.044:325:60//AL022727

F-HEM BB1000774

F-HEM BB1000781//Sequence 3 from patent US 5753446//1.2e-92:599:86//AR008277

35 F-HEM BB1000789//Homo sapiens mRNA for KIAA0677 protein, complete cds//9.3e-64:672:71//AB014577

F-HEM BB1000790//Homo sapiens 12q13.1 PAC RPC11-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence//2.4e-41:460:74//AC004801

F-HEM BB1000794//HS_3034_B2_D12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3034 Col=24 Row=H, genomic survey sequence//1.8e-74:378:97//AQ117099

40 F-HEM BB1000807//H.sapiens CpG island DNA genomic Mse1 fragment, clone 39d7, reverse read cpg39d7.rt1a.//8.5e-14:95:97//Z58412

F-HEM BB1000810//H.sapiens chromosome 22 CpG island DNA genomic Mse1 fragment, clone 303a8, complete read//3.2e-05:138:71//Z79983

45 F-HEM BB1000821//HS_2168_B1_A12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2168 Col=23 Row=B, genomic survey sequence//0.85 :208:60//AQ086361

F-HEM BB1000822//Human BAC clone GS113H23 from 5p15.2, complete sequence//3.0e-06:361:60//AC003015

F-HEM BB1000826//Human BAC clone RG180F08 from 7q31, complete sequence//1.1e-27:360:69//AC002431

F-HEM BB1000827

F-HEM BB1000831

50 F-HEM BB1000835//Human DNA sequence from clone 45I4 on chromosome 6q24.1-24.3. Contains two putative unknown genes, ESTs, STSs and GSSs, complete sequence//0.00098:234:63//AL023581

F-HEM BB1000840//Human Chromosome 11 Cosmid cSRL97a6, complete sequence//4.5e-61:328:79//U73649

F-HEM BB1000848//Homo sapiens DNA sequence from PAC 206D15 on chromosome 1q24. Contains a Reduced Folate Carrier protein (RFC) LIKE gene, a mitochondrial ATP Synthetase protein 8 (ATP8, MTATP8) LIKE pseudogene, an unknown gene and the last exon of the JEM1 gene coding for the Basic-Leucine Zipper nuclear factor

JEM1. Contains ESTs, STS, and a BAC end sequence. GSS. Location: chr1:111,899,871-111,900,871

111,899,871-111,900,871

F-HEM BB1000849//Human DNA sequence from clone 45I4 on chromosome 6q24.1-24.3. Contains two putative unknown genes, ESTs, STSs and GSSs, complete sequence//0.00098:234:63//AL023581

DRAFT SEQUENCE, 9 unordered pieces.//0.12:492:58//AC004157

F-HEM BB1000870//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0024:212:67//AC004157

F-HEM BB1000876//Homo sapiens ELISC-1 mRNA, partial cds.//1.5e-32:200:94//AF085351

5 F-HEM BB1000883//HS_3065_B2_C04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3065 Col=8 Row=F, genomic survey sequence.//0.0017:152:66//AQ137687

F-HEM BB1000887

F-HEM BB1000888//CIT-HSP-2329A10.TR CIT-HSP Homo sapiens genomic clone 2329A10, genomic survey sequence.//1.5e-31:172:98//AQ044369

10 F-HEM BB1000890

F-HEM BB1000893//Plasmodium falciparum MAL3P2, complete sequence.//9.5e-06:768:56//AL034558

F-HEM BB1000908//Homo sapiens clone DJ1119N05, complete sequence.//4.5e-21:199:82//AC004968

F-HEM BB1000910//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE.//0.72:366:59//AL034557

15 F-HEM BB1000913//HS_3078_B1_C02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3078 Col=3 Row=F, genomic survey sequence.//9.9e-12:221:63//AQ144507

F-HEM BB1000915//Homo sapiens DNA for (CGG)_n trinucleotide repeat region, isolate P4.//1.2e-49:252:99//AJ001215

20 F-HEM BB1000917//Homo sapiens chromosome 5, P1 clone 254f11 (LBNL H62), complete sequence.//2.3e-42:316:76//AC006077

F-HEM BB1000927//Human BDR-2 mRNA for hippocalcin, complete cds.//3.6e-30:528:65/D16593

F-HEM BB1000947//CpG0856B CplOWAgDNA1 Cryptosporidium parvum genomic, genomic survey sequence.//0.81:262:62//AQ254493

25 F-HEM BB1000959//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 34606, WORKING DRAFT SEQUENCE.//1.2e-43:454:75//Z84487

F-HEM BB1000973//Mus musculus schlafen2 (Slfn2) mRNA, complete cds.//8.3e-42:458:72//AF099973

F-HEM BB1000975//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK5, complete sequence.//0.98:196:63//AB005234

F-HEM BB1000981

30 F-HEM BB1000985//Homo sapiens chromosome 19, cosmid R29388, complete sequence.//2.9e-06:566:57//AC004476

F-HEM BB1000991//Human DNA sequence from PAC 238J17 on chromosome 6q22. Contains EST and STS.//0.099:391:57//Z98753

F-HEM BB1000996//Human DNA sequence from BAC 999D10 on chromosome 22q13.3. Contains two BAC end-sequences (GSSs).//6.2e-33:227:80//Z94802

35 F-HEM BB1001004

F-HEM BB1001008//Human Chromosome 16 BAC clone CIT987SK-A-951C11, complete sequence.//4.0e-13:164:79//AC002551

F-HEM BB1001011//Human Chromosome 16 BAC clone CIT987SK-A-635H12, complete sequence.//7.5e-13:229:69//AC002310

40 F-HEM BB1001014//Homo sapiens chromosome 16, BAC clone 375G12 (LANL), complete sequence.//0.32:474:58//AC005751

F-HEM BB1001020//Homo sapiens BAC clone 255A7 from 8q21 containing NBS1 gene, complete sequence.//2.6e-39:218:80//AF069291

45 F-HEM BB1001024//Homo sapiens BAC clone 393I22 from 8q21, complete sequence.//5.3e-05:656:59//AF070717

F-HEM BB1001037//CIT-HSP-2358K16.TF CIT-HSP Homo sapiens genomic clone 2358K16, genomic survey sequence.//6.6e-05:228:64//AQ080539

F-HEM BB1001047//Homo sapiens cosmids Qc14E2, Qc12H12, Qc11F9, Qc10G9, LA1733 and Qc17B8 from Xq28, complete sequence.//4.0e-27:385:71//U82671

50 F-HEM BB1001051//H.sapiens mRNA for FAN protein.//1.2e-27:160:98//X96586

F-HEM BB1001056//Homo sapiens clone DJ0953A04, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.3e-89:180:91//AC006014

F-HEM BB1001058//Homo sapiens 3p22-8 PAC RPC14-736H12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.2e-41:468:74//AC006060

55 F-HEM BB1001060//Human Tigger1 transposable element, complete consensus sequence.//4.3e-122:785:86//U49973

F-HEM BB1001061//Homo sapiens 3p22-8 PAC RPC14-736H12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.2e-41:468:74//AC006060

F-HEM BB1001068//Homo sapiens liprin-beta2 mRNA, partial cds.//3.1e-146:736:95//AF034803

F-HEM BB1001096//Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene, partial cds.//0.00088:690:57//AF008210

5 F-HEM BB1001102//Homo sapiens huntingtin interacting protein HYPH mRNA, partial cds.//2.1e-76:368:99//AF049612

F-HEM BB1001105//CIT-HSP-2185N1.TR CIT-HSP Homo sapiens genomic clone 2185N1, genomic survey sequence.//1.0e-09:136:76//AQ002987

F-HEM BB1001112//Rattus rattus sec61 homologue mRNA, complete cds.//1.0e-108:909:76//M96630

10 F-HEM BB1001114//Homo sapiens chromosome 17, clone hRPK.795_F_17, complete sequence.//7.2e-07:459:59//AC005284

F-HEM BB1001117//HS_2178_B1_E12_MR CIT Approved-Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2178 Col=23 Row=J, genomic survey sequence.//7.8e-50:331:86//AQ068244

F-HEM BB1001119//Human collagen type XII alpha-1 precursor (COL12A1) mRNA, complete cds.//1.6e-25:150:98//U73778

15 F-HEM BB1001126

F-HEM BB1001133//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//2.8e-24:228:80//AC004673

F-HEM BB1001137

20 F-HEM BB1001142//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//1.0e-40:231:76//AC004617

F-HEM BB1001151//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//2.9e-47:640:67//AF015264

F-HEM BB1001153//CIT-HSP-2359K11.TR CIT-HSP Homo sapiens genomic clone 2359K11, genomic survey sequence.//0.76:136:67//AQ075724

25 F-HEM BB1001169//Human DNA sequence from PAC 84F12 on chromosome Xq25-Xq26.3. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2), ESTs and CA repeat.//9.9e-63:259:79//AL008712

F-HEM BB1001175//Human mRNA for ankyrin motif, complete cds.//2.2e-34:509:66//D78334

F-HEM BB1001177//CIT-HSP-2321I17.TR CIT-HSP Homo sapiens genomic clone 2321I17, genomic survey sequence.//5.9e-27:320:75//AQ036473

30 F-HEM BB1001182//RPCI11-30J5.TV RPCI-11 Homo sapiens genomic clone RPCI-11-30J5, genomic survey sequence.//5.7e-06:62:96//B85188

F-HEM BB1001199

F-HEM BB1001208//HS_2026_B1_C07_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026 Col=13 Row=F, genomic survey sequence.//0.00018:134:70//AQ229237

35 F-HEM BB1001209//CITBI-E1-2521F23.TF CITBI-E1 Homo sapiens genomic clone 2521F23, genomic survey sequence.//1.4e-95:464:98//AQ278357

F-HEM BB1001210//HS_3102_A2_F09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3102 Col=18 Row=K, genomic survey sequence.//2.6e-90:446:98//AQ119196

40 F-HEM BB1001218//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 796F18, WORKING DRAFT SEQUENCE.//1.0e-31:315:72//AL031291

F-HEM BB1001221//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//9.7e-17:770:59//AC005504

F-HEM BB1001234//H.sapiens CpG island DNA genomic Mse1 fragment, clone 39f9, forward read cpg39f9.ft1e//4.0e-30:171:97//Z65435

45 F-HEM BB1001242//Homo sapiens mRNA for LAK-1, complete cds.//3.8e-30:458:67//AB005754

F-HEM BB1001249//CIT-HSP-2375N19.TF CIT-HSP Homo sapiens genomic clone 2375N19, genomic survey sequence.//0.0076:250:63//AQ109087

F-HEM BB1001253//Homo sapiens genomic DNA, chromosome 21q11.1, segment 3/28, WORKING DRAFT SEQUENCE.//0.0097:89:80//AP000032

50 F-HEM BB1001254//CIT-HSP-2320E5.TF CIT-HSP Homo sapiens genomic clone 2320E5, genomic survey sequence.//3.7e-54:284:97//AQ037173

F-HEM BB1001267//Homo sapiens chromosome 17, clone hRPK.488_L_1, complete sequence.//3.5e-30:236:78//AC005303

55 F-HEM BB1001271//HS_3011_A1_G02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3011 Col=3 Row=M, genomic survey sequence.//5.2e-07:364:62//AQ214217

F-HEMBB1001288//R.norvegicus mRNA for gephyrin.//3.4e-18:194:77//X66366
 F-HEMBB1001289//Genomic sequence from Human 9q34, complete sequence.//4.8e-66:434:74//AC000387
 F-HEMBB1001294//HS_3039_B1_D01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3039 Col=1 Row=H, genomic survey sequence.//2.0e-90:437:99//AQ155035
 5 F-HEMBB1001302
 F-HEMBB1001304//CIT-HSP-2053E15.TF CIT-HSP Homo sapiens genomic clone 2053E15, genomic survey se-
 quence.//2.2e-07:370:61//B69144
 F-HEMBB1001314//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//5.7e-116:
 663:85//J92703
 10 F-HEMBB1001315//Homo sapiens chromosome 10 clone LA10NC01_40_G_3 map 10q26.1-10q26.2, WORKING
 DRAFT SEQUENCE, 1 ordered pieces.//2.5e-33:328:77//AC006096
 F-HEMBB1001317//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) com-
 plete sequence.//1.4e-122:680:91//AC006210
 F-HEMBB1001326//Homo sapiens BAC clone RG136N17 from 7p15-p21, complete sequence.//2.8e-09:518:60//
 15 AC004129
 F-HEMBB1001331//Mus musculus mRNA for hepatoma-derived growth factor, complete cds, strain:BALB/c.//3.7e-
 56:458:79//D63850
 F-HEMBB1001335//HS_3055_A1_H10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3055 Col=19 Row=O, genomic survey sequence.//1.0:222:63//AQ147384
 20 F-HEMBB1001337//Human PAC clone DJ0093I03 from Xq23, complete sequence.//1.0e-74:319:85//AC003983
 F-HEMBB1001339//Homo sapiens FSHD-associated repeat DNA, proximal region.//4.0e-135:856:87//J85056
 F-HEMBB1001346//Human familial Alzheimer's disease (STM2) gene, complete cds.//3.3e-44:481:74//J50871
 F-HEMBB1001348//Homo sapiens BAC clone NH0491B03 from 7p21-p15, complete sequence.//1.8e-17:210:73//
 AC006041
 25 F-HEMBB1001356//Homo sapiens clone RG252P22, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.0:
 386:59//AC005079
 F-HEMBB1001364//Homo sapiens chromosome 17, clone hRPC.842_A_23, complete sequence.//0.97:349:61//
 AC004662
 F-HEMBB1001366//Homo sapiens chromosome 10 clone CIT987SK-1188I5 map 10p11.2-10p12.1, complete se-
 30 quence.//5.5e-161:766:98//AC005876
 F-HEMBB1001367//Homo sapiens chromosome 17, clone hRPC.906_A_24, complete sequence.//3.0e-55:510:
 76//AC004408
 F-HEMBB1001369//Homo sapiens BAC clone RG163K11 from 7q31, complete sequence.//0.048:244:64//
 AC005192
 35 F-HEMBB1001380//Homo sapiens PAC clone DJ1102B04 from 7q11.23-7q21, complete sequence.//2.5e-26:257:
 78//AC006204
 F-HEMBB1001384//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, complete cds.//5.1e-99:571:89//
 AF071314
 F-HEMBB1001387//Leishmania tarentolae mitochondrial 12S ribosomal RNA gene.//7.1e-05:546:58//X02354
 40 F-HEMBB1001394//Homo sapiens BAC clone GS421I03 from Xq25-q26, complete sequence.//4.0e-129:788:88//
 AC005023
 F-HEMBB1001410//Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete
 cds.//4.8e-11:632:59//AF045555
 F-HEMBB1001424//Mus musculus Chromosome 4 BAC clone BacB6, complete sequence.//0.0012:435:59//
 45 AC003019
 F-HEMBB1001426//Homo sapiens clone DJ0736H05, WORKING DRAFT SEQUENCE, 5 unordered pieces.//
 3.8e-17:360:64//AC005482
 F-HEMBB1001429//leucine aminopeptidase [cattle, kidney, mRNA, 2056 nt].//4.1e-114:668:88//S65367
 F-HEMBB1001436//Homo sapiens FUT2 gene, intron 1, complete sequence.//2.3e-37:438:74//AB000931
 50 F-HEMBB1001443//Bos taurus pyruvate dehydrogenase phosphatase mRNA, complete cds.//9.1e-92:550:88//
 L18966
 F-HEMBB1001449//Homo sapiens chromosome 5, PAC clone 228g9 (LBNLH142), complete sequence.//0.00024:
 385:62//AC004768
 F-HEMBB1001454//Homo sapiens chromosome 19, cosmid R34169, complete sequence.//0.84:577:57//
 55 AC005790
 F-HEMBB1001458//Human Chromosome 11, clone 107H17, WORKING DRAFT SEQUENCE, 11 unordered
 pieces.//1.0e-10:107:17//AC005876
 F-HEMBB1001459//Human Chromosome 11, clone 107H17, WORKING DRAFT SEQUENCE, 11 unordered
 pieces.//1.0e-10:107:17//AC005876

59//AF001549

F-HEMBB1001464//Human chromosome 16p13 BAC clone CIT987SK-3H8 complete sequence//0.019:263:61//U91320

F-HEMBB1001482//Rattus norvegicus Olf-1/EBF associated Zn finger protein Roaz mRNA, alternatively spliced form, complete cds//1.0e-30:521:66//U92564

F-HEMBB1001500//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces//1.3e-31:479:71//AC004873

F-HEMBB1001521//Homo sapiens clone RG269P13, WORKING DRAFT SEQUENCE, 6 unordered pieces//3.7e-51:680:70//AC005080

F-HEMBB1001527

F-HEMBB1001531//Homo sapiens Chromosome 22q11.2 Cosmid Clone 89h In DGCR Region, complete sequence//1.3e-79:696:79//AC000089

F-HEMBB1001535//O. aries DNA for polymorphic marker 'OVINRA01' (339 bp)//0.00034:217:62//X89268

F-HEMBB1001536//Homo sapiens PAC clone DJ1182N03 from 7q11.23-q21.1, complete sequence//0.54:266:60//AC004548

F-HEMBB1001537//Homo sapiens chromosome 19, cosmid R29368, complete sequence//4.6e-25:784:61//AC004262

F-HEMBB1001555//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence//6.9e-50:213:80//AC004605

F-HEMBB1001562//Homo sapiens clone NH0523H20, complete sequence//0.46:269:60//AC005041

F-HEMBB1001564//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudo-gene similar to rat Plasmolipin, ESTs and GSSs, complete sequence//1.7e-107:620:83//AL020989

F-HEMBB1001565//Homo sapiens BAC clone RG437L15 from 8q21, complete sequence//2.4e-50:734:67//AC004003

F-HEMBB1001585//Human DNA sequence from clone 790B6 on chromosome 20p11.22-12.2. Contains STSs and GSSs, complete sequence//1.4e-166:816:97//AL031677

F-HEMBB1001586

F-HEMBB1001588//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence//1.6e-21:419:65//AC005261

F-HEMBB1001603

F-HEMBB1001618//Homo sapiens DNA sequence from PAC 142L7 on chromosome 6q21. Contains a Laminin Alpha 4 (LAMA4) LIKE gene coding for two alternatively spliced transcripts, a Tubulin Beta LIKE pseudogene, a Connective tissue growth factor (NOV, GIG) LIKE gene, A predicted CpG island, ESTs, STSs and genomic marker D6S416, complete sequence//4.5e-29:422:72//Z99289

F-HEMBB1001619//HS_3079_B1_A04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3079 Col=7 Row=B, genomic survey sequence//0.0010:77:79//AQ123388

F-HEMBB1001630//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces//3.2e-12:667:59//AC005089

F-HEMBB1001635//Plasmodium falciparum MAL3P7, complete sequence//3.8e-05:475:57//AL034559

F-HEMBB1001637//Homo sapiens DNA sequence from PAC 934G17 on chromosome 1p36.21. Contains the alternatively spliced CLCN6 gene for chloride channel proteins CLC-6A (KIAA0046) -B, -C and -D, the alternatively spliced NPPA gene coding for Atrial Natriuretic Factor ANF precursor (Atrial Natriuretic peptide ANP, Prepronatriuretin), the NPPB gene for Brain Natriuretic Protein BNP, and a pseudogene similar to SBF1 (and other Myotubularin-related protein genes). Contains ESTs, STSs and the genomic marker D1S2740, complete sequence//9.2e-13:168:76//AL021155

F-HEMBB1001641//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPO12, complete sequence//0.00097:721:58//AB006702

F-HEMBB1001653//Homo sapiens chromosome 2 clone 101B6 map 2p11, complete sequence//0.15:276:63//AC002038

F-HEMBB1001665//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds//0.43:393:61//L14320

F-HEMBB1001668//F16C15-T7 IGF Arabidopsis thaliana genomic clone F16C15, genomic survey sequence//0.040:275:60//B12308

F-HEMBB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds//7.2e-171:803:98//AB014546

F-HEMBB1001684//Sequence 1 from patent US 5700927//7.5e-124:883:81//I86429

F-HEMBB1001685//CIT HSP 628706 T7 P1 1000 bp DNA sequence from clone 628706

F-HEMBB1001686//CIT HSP 628706 T7 P1 1000 bp DNA sequence from clone 628706

F-HEMBB1001687//CIT HSP 628706 T7 P1 1000 bp DNA sequence from clone 628706

F-HEMBB1001688//CIT HSP 628706 T7 P1 1000 bp DNA sequence from clone 628706

exon of the MLLT4 gene for myeloid/lymphoid or mixed-lineage leukemia (trithorax (*Drosophila*) homolog); translocated to, 4 (AF-6, Afadin, MLLT-4, ALL-1 fusion partner), and a Serine Palmitoyltransferase 2 (EC 2.3.1.50, Long Chain Base Biosynthesis protein 2, LCB-2, SPT-2) pseudogene. Contains ESTs, STss, GSSs, and a putative CpG island, complete sequence.//0.0091:334:63//AL009178

F-HEM BB1001704//Human DNA sequence from clone 931E15 on chromosome Xq25. Contains STss, GSSs and genomic marker DXS8098, complete sequence.//1.2e-17:144:87//AL023575

F-HEM BB1001706

F-HEM BB1001707//Guinea pig CD19 mRNA, complete cds.//0.57:232:62//M62543

F-HEM BB1001717//*Saccharomyces cerevisiae* mitochondrial tRNA-Tyr, tRNA-Asn, & amp; tRNA-Met genes.//

1.1e-13:723:58//AJ223323

F-HEM BB1001735//Human PAC clone DJ0596O09 from 7p15, complete sequence.//1.3e-36:427:73//AC003074

F-HEM BB1001736//*S.pombe* chromosome II cosmid c4B4.//0.0085:479:57//AL023706

F-HEM BB1001747//Homo sapiens PAC clone DJ1002N02 from 7p21-p22, complete sequence.//4.0e-112:532:84//AC005376

F-HEM BB1001749//Homo sapiens chromosome 17, clone hRPK.259_G_18, complete sequence.//1.3e-98:395:82//AC005829

F-HEM BB1001753//*S.maximus* repeat region, 342bp.//4.2e-11:69:85//Z78099

F-HEM BB1001756//Homo sapiens full-length insert cDNA clone ZD86A11.//0.0015:302:62//AF088064

F-HEM BB1001760//*P.falciparum* complete gene map of plastid-like DNA (IR-A).//0.011:615:56//X95275

F-HEM BB1001762//CIT-HSP-2290J16.TF CIT-HSP Homo sapiens genomic clone 2290J16, genomic survey sequence.//0.84:208:64//AQ005184

F-HEM BB1001785//*Plasmodium falciparum* DNA *** SEQUENCING IN PROGRESS *** from MAL1P3, WORKING DRAFT SEQUENCE.//0.0019:469:60//AL031746

F-HEM BB1001797//Human heterogenous nuclear RNA W16W.//0.00012:83:86//X17272

F-HEM BB1001802//*Plasmodium falciparum* MAL3P7, complete sequence.//1.8e-11:538:60//AL034559

F-HEM BB1001812//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 356B8, WORKING DRAFT SEQUENCE.//1.0e-56:304:84//Z98882

F-HEM BB1001816//Homo sapiens chromosome 19, cosmid F24083, complete sequence.//3.6e-75:300:87//AC005204

F-HEM BB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds.//2.3e-162:763:98//AF056209

F-HEM BB1001834//CIT-HSP-2291012.TF CIT-HSP Homo sapiens genomic clone 2291O12, genomic survey sequence.//7.6e-08:73:94//AQ004168

F-HEM BB1001836//Homo sapiens 12q13.1 PAC RPC1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//5.7e-30:297:79//AC004801

F-HEM BB1001839//Human Chromosome X, complete sequence.//0.016:293:63//AC004073

F-HEM BB1001850//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.0027:812:58//AC005504

F-HEM BB1001863//Human Chromosome 15q26.1 PAC clone pDJ460g16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//8.3e-43:520:72//AC004581

F-HEM BB1001867//Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds.//1.7e-56:399:86//U07563

F-HEM BB1001868//*Rattus norvegicus* clone 923 polymeric immunoglobulin receptor mRNA 3' untranslated region, GA rich region, and microsatellites with GGA-triplet and GAA-triplet repeats.//6.1e-08:234:67//U01145

F-HEM BB1001869//Homo sapiens full-length insert cDNA clone YT86F01.//7.4e-87:432:97//AF085974

F-HEM BB1001872

F-HEM BB1001874//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.4e-14:631:61//AC005000

F-HEM BB1001875//Human DNA sequence from clone J428A131, WORKING DRAFT SEQUENCE.//0.93:415:57//Z82209

F-HEM BB1001880//Human genomic DNA sequence from clone 308O1 on chromosome Xp11.3-11.4. Contains EST, CA repeat, STS, GSS, CpG island.//1.0e-18:729:60//Z93403

F-HEM BB1001899//*Plasmodium falciparum* DNA *** SEQUENCING IN PROGRESS *** from contig 4-10, complete sequence.//0.0038:425:58//AL010216

F-HEM BB1001905//*S.pombe* chromosome III cosmid c330.//1.1e-23:520:62//AL031603

F-HEM BB1001906

F-HEM BB1001907//Human DNA sequence from clone J428A131, WORKING DRAFT SEQUENCE.//0.93:415:57//Z82209

U04774.

F-HEM BB1001910//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0033:566:55//AC005505

F-HEM BB1001911//*Arabidopsis thaliana* chromosome II BAC F26C24 genomic sequence, complete sequence.//1.0:581:58//AC004705

5 F-HEM BB1001915//*Caenorhabditis elegans* cosmid T05H10, complete sequence.//1.2e-16:283:67//Z47812

F-HEM BB1001921//*Homo sapiens* chromosome 17, clone hCIT.123_J_14, complete sequence.//3.4e-07:803:58//AC003950

F-HEM BB1001922//*Plasmodium falciparum* chromosome 2, section 28 of 73 of the complete sequence.//5.0e-06:756:56//AE001391

10 F-HEM BB1001925//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1p35. Contains delta opiate receptor, CpG island, CA repeat.//3.1e-45:609:73//AL009181

F-HEM BB1001930//*Homo sapiens* genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 10/11.//3.2e-158:745:99//AB020867

F-HEM BB1001944//, complete sequence.//4.1e-60:638:73//AC005815

15 F-HEM BB1001945//HS_3185_B1_G05_MR CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3185 Col=9 Row=N, genomic survey sequence.//1.0:280:58//AQ188882

F-HEM BB1001947//Human mRNA for KIAA0392 gene, partial cds.//5.6e-20:333:66//AB002390

F-HEM BB1001950//Human lipocortin (LIP) 2 gene, upstream region.//0.0094:180:63//M62899

20 F-HEM BB1001952//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 101A4, WORKING DRAFT SEQUENCE.//5.4e-19:329:70//Z93341

F-HEM BB1001953//*Homo sapiens* chromosome 17, clone hRPK.795_F_17, complete sequence.//0.11:589:58//AC005284

25 F-HEM BB1001957//Human DNA sequence from PAC 204E5 on chromosome 12. Contains exon similar to Wilms' Tumour-related protein QM-like P2X-like receptor, ATP ligand gated ion channel, ESTs, CpG island.//9.8e-25:446:67//Z98941

F-HEM BB1001962//*Homo sapiens* chromosome 16, BAC clone 462G18 (LANL), complete sequence.//2.8e-147:727:97//AC005736

F-HEM BB1001967//*Homo sapiens* clone DJ1102A12, WORKING DRAFT SEQUENCE, 15 unordered pieces.//3.2e-56:650:71//AC004963

30 F-HEM BB1001973//*Homo sapiens* chromosome 12p13.3-clone RPCI11-350L7, WORKING DRAFT SEQUENCE, 72 unordered pieces.//1.2e-42:327:84//AC005844

F-HEM BB1001983//CIT-HSP-2315M4.TF CIT-HSP *Homo sapiens* genomic clone 2315M4, genomic survey sequence.//8.8e-35:198:96//AQ028071

F-HEM BB1001988//*D. polychroa* microsatellite sequence (clone Dp 1C e12).//4.5e-07:337:62//X92189

35 F-HEM BB1001990//HS_3234_A1_G08_T7 CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3234 Col=15 Row=M, genomic survey sequence.//0.039:279:59//AQ204689

F-HEM BB1001996//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 191J18, WORKING DRAFT SEQUENCE.//0.18:392:58//AL024507

40 F-HEM BB1001997//*Homo sapiens* clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//1.3e-43:446:71//AC005069

F-HEM BB1002002//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.077:444:58//AC004153

F-HEM BB1002005//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 963K23, WORKING DRAFT SEQUENCE.//3.4e-16:173:78//AL031685

45 F-HEM BB1002009//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.00033:790:56//AC005506

F-HEM BB1002015//*Homo sapiens* genomic DNA, chromosome 21q11.1, segment 27/28, WORKING DRAFT SEQUENCE.//6.7e-05:126:76//AP000056

50 F-HEM BB1002042//*Oncorhynchus mykiss* cytochrome P450 (CYP4V1) mRNA, partial cds.//6.4e-33:402:69//AF046012

F-HEM BB1002043

F-HEM BB1002044//*Homo sapiens* chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//3.0e-167:809:97//AC005740

F-HEM BB1002045

55 F-HEM BB1002049//*Homo sapiens* chromosome 17, clone hRPC.161 P_9, complete sequence.//0.87:177:65//AF006231

F-HEM BB1002050//*Streptomyces* genomic DNA cosmid clone 1044 BB AC004935

F-HEM BB1002068//*Homo sapiens* mRNA for KIAA0612 protein, partial cds.//2.5e-05:402:69//AB004935

F-HEM BB1002069

F-HEM BB1002092//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone B33108; HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//7.8e-104:550:83//AC004064

F-HEM BB1002094//Homo sapiens genomic DNA, 21q region, clone: 125H6N2, genomic survey sequence.//2.9e-49:302:83//AG001476

F-HEM BB1002115//Homo sapiens chromosome 16, cosmid clone 378E2 (LANL), complete sequence.//0.00023:542:61//AC004035

F-HEM BB1002134//Human h-neuro-d4 protein mRNA, complete cds.//7.3e-43:533:70//U43843

F-HEM BB1002139//HS-1048-A2-B02-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 831 Col=4 Row=C, genomic survey sequence.//0.055:228:66//B38714

F-HEM BB1002142//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P5, WORKING DRAFT SEQUENCE.//0.0095:276:64//AL031748

F-HEM BB1002152//Human Chromosome X, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.055:520:57//AC002421

F-HEM BB1002189//Homo sapiens cosmid ICRFc104I0935Q8 from Xq28, complete sequence.//2.6e-05:311:63//AF002998

F-HEM BB1002190//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//5.4e-05:647:59//AC005140

F-HEM BB1002193//Sequence 5 from patent US 5709858.//1.8e-34:179:100//I80846

F-HEM BB1002217//Homo sapiens mRNA for zinc finger protein 10.//1.2e-23:405:67//X52332

F-HEM BB1002218//HS_2056_B1_C09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2056 Col=17 Row=F, genomic survey sequence.//3.3e-45:245:97//AQ244711

F-HEM BB1002232//Human chromosome 11 72g7 cosmid, complete sequence.//1.9e-21:314:70//U73648

F-HEM BB1002247

F-HEM BB1002249//Homo sapiens DNA sequence from BAC 34I8 on chromosome 6p21.3-22.1. Contains ZNF184 gene coding for Kruppel related Zinc Finger protein 184, a hnRNP core protein A1 (mouse Fli-2, rat helix destabilizing protein, mouse Topoisomerase-inhibitor suppressed gene TIS) LIKE pseudogene, a HB15 (CD83 antigen precursor) LIKE pseudogene, Ser-tRNA, Glu-tRNA and Met-tRNA (Met-tRNA-i gene 1) genes. Contains ESTs, STSs and GSSs, complete sequence.//4.1e-45:327:83//AL021918

F-HEM BB1002254//Human chromosome 16 BAC clone LANL cosmid-440E5, WORKING DRAFT SEQUENCE, 2 unordered pieces.//9.8e-40:315:82//AC002506

F-HEM BB1002255//Plasmodium falciparum MAL3P3, complete sequence.//0.0035:312:62//Z98547

F-HEM BB1002266//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.013:469:59//AC005504

F-HEM BB1002280//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-259H10, complete sequence.//5.3e-18:527:61//AC004682

F-HEM BB1002300//Human Chromosome 11 Cosmid cSRL30h11, complete sequence.//8.6e-139:818:88//U73642

F-HEM BB1002306//HS_3109_A2_H01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3109 Col=2 Row=O, genomic survey sequence.//1.3e-75:371:98//AQ148164

F-HEM BB1002327//HS_3235_B2_G10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3235 Col=20 Row=N, genomic survey sequence.//3.3e-83:418:97//AQ209752

F-HEM BB1002329//CITBI-E1-2503J7.TR CITBI-E1 Homo sapiens genomic clone 2503J7, genomic survey sequence.//3.3e-31:220:88//AQ263402

F-HEM BB1002340

F-HEM BB1002342//Homo sapiens mRNA for putative thioredoxin-like protein.//4.1e-154:724:98//AJ010841

F-HEM BB1002358//Human thymidylate kinase (CDC8) mRNA, complete cds.//3.3e-36:192:98//L16991

F-HEM BB1002359//Human Rev interacting protein Rip-1 mRNA, complete cds.//1.8e-13:96:96//U55766

F-HEM BB1002364//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 376D21, WORKING DRAFT SEQUENCE.//7.5e-24:202:71//Z98946

F-HEM BB1002371//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.9e-06:674:56//AC004153

F-HEM BB1002381//Homo sapiens chromosome 16, cosmid clone RT163 (LANL), complete sequence.//0.34:238:61//AC005222

F-HEM BB1002383

F-HEM BB1002387//Homo sapiens chromosome 16, cosmid clone RT163 (LANL), complete sequence.//0.34:238:61//AC005222

F-HEM BB1002388//Homo sapiens chromosome 16, cosmid clone RT163 (LANL), complete sequence.//0.34:238:61//AC005222

F-HEM BB1002389//Homo sapiens chromosome 16, cosmid clone RT163 (LANL), complete sequence.//0.34:238:61//AC005222

precursor (intestinal protein OCI-5) (GTR2-2), ESTs and CA repeat.//1.2e-56:324:88//AL008712
F-HEM BB1002415//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 364I1, WORKING DRAFT SEQUENCE.//8.9e-35:334:75//AL031319
F-HEM BB1002425//Chromosome 22q13 BAC Clone CIT987SK-384D8 complete sequence.//1.0e-36:317:76//U62317
F-HEM BB1002442//Rattus norvegicus lin-10 protein homolog (lin-10) mRNA, complete cds.//4.3e-88:296:92//U92010
F-HEM BB1002453//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 86D1, WORKING DRAFT SEQUENCE.//2.7e-43:419:78//AL034349
F-HEM BB1002457//Homo sapiens clone DJ0982E09, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.3e-27:542:68//AC005534
F-HEM BB1002458//HS_3246_A2_G05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3246 Col=10 Row=M, genomic survey sequence.//3.2e-51:257:99//AQ217993
F-HEM BB1002477//Human Grb2-associated binder-1 mRNA, complete cds.//1.9e-87:493:92//U43885
F-HEM BB1002489
F-HEM BB1002492//Arabidopsis thaliana BAC T15B16.//0.028:516:57//AF104919
F-HEM BB1002495//Homo sapiens chromosome 17, clone hRPK.421_E_14, complete sequence.//1.1e-16:297:68//AC006141
F-HEM BB1002502//Homo sapiens clone DJ1163L11, complete sequence.//1.1e-91:675:82//AC005230
F-HEM BB1002509//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//2.7e-11:648:60//AC004605
F-HEM BB1002510//HS_3236_B1_H11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3236 Col=21 Row=P, genomic survey sequence.//1.2e-06:67:94//AQ205992
F-HEM BB1002520//Homo sapiens BAC clone NH0004N07 from Y, complete sequence.//1.2e-70:580:72//AC006152
F-HEM BB1002522//Homo sapiens Xp22 bin 150 clone GSHB-223P11 (Genome Systems Human BAC library) complete sequence.//5.6e-22:516:64//AC004553 F-HEM BB1002531
F-HEM BB1002534//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 668J24, WORKING DRAFT SEQUENCE.//6.9e-62:265:87//AL034346
F-HEM BB1002545//Human BAC clone RG128M16 from 7q21-7q22, complete sequence.//2.7e-44:200:82//AC000059
F-HEM BB1002550//Homo sapiens PAC clone DJ0910I17 from 7q11.21-q11.23, complete sequence.//0.22:161:68//AC004927
F-HEM BB1002556//Homo sapiens PAC clone DJ0696N01 from 7p21-p22, complete sequence.//7.5e-43:306:77//AC004861
F-HEM BB1002579
F-HEM BB1002582//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 349A12, WORKING DRAFT SEQUENCE.//0.00018:431:61//AL033520
F-HEM BB1002590//Yeast (*S.cerevisiae*) mitochondrial apocytochrome b gene, 3' flank.//0.78:147:64//J01471
F-HEM BB1002596//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 9E21, WORKING DRAFT SEQUENCE.//3.6e-50:692:69//AL008639
F-HEM BB1002600//Homo sapiens tetraspan NET-5 mRNA, complete cds.//9.1e-151:710:98//AF089749
F-HEM BB1002601//Human BAC clone RG020D02 from 7q22, complete sequence.//1.5e-07:416:60//AC002381
F-HEM BB1002603//Human BAC clone GS552A01 from 7q21-q22, complete sequence.//0.40:341:60//AC002454
F-HEM BB1002607//Mus musculus homeobox containing nuclear transcriptional factor Hmx1 (Hmx1) gene, complete cds.//0.0042:460:60//AF009614
F-HEM BB1002610//Homo sapiens Chromosome 12q24 PAC RPCI3-462E2 (Roswell Park Cancer Institute Human PAC library) complete sequence.//6.3e-23:559:63//AC003029
F-HEM BB1002613//Homo sapiens Chromosome 22q12 BAC Clone 566c1, complete sequence.//4.2e-17:441:63//AC000025
F-HEM BB1002614//Plasmodium falciparum chromosome 2, section 54 of 73 of the complete sequence.//0.013:324:56//AE001417
F-HEM BB1002617//Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence.//2.1e-07:441:60//AF001550
F-HEM BB1002623//C.hyalina microsatellite marker DNA (id ATCC4).//0.57:106:66//Z95304
F-HEM BB1002635//Homo sapiens chromosome 12p11.2 BAC clone C12orf10.1 (human chromosome 12 open reading frame 10.1) complete cds.
F-HEM BB1002636//Homo sapiens chromosome 12p11.2 BAC clone C12orf10.1 (human chromosome 12 open reading frame 10.1) complete cds.

omic clone Plate=2265 Col=11 Row=O, genomic survey sequence//0.54:115:67//AQ101557

F-HEMBB1002677//Homo sapiens (subclone 3_d1 from P1 H25) DNA sequence, complete sequence//2.2e-49:784:68//L81774

F-HEMBB1002683//Homo sapiens type IV collagen 5a chain (COL4A5) gene, exon 23//1.0:112:63//U04492

F-HEMBB1002684//HS-1050-A2-G06-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 772 Col=12 Row=M, genomic survey sequence//4.4e-07:86:84//B39748

F-HEMBB1002686//HS-1023-B2-F10-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 802 Col=20 Row=L, genomic survey sequence//0.98:183:61//B34077

F-HEMBB1002692//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1108H3, WORKING DRAFT SEQUENCE//0.00039:408:60//AL033525

F-HEMBB1002697//Homo sapiens clone DJ1087M19, WORKING DRAFT SEQUENCE, 7 unordered pieces//7.3e-35:323:74//AC004955

F-HEMBB1002699//Mus musculus D6MM5e protein (D6Mm5e) and DOK protein (Dok) genes, complete cds; and LOR2 protein (Lor2) gene, partial cds//0.031:325:62//AF084363

F-HEMBB1002702//HS-1025-A2-D01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 804 Col=2 Row=G, genomic survey sequence//1.8e-25:158:95//B34720

F-HEMBB1002705//Homo sapiens DNA, chromosome 21q22.2, PAC clone 25P16 complete sequence, encoding carbonyl reductase and carbonyl reductase 3 (complete cds)//1.7e-137:534:96//AB003151

F-HEMBB1002712//Human DNA sequence from cosmid cU115G11, between markers DXS6791 and DXS8038 on chromosome X contains ESTs and STS//0.0019:612:58//Z71187

F-MAMMA1000009//Human chromosome 1 BAC 308G1 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces//6.1e-43:354:81//AC003117

F-MAMMA1000019

F-MAMMA1000020//H.sapiens mRNA for flavin-containing monooxygenase 5 (FMO5)//2.0e-40:185:97//Z47553

F-MAMMA1000025//Homo sapiens PAC clone DJ0806A17 from 7p13-p14, complete sequence//1.0:211:65//AC005483

F-MAMMA1000043//Human angiotensin I-converting enzyme (ACE) gene, intron 12//0.075:204:65//M73275

F-MAMMA1000045//Human DNA sequence from clone 142F18 on chromosome Xq26.3-27.2 Contains part of a gene similar to melanoma-associated antigen, EST, GSS and an inverted repeat, complete sequence//4.1e-122:495:79//AL031073

F-MAMMA1000055//M.musculus mRNA for testin//2.1e-35:559:66//X78989

F-MAMMA1000057//Homo sapiens chromosome 17, clone hRPK.259_G_18, complete sequence//5.5e-121:703:89//AC005829

F-MAMMA1000069//Homo sapiens minisatellite ceb1 repeat region//0.00013:329:60//AF048727

F-MAMMA1000084//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island//2.1e-53:445:79//Z93023

F-MAMMA1000085//Caenorhabditis elegans cosmid Y23H5A//0.0017:164:64//AF077541

F-MAMMA1000092//Homo sapiens BAC clone GS465N13 from 7p15-p21, complete sequence//1.2e-70:598:78//AC004744

F-MAMMA1000103//Homo sapiens chromosome 17, clone hCIT.91_J_4, complete sequence//1.1e-156:857:92//AC003976

F-MAMMA1000117//HS_3223_B2_D08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3223 Col=16 Row=H, genomic survey sequence//5.4e-100:527:94//AQ221160

F-MAMMA1000129//ryanodine receptor//0.055:492:59//A20359

F-MAMMA1000133

F-MAMMA1000134//HS_3078_B1_C02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3078 Col=3 Row=F, genomic survey sequence//2.1e-93:462:97//AQ144362

F-MAMMA1000139//Homo sapiens Xp22 PAC RPC11-5G11 (from Roswell Park Cancer Center) complete sequence//3.3e-14:322:65//AC002369

F-MAMMA1000143//Homo sapiens mRNA for KIAA0685 protein, complete cds//6.9e-25:148:97//AB014585

F-MAMMA1000155//Homo sapiens homeobox transcription factor barx2 (BARX2) mRNA, complete cds//1.0e-29:219:87//AF031924

F-MAMMA1000163

F-MAMMA1000171//Homo sapiens chromosome 19, CIT-HSP BAC 470n8, complete sequence//6.3e-14:92:88//AC005393

F-MAMMA1000175//M.musculus

F-MAMMA1000176//M.musculus

F-MAMMA1000177//Homo sapiens chromosome 19, CIT-HSP BAC 470n8, complete sequence//6.3e-14:92:88//AC005393

nomic clone Plate=3050 Col=5 Row=D, genomic survey sequence.//6.2e-73:357:99//AQ102678
 F-MAMMA1000183//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING
 DRAFT SEQUENCE.//4.6e-94:904:73//AL023808
 F-MAMMA1000198//Z.diploperennis repetitive DNA (clone ZEAR 266).//0.18:152:70//X53610
 5 F-MAMMA1000221//Human Chromosome 15q11-q13 PAC clone pDJ778a2, complete sequence.//0.017:99:75//
 AC004583
 F-MAMMA1000227//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 467K16, WORKING
 DRAFT SEQUENCE.//0.36:312:62//AL031283
 F-MAMMA1000241//HS_3217_B1_B02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 10 nomic clone Plate=3217 Col=3 Row=D, genomic survey sequence.//1.9e-94:456:98//AQ193401
 F-MAMMA1000251//Homo sapiens NF2 gene.//0.00092:270:64//Y18000
 F-MAMMA1000254//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING
 DRAFT SEQUENCE, 14 unordered pieces.//0.0034:777:57//AC005140
 F-MAMMA1000257//Homo sapiens DNA sequence from PAC 201D7 on chromosome 6p22.1-22.3. Contains EST
 15 and STS.//0.00036:230:65//AL022717
 F-MAMMA1000264//Homo sapiens (subclone 9_f5 from P1 H17) DNA sequence, complete sequence.//1.5e-30:
 499:68//L81612
 F-MAMMA1000266//Bacillus lynceorum strain pMEL12 Bag320 satellite DNA.//0.28:218:64//AF034430
 F-MAMMA1000270//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//1.4e-157:
 20 788:96//AF001549
 F-MAMMA1000277//Mycobacterium tuberculosis H37Rv complete genome; segment 48/162.//0.70:320:61//
 AL021897
 F-MAMMA1000278//Sequence 23 from patent US 5708157.//9.3e-103:540:95//I80055
 F-MAMMA1000279//Human DNA sequence from clone 769D20 on chromosome Xp21.1-21.3 Contains EST, STS,
 25 GSS, complete sequence.//2.4e-49:262:77//AL031643
 F-MAMMA1000284//cSRL-165E12-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic
 clone cSRL-165E12, genomic survey sequence.//1.1e-30:324:75//B03004
 F-MAMMA1000287//Homo sapiens, clone hRPK.15_A_1, complete sequence.//2.7e-54:401:83//AC006213
 F-MAMMA1000302//Drosophila melanogaster complete mitochondrial genome.//0.0051:307:61//U37541
 30 F-MAMMA1000307//Homo sapiens chromosome 12p13.3 clone RPC15-1154L15, WORKING DRAFT SE-
 QUENCE, 67 unordered pieces.//0.15:449:59//AC006205
 F-MAMMA1000309//cDNA coding human apolipoprotein E3.//0.00010:691:58//E00359
 F-MAMMA1000312//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 798A17, WORKING
 DRAFT SEQUENCE.//0.27:301:60//AL031274
 35 F-MAMMA1000313
 F-MAMMA1000331//Human Chromosome 16 BAC clone CIT987SK-A-735G6, complete sequence.//9.8e-06:151:
 71//AC002400
 F-MAMMA1000339
 F-MAMMA1000340//HS_2181_B2_F07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 40 nomic clone Plate=2181 Col=14 Row=L, genomic survey sequence.//4.3e-05:181:68//AQ024288
 F-MAMMA1000348//Homo sapiens chromosome 17, clone HRC843B9, complete sequence.//5.3e-30:575:66//
 AC004139
 F-MAMMA1000356//Homo sapiens clone RG038K21, WORKING DRAFT SEQUENCE, 3 unordered pieces.//
 1.8e-52:264:76//AC005052
 45 F-MAMMA1000360//Homo sapiens PAC clone DJ0755G17 from 7p21-p22, complete sequence.//6.5e-91:569:88//
 AC004879
 F-MAMMA1000361//Human DNA sequence from PAC 507I15 on chromosome Xq26.3-27.3. Contains 60S ribos-
 omal protein L44 (L41, L36) like gene, ESTs, STSs and a polymorphic CA repeat.//1.4e-42:315:83//Z98950
 F-MAMMA1000372//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y738F9, WORKING
 50 DRAFT SEQUENCE.//2.9e-114:516:89//AL022345
 F-MAMMA1000385//CITBI-E1-2517E13.TF CITBI-E1 Homo sapiens genomic clone 2517E13, genomic survey
 sequence.//6.9e-26:377:71//AQ279944
 F-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds.//3.7e-148:710:
 98//AB015132
 55 F-MAMMA1000395
 F-MAMMA1000402//Human chromosome 10p11-p12 BAC clone CIT987SK-A-735G6, complete sequence.//9.8e-06:151:
 71//AC002400
 F-MAMMA1000403//HS_3217_B1_B02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3217 Col=3 Row=D, genomic survey sequence.//1.9e-94:456:98//AQ193401

F-MAMMA1000413//HS_3223_B2_F01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3223 Col=2 Row=L, genomic survey sequence//1.6e-48:318:89//AQ188456

F-MAMMA1000414//HS_2027_B2_C04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2027 Col=8 Row=F, genomic survey sequence//1.4e-46:286:92//AQ231369

5 F-MAMMA1000416//Drosophila melanogaster DNA sequence (P1s DS07528 (D169) and DS06665 (D220)), complete sequence//9.4e-33:310:72//AC004640

F-MAMMA1000421//Homo sapiens clone DJ1129D05, complete sequence//3.3e-29:223:84//AC005630

F-MAMMA1000422

F-MAMMA1000423//Drosophila yakuba mitochondrial DNA molecule//2.2e-10:639:57//X03240

10 F-MAMMA1000424//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence//4.6e-47:556:68//AC003973

F-MAMMA1000429//Mus musculus SDP8 mRNA, complete cds//8.0e-99:545:92//AF062484

F-MAMMA1000431//Homo sapiens clone DJ1039L24, WORKING DRAFT SEQUENCE, 3 unordered pieces//4.8e-41:289:79//AC005283

15 F-MAMMA1000444//Human DNA sequence from clone 714B7 on chromosome 22q12.2-13.2 Contains CYTOCHROME C OXIDASE VIIB precursor like pseudogene and ESTs, complete sequence//2.3e-34:291:80//Z99755

F-MAMMA1000446

F-MAMMA1000458//Mus musculus clone OST9003, genomic survey sequence//5.0e-53:231:84//AF046620

F-MAMMA1000468//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 291J10, WORKING

20 DRAFT SEQUENCE//0.75:303:60//Z93017

F-MAMMA1000472//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 414D7, WORKING DRAFT SEQUENCE//4.0e-41:403:77//AL033543

F-MAMMA1000478//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces//9.5e-54:369:77//AC005081

25 F-MAMMA1000483//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence//3.6e-34:332:77//AC004381

F-MAMMA1000490//Homo sapiens 12q13.1 PAC RPCI1-90J4 (Roswell Park Cancer Institute Human PAC library) complete sequence//8.9e-128:822:87//AC003686

F-MAMMA1000500//CIT-HSP-231905.TF CIT-HSP Homo sapiens genomic clone 2319O5, genomic survey sequence//4.8e-29:175:94//AQ044812

30 F-MAMMA1000501//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence//5.7e-45:334:82//AL022336

F-MAMMA1000516//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATPSG1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat//2.9e-43:529:69//Z92545

35 F-MAMMA1000522//Human DNA sequence from clone 20J23 on chromosome Xq26.2-27.2 Contains ras-related C3 botulinum toxin substrate 1 (P21-RAC1) (ras-like protein TC25) EST, CA repeat, STS, CpG island, complete sequence//2.0e-14:380:63//AL022576

40 F-MAMMA1000524//Homo sapiens chromosome 10 clone CIT-HSP-1338F24 map 10p11.2-10p12.1, complete sequence//1.4e-22:420:66//AC006101

F-MAMMA1000559//Human HepG2 3' region cDNA, clone hmd3f08//5.4e-29:168:97//D16922

F-MAMMA1000565//RPCI11-61K6.TJ RPCI11 Homo sapiens genomic clone R-61K6, genomic survey sequence//1.7e-120:561:100//AQ194238

45 F-MAMMA1000567//Human DNA sequence from PAC 179D3, between markers DXS6791 and DXS8038 on chromosome X contains S10 GTP-binding protein, ESTs and CpG island//3.1e-43:387:80//Z81370

F-MAMMA1000576//Homo sapiens BAC clone RG442F18 from 2, complete sequence//1.2e-30:237:75//AC005104

F-MAMMA1000583//RPCI11-60M22.TJ RPCI11 Homo sapiens genomic clone R-60M22, genomic survey sequence//9.6e-102:487:99//AQ198091

50 F-MAMMA1000585//Homo sapiens clone UWGC:djs14 from 7p14-15, complete sequence//5.2e-39:370:78//AC006195

F-MAMMA1000594//Homo sapiens chromosome 19, cosmid R31646, complete sequence//3.9e-43:328:83//AC005338

55 F-MAMMA1000597//Homo sapiens chromosome 17, clone hRPK.481_C_4, complete sequence//1.5e-32:259:

F-MAMMA1000597//Homo sapiens chromosome 17, clone hRPK.481_C_4, complete sequence//1.5e-32:259:
F-MAMMA1000597//Homo sapiens chromosome 17, clone hRPK.481_C_4, complete sequence//1.5e-32:259:

F-MAMMA1000612//HS_2188_A2_D02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2188 Col=4 Row=G, genomic survey sequence.//4.8e-30:171:96//AQ116793

F-MAMMA1000616//HS_3176_A1_E06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3176 Col=11 Row=I, genomic survey sequence.//4.7e-28:287:79//AQ300310

F-MAMMA1000621//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 273F20, WORKING DRAFT SEQUENCE.//0.015:478:58//AL034371

F-MAMMA1000623

F-MAMMA1000625//DNA encoding Hepatitis C virus antigen.//0.93:196:61//E06898

F-MAMMA1000643//Homo sapiens nephrocystin (NPHP1) mRNA, partial cds.//0.95:365:59//AF023674

F-MAMMA1000664//HS_3096_B1_C02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3096 Col=3 Row=F, genomic survey sequence.//2.7e-51:257:99//AQ145137

F-MAMMA1000669//Homo sapiens chromosome 19, cosmid R26908, complete sequence.//2.0e-66:586:67//AC004785

F-MAMMA1000670//HS_2243_B2_A08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2243 Col=16 Row=B, genomic survey sequence.//8.7e-05:94:80//AQ153650

F-MAMMA1000672//Mus musculus clone OST8270, genomic survey sequence.//3.9e-64:471:81//AF046705

F-MAMMA1000684//Suid herpesvirus 1 Rsp40 mRNA, partial cds.//1.2e-07:186:67//U27489

F-MAMMA1000696//Human oligodendrocyte myelin glycoprotein (OMG) exons 1-2; neurofibromatosis 1 (NF1) exons 28-49; ecotropic viral integration site 2B (EVI2B) exons 1-2; ecotropic viral integration site 2A (EVI2A) exons 1-2; adenylate kinase (AK3) exons 1-2.//3.0e-53:653:70//L05367

F-MAMMA1000707//CIT-HSP-2302019.TR CIT-HSP Homo sapiens genomic clone 2302O19, genomic survey sequence.//1.8e-08:131:77//AQ017947

F-MAMMA1000713//Rattus norvegicus clonel polymeric immunoglobulin receptor mRNA 3' untranslated region, GA rich region, and microsatellites with GGA-triplet and GAA-triplet repeats.//0.062:134:67//U00762

F-MAMMA1000714//Chicken hsp90 gene for 90 kDa-heat shock protein 5'-end.//1.0:266:61//X15028

F-MAMMA1000718//CIT-HSP-2171B10.TF CIT-HSP Homo sapiens genomic clone 2171B10, genomic survey sequence.//3.6e-05:289:60//B95401

F-MAMMA1000720//Homo sapiens chromosome 19, cosmid R33632, complete sequence.//4.4e-184:842:98//AC005781

F-MAMMA1000723//Homo sapiens clone DJ0892G19, complete sequence.//8.8e-05:430:60//AC004917

F-MAMMA1000731//Drosophila melanogaster DNA sequence (P1 DS07049 (D133)), complete sequence.//3.8e-55:796:66//AC004274

F-MAMMA1000732//Homo sapiens chromosome 21q22.3 PAC 141B3, complete sequence, containing ribosomal protein homologue pseudogene L23a.//6.6e-77:555:74//AF064859

F-MAMMA1000733//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P6, WORKING DRAFT SEQUENCE.//0.98:479:58//AL031749

F-MAMMA1000734//Homo sapiens SEC63 (SEC63) mRNA, complete cds.//7.3e-168:802:98//AF100141

F-MAMMA1000738//S.cerevisiae chromosome XIV reading frame ORF YNL132w.//8.6e-31:626:63//Z71408

F-MAMMA1000744//Gorilla Alu-repetitive sequence in beta-globin gene cluster.//2.7e-54:410:82//X06123

F-MAMMA1000746//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-10F4, complete sequence.//3.7e-109:779:83//AC004158

F-MAMMA1000752//Homo sapiens clone RG219E16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.2e-20:444:63//AC005075

F-MAMMA1000760//Homo sapiens clone RG015P03, complete sequence.//1.5e-44:403:79//AC005048

F-MAMMA1000761//Homo sapiens Chromosome 7 BAC Clone 239c10, WORKING DRAFT SEQUENCE, 9 unordered pieces.//2.3e-22:159:81//AC004166

F-MAMMA1000775//Homo sapiens chromosome 17, clone hRPK.849_N_15, complete sequence.//1.3e-51:789:68//AC005703

F-MAMMA1000776//Human DNA sequence from BAC 57G9 on chromosome 22q12.1 Contains ESTs, CA repeat, GSS.//5.7e-40:238:78//Z95116

F-MAMMA1000778//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 153G14, WORKING DRAFT SEQUENCE.//7.6e-29:222:84//AL031118

F-MAMMA1000782//Human 2,4-dienoyl-CoA reductase gene, exon 9.//0.90:137:62//U94987

F-MAMMA1000798//*** SEQUENCING IN PROGRESS *** EPM1/APECED region of chromosome 21, clones A68E8, B127P21, B173L3, B23N8, C1242C9, C579E2, A70B6, B159G9, B175D10, B52C10, C124G1 Note: Sequencing in this region has been discontinued by the Stanford Human Genome Center. WORKING DRAFT SEQUENCE.//1.2e-20:444:63//AC005075

F-MAMMA100802//Homo sapiens chromosome 19, cosmid R33632, complete sequence.//4.4e-184:842:98//AC005781

AC005339

F-MAMMA1000824//Homo sapiens 12p13.3 BAC RPC111-543P15 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//4.2e-104:503:99//AC005912

F-MAMMA1000831//Homo sapiens clone UWGC:g1211a139, complete sequence.//0.76:302:58//AC005502

F-MAMMA1000839//Human BAC clone RG013L03 from 7q21, complete sequence.//1.9e-54:322:68//AC002456

F-MAMMA1000841//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 968D22, WORKING DRAFT SEQUENCE.//6.7e-140:647:92//AL023755

F-MAMMA1000842//, complete sequence.//0.0068:499:59//AC005817

F-MAMMA1000843//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING

DRAFT SEQUENCE, 2 unordered pieces.//0.13:439:59//AC004710

F-MAMMA1000845//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE.//2.2e-05:208:64//AL034557

F-MAMMA1000851//Gallus domesticus filamin gene 5' region, partial cds.//0.86:193:63//U00146

F-MAMMA1000855//Human minisatellite region detected by myoglobin 33-repeat probe, clone lambda 33.10.//0.081:229:62//M30549

F-MAMMA1000856//B.taurus microsatellite marker ETH8 (D6S3) DNA.//0.0024:253:60//Z22747

F-MAMMA1000859//Sequence 6 from Patent WO9722695.//2.3e-79:533:82//A63553

F-MAMMA1000862

F-MAMMA1000863//Homo sapiens genomic DNA, chromosome 21q11.1, segment 21/28, WORKING DRAFT SEQUENCE.//1.0e-28:439:64//AP000050

F-MAMMA1000865

F-MAMMA1000867//CIT-HSP-2385J8.TR.1 CIT-HSP Homo sapiens genomic clone 2385J8, genomic survey sequence.//0.00017:158:70//AQ240906

F-MAMMA1000875//Homo sapiens DNA sequence from PAC 232G24 on chromosome Xq27.1-q27.3. Contains two exons similar to MAGE gene family, EST, CA repeat, STS, complete sequence.//1.0:121:68//AL022152

F-MAMMA1000876//Homo sapiens clone HS19.6 Alu-Ya5 sequence.//8.4e-41:185:90//AF015152

F-MAMMA1000877//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//8.3e-57:522:75//AL022336

F-MAMMA1000880//Homo sapiens full-length insert cDNA clone ZD54A10.//5.2e-26:143:100//AF086327

F-MAMMA1000883//Human DNA sequence from clone 786D3 on chromosome 22q13.31-33 Contains GSS, complete sequence.//0.99:225:63//AL023801

F-MAMMA1000897//R.norvegicus mRNA for plasma protein.//4.8e-07:479:58//Y11283

F-MAMMA1000905//F26L5TRB IGF Arabidopsis thaliana genomic clone F26L5, genomic survey sequence.//0.94:115:66//B61433

F-MAMMA1000906//HS_3110_B2_A11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3110 Col=22 Row=B, genomic survey sequence.//2.5e-63:548:78//AQ182819

F-MAMMA1000908//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 27K12, WORKING DRAFT SEQUENCE.//5.2e-80:480:90//AL033397

F-MAMMA1000914//Plasmodium falciparum MAL3P8, complete sequence.//7.6e-09:596:58//AL034560

F-MAMMA1000921//CIT-HSP-2171D8.TR CIT-HSP Homo sapiens genomic clone 2171D8, genomic survey sequence.//6.6e-07:249:66//889575

F-MAMMA1000931//Homo sapiens clone DJ0892G19, complete sequence.//2.9e-43:415:66//AC004917

F-MAMMA1000940//HS-1056-A2-E02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 778 Col=4 Row=I, genomic survey sequence.//6.1e-44:235:78//B47296

F-MAMMA1000941//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-113A6 complete genomic sequence, complete sequence.//9.4e-48:443:75//AC002299

F-MAMMA1000942//Human DNA sequence from clone 914P14 on chromosome Xq23 Contains calpain-like protease gene, DCX (doublecortin) ESTs, CA repeat, GSS, complete sequence.//1.8e-14:175:76//AL031117

F-MAMMA1000943//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.0082:684:56//AC005308

F-MAMMA1000956//Homo sapiens chromosome 16, cosmid clone 363E3 (LANL), complete sequence.//3.3e-30:530:67//AC004643

F-MAMMA1000957//HS_3039_A2_C08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3039 Col=16 Row=E, genomic survey sequence.//1.3e-72:390:94//AQ155121

F-MAMMA1000962//Homo sapiens clone DJ0756H11 WORKING DRAFT SEQUENCE, 5 unordered pieces

F-MAMMA1000963

F-MAMMA1000968//Homo sapiens clone DJ0756H11 WORKING DRAFT SEQUENCE, 5 unordered pieces

TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 PLC-II, PLC-148), the KIAA0395 gene for a probable Zinc Finger Homeobox protein and a 60S Ribosomal Protein L23 LIKE pseudogene. Contains a predicted CpG island, ESTs, STSs and GSSs, complete sequence.//1.4e-18:396:65//AL022394

5 F-MAMMA1000975//Human DNA sequence from clone 34417 on chromosome Xp11.21-11.3. Contains a Keratin, Type II Cytoskeletal 8 (Cytokeratin 8, CYK8, KRT8) pseudogene, ESTs and a GSS, complete sequence.//1.4e-79:690:77//AL024458

F-MAMMA1000979//Homo sapiens PAC clone DJ1186C01 from 7q21.2-q31.1, complete sequence.//0.089:214:66//AC004991

10 F-MAMMA1000987//Human PAC clone DJ527C21 from Xq23, complete sequence.//1.1e-58:458:82//AC000114

F-MAMMA1000998//Human DNA sequence from PAC 997K18 on chromosome 20p12. Contains ESTs and CA repeat.//1.1e-05:439:62//AL021406

F-MAMMA1001003//Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Choroideraemia protein, Tapetochoroidal Dystrophy (TCD) protein). Contains ESTs and an STS, complete sequence.//0.24:166:68//AL022401

15 F-MAMMA1001008//Homo sapiens *** SEQUENCING IN PROGRESS *** , WORKING DRAFT SEQUENCE.//1.6e-103:139:99//AJ011929

F-MAMMA1001021//Homo sapiens clone 24544 beta-dystrobrevin mRNA, partial cds.//6.5e-48:465:76//AF070567

20 F-MAMMA1001024//CITBI-E1-2501L21.TF.1 CITBI-E1 Homo sapiens genomic clone 2501L21, genomic survey sequence.//1.0:175:62//AQ241701

F-MAMMA1001030//Homo sapiens G protein-coupled receptor LGR5 (LGR5) mRNA, complete cds.//1.1e-30:753:6//AF061444

25 F-MAMMA1001035//Human Chromosome 16 BAC clone CIT987SK-A-1000D7, complete sequence.//7.9e-24:256:76//AC002990

F-MAMMA1001038//CIT-HSP-2284N21.TF CIT-HSP Homo sapiens genomic clone 2284N21, genomic survey sequence.//0.96:78:75//AQ000903

F-MAMMA1001041//chicken mRNA for alpha-actinin, complete cds.//2.8e-09:355:63//D26597

30 F-MAMMA1001050//Homo sapiens BAC clone RG060P12 from 7q21, complete sequence.//2.6e-40:378:76//AC002457

F-MAMMA1001059//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete cds.//4.8e-97:661:83//L25125

35 F-MAMMA1001067//Homo sapiens genomic intron breakpoint sequence of MLL rearrangement, 285 bp.//2.8e-18:110:100//AJ000169

F-MAMMA1001073//HS_3046_A2_G08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3046 Col=16 Row=M, genomic survey sequence.//1.0:142:68//AQ098420

F-MAMMA1001074//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 455J7, WORKING DRAFT SEQUENCE.//1.2e-23:386:70//AL031733

40 F-MAMMA1001075//Homo sapiens (clone F4) transmembrane protein mRNA sequence.//1.1e-27:559:65//L09749

F-MAMMA1001078//Homo sapiens chromosome 17, clone hRPK.346_K_10, complete sequence.//2.0e-22:334:69//AC006120

F-MAMMA1001080//Human immunoglobulin heavy chain variable region (VH III family) from IgM rheumatoid factor.//6.4e-58:327:92//L29155

45 F-MAMMA1001082//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete sequence.//3.8e-87:695:77//AC004087

F-MAMMA1001091//Homo sapiens chromosome 19, cosmid F21967, complete sequence.//7.0e-05:594:60//AC005256

F-MAMMA1001092//Human DNA sequence from PAC 49C23 on chromosome X contains malate dehydrogenase pseudogene and STS.//1.6e-91:174:87//Z93019

50 F-MAMMA1001105//Homo sapiens OVO-like 1 binding protein (OVOL1) mRNA, complete cds.//6.4e-23:507:66//AF016045

F-MAMMA1001110//Homo sapiens chromosome 19, cosmid F16815, complete sequence.//0.77:316:60//AC004637

55 F-MAMMA1001126//Homo sapiens PAC 50H2 in the CUTL1 locus, complete sequence.//3.3e-21:237:73//AF047825

F-MAMMA

GSS 1001126

F-MAMMA1001139//tricarboxylate carrier [rats, liver, mRNA Partial, 2986 nt]//1.6e-84:406:82//S70011
 F-MAMMA1001143//Homo sapiens DNA sequence from cosmid N75B3 on chromosome 22 Contains EST, exon trap, complete sequence//1.3e-14:182:76//AL022339
 F-MAMMA1001145//Human DNA sequence from cosmid cU115G11, between markers DXS6791 and DXS8038 on chromosome X contains ESTs and STS//5.2e-87:714:78//Z71187
 5 F-MAMMA1001154//CIT-HSP-2341D13.TF CIT-HSP Homo sapiens genomic clone 2341D13 genomic survey sequence//0.00051:249:61//AQ055735
 F-MAMMA1001161//Homo sapiens chromosome 14, BAC CITB-135H17 containing the RAD51L1 gene, complete sequence//2.2e-30:410:70//AC004518
 10 F-MAMMA1001162//Homo sapiens full-length insert cDNA clone ZA79C01//2.4e-13:87:100//AF086123
 F-MAMMA1001181//Mus musculus C2C12 unknown mRNA, partial cds//9.3e-15:432:60//U31629
 F-MAMMA1001186//Homo sapiens chromosome 17, clone hRPK.74_E_22, complete sequence//6.8e-57:670:72//AC005696
 F-MAMMA1001191
 15 F-MAMMA1001198//Mus musculus eps15R mRNA, complete cds//1.5e-117:759:84//U29156
 F-MAMMA1001202
 F-MAMMA1001203//Homo sapiens chromosome 17, clone hRPK.22_N_12, WORKING DRAFT SEQUENCE, 2 ordered pieces//1.5e-161:764:98//AC005412
 F-MAMMA1001206//Homo sapiens chromosome 17, clone HCIT421K24, complete sequence//5:1e-30:535:65//AC004099
 20 F-MAMMA1001215//Homo sapiens chromosome 19, CIT-HSP BAC 470n8, complete sequence//8.4e-182:860:98//AC005393
 F-MAMMA1001220//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence//7.7e-58:690:70//AC004875
 25 F-MAMMA1001222//Mouse loricrin mRNA, complete cds//2.7e-07:624:58//M34398
 F-MAMMA1001243//Homo sapiens chromosome 17, clone hRPK.192_H_23, complete sequence//0.91:177:66//AC005726
 F-MAMMA1001244
 F-MAMMA1001249//Human 28S ribosomal RNA psuedogenes and alu repeat region sequence//6.7e-09:502:58//U67616
 30 F-MAMMA1001256//Human DNA sequence from clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence//5.0e-37:342:80//Z99495
 F-MAMMA1001259
 F-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds//8.7e-40:659:64//AB014561
 35 F-MAMMA1001268//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence//4.9e-43:265:81//AC004453
 F-MAMMA1001271//Salmo salar DNA for a cryptic repeat//2.6e-06:311:63//AJ012206
 F-MAMMA1001274//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12 unordered pieces//6.6e-70:327:83//AC004840
 40 F-MAMMA1001280//Homo sapiens Xp22 bins 87-93 PAC RPCI1-122K4 (Roswell Park Cancer Institute Human PAC Library) complete sequence//1.0e-05:276:66//AC003035
 F-MAMMA1001292//Human DNA sequence from clone 1170K4 on chromosome 22q12.2-13.1. Contains three novel genes, one of which codes for a Trypsin family protein with class A LDL receptor domains, and the IL2RB gene for Interleukin 2 Receptor, Beta (IL-2 Receptor, CD122 antigen). Contains a putative CpG island, ESTs, and GSSs, complete sequence//3.6e-98:199:98//AL022314
 45 F-MAMMA1001296//RPCI11-38B4.TV RPCI-11 Homo sapiens genomic clone RPCI-11-38B4, genomic survey sequence//4.7e-33:292:71//AQ030084
 F-MAMMA1001298//Homo sapiens chromosome 17, clone hRPK.849_N_15, complete sequence//1.6e-182:860:98//AC005703
 50 F-MAMMA1001305//Human DNA sequence from clone 116F5 on chromosome 22q13. Contains part of an unknown gene and part of a RhoGAP (CDC42 GTPase Activating Protein) LIKE gene. Contains ESTs, STSs, GSSs, genomic marker D22S1168 and a CA repeat polymorphism, complete sequence//1.9e-70:163:97//Z93244
 F-MAMMA1001322//Human DNA sequence from clone 774I24 on chromosome 1q24.1-24.3 Contains protein similar to pregnancy-associated plasma protein A precursor neuronal migration protein astrotactin, ESTs, STS and GSS, complete sequence//2.6e-19:379:68//AL031290
 55 F-MAMMA1001324//Human DNA sequence *** SEQUENCE ***
 F-MAMMA1001325//Human DNA sequence *** SEQUENCE ***
 F-MAMMA1001326//Human DNA sequence *** SEQUENCE ***
 F-MAMMA1001327//Human DNA sequence *** SEQUENCE ***
 F-MAMMA1001328//Human DNA sequence *** SEQUENCE ***
 F-MAMMA1001329//Human DNA sequence *** SEQUENCE ***
 F-MAMMA1001330//Human DNA sequence *** SEQUENCE ***
 F-MAMMA1001331//Human DNA sequence *** SEQUENCE ***
 F-MAMMA1001332//Human DNA sequence *** SEQUENCE ***
 F-MAMMA1001333//Human DNA sequence *** SEQUENCE ***
 F-MAMMA1001334//Human DNA sequence *** SEQUENCE ***
 F-MAMMA1001335//Human DNA sequence *** SEQUENCE ***

F-MAMMA1001341//Sus scrofa//1.6e-36:420:73/Z46906

F-MAMMA1001343//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P1, WORKING DRAFT SEQUENCE//1.1e-05:818:58//AL031744

F-MAMMA1001346

5 F-MAMMA1001383//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces//2.0e-44:505:74//AC004086

F-MAMMA1001388//Human IGF binding protein complex acid-labile subunit a mRNA, complete cds//1.5e-07:415:58//M86826

10 F-MAMMA1001397//Human DNA sequence from clone 462D8 on chromosome 22q11.21-12.1 Contains EST, STS and GSS, complete sequence//1.6e-23:209:75//AL022332

F-MAMMA1001408//HS_3242_A1_H11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3242 Col=21 Row=O, genomic survey sequence//2.7e-07:181:69//AQ207300

F-MAMMA1001411//Homo sapiens autosomal dominant polycystic kidney disease type II protein (PKD2) gene, exon 14//0.98:120:68//AF004872

15 F-MAMMA1001419//HS_2053_B1_F12_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2053 Col=23 Row=L, genomic survey sequence//1.9e-75:424:93//AQ244585

F-MAMMA1001420//Homo sapiens chromosome 4 clone B203C23 map 4q25, complete sequence//2.4e-09:199:70//AC004049

20 F-MAMMA1001435//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-2011O4, WORKING DRAFT SEQUENCE, 4 unordered pieces//5.1e-42:558:69//AC004529 F-MAMMA1001442//Plasmodium falciparum chromosome 2, section 37 of 73 of the complete sequence//0.0019:516:56//AE001400

F-MAMMA1001446//Homo sapiens Xp22 BAC GSHB-519E5 (Genome Systems Human BAC library) complete sequence//3.6e-42:486:70//AC003684

25 F-MAMMA1001452//RPC111-48022.TJ RPC111 Homo sapiens genomic clone R-48022, genomic survey sequence//5.3e-87:423:98//AQ199294

F-MAMMA1001465//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 414D7, WORKING DRAFT SEQUENCE//0.00038:114:75//AL033543

F-MAMMA1001476//Mus musculus uridine kinase mRNA, partial cds//4.1e-99:604:87//L31783

30 F-MAMMA1001487//Homo sapiens clone DJ1070G24, WORKING DRAFT SEQUENCE, 12 unordered pieces//1.0e-13:158:77//AC005486

F-MAMMA1001501//Human mRNA for calcium activated neutral protease large subunit (muCANP, calpain, EC 3.4.22.17)//9.6e-52:438:81//X04366

F-MAMMA1001502//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 356B7, WORKING DRAFT SEQUENCE//3.7e-152:720:99//AL031714

35 F-MAMMA1001510//Human PAC clone DJ438O4 from 22q12.1-qter, complete sequence//1.1e-05:371:61//AC002378

F-MAMMA1001522

F-MAMMA1001547

F-MAMMA1001551//Homo sapiens mRNA for KIAA0462 protein, partial cds//2.3e-128:614:98//AB007931

40 F-MAMMA1001575//Human Chromosome 16 BAC clone CIT987SK-A-815A9, complete sequence//0.97:154:68//AF001548

F-MAMMA1001576//Human gamma-tubulin mRNA, complete cds//1.8e-95:529:91//M61764

F-MAMMA1001590//Human DNA sequence from clone 125H2 on chromosome 22q11-12 Contains part of myosin heavy chain gene, EST, CA repeat, STS, GSS, complete sequence//1.8e-07:104:84//Z98949

45 F-MAMMA1001600//HS_3022_A2_H01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3022 Col=2 Row=O, genomic survey sequence//1.6e-66:405:90//AQ163791

F-MAMMA1001604//Human DNA sequence from clone 1114G22 on chromosome 1q24-25 Contains EST, CA repeat, Ninenin like sequence, complete sequence//0.00043:715:58//AL008626

50 F-MAMMA1001606//jd114 Trypanosome Shotgun M13 genomic Trypanosoma brucei brucei genomic clone 2G6, genomic survey sequence//0.19:266:62//B13685

F-MAMMA1001620//Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds//9.7e-54:442:69//AF053630

F-MAMMA1001627//X.borealis ribosomal spacer DNA, with a DNaseI-hypersensitive site//0.14:221:62//M29833

55 F-MAMMA1001630//Homo sapiens chromosome 17, clone hRPK.22_N_12, WORKING DRAFT SEQUENCE, 2 ordered pieces//2.0e-47:611:71//AC005412

F-MAMMA1001633//Human zinc finger protein 175, complete cds//1.1e-99:100:100//U00111

F-MAMMA1001634//Human zinc finger protein 175, complete cds//1.1e-99:100:100//U00111

F-MAMMA1001663/CIT-HSP-2165E16.TR CIT-HSP Homo sapiens genomic clone 2165E16, genomic survey sequence.//9.7e-05:146:66//B95491

F-MAMMA1001671//Homo sapiens chromosome 19, cosmid F23269, complete sequence.//3.3e-181:863:98//AC005614

F-MAMMA1001679/HS_3054_A1_H11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=21 Row=O, genomic survey sequence.//1.0:89:70//AQ106118

F-MAMMA1001683//Spermatozopsis similis mRNA for 90 kD basal apparatus-protein.//8.3e-07:480:62//AJ224970

F-MAMMA1001686//HS_3219_B1_A03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3219 Col=5 Row=B, genomic survey sequence.//0.00072:180:65//AQ180345

F-MAMMA1001692//HS_3047_B1_B10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=19 Row=D, genomic survey sequence.//2.5e-94:459:98//AQ134228

F-MAMMA1001711//Homo sapiens clone DJ0635O05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//
1.2e-42:316:82//AC004845

F-MAMMA1001715//CIT-HSP-2347A14.TF CIT-HSP Homo sapiens genomic clone 2347A14, genomic survey sequence.//1.1e-60:413:87//AQ059125

F-MAMMA1001730//Homo sapiens brain and nasopharyngeal carcinoma susceptibility protein NSG-x mRNA, partial cds.//1.8e-133.646:97//AF095687

F-MAMMA1001735//chicken brain tubulin beta chain mrna.//3.5e-110:740:84//J00913

F-MAMMA1001740//Human DNA sequence from PAC 136017 on chromosome X contains ESTs and STS //0.98:
416:57//Z72001

F-MAMMA1001743//Homo sapiens clone DJ0981007, complete sequence.//3.2e-16:194:75//AC006017

F-MAMMA1001744//Homo sapiens DNA sequence from clone 46618 on chromosome Xq11.1-13.2. Contains an unknown gene similar to Coagulation Factor V (Activated Protein C Cofactor), Coagulation Factor VIII (Procoagulant Component) and Ceruloplasmin (EC 1.16.3.1, Ferroxidase). Contains ESTs and an STS, complete sequence.//0.0036:181:66//AL030998

F-MAMMA1001745//Homo sapiens BAC clone 529F11 from 8q21, complete sequence.//1.2e-60:822:68//AF070718

F-MAMMA1001751//Human potassium channel KCNO1 mRNA, complete cds//1.2e-35:583:65//U90065

F-MAMMA1001754//Bos taurus vacuolar proton pump subunit SFD alpha isoform (SFD) mRNA, complete cds.//
8.4e-102:627:87//AF041338

F-MAMMA1001757//HS_2058_B2_C04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
nomic clone Plate=2058 Col=8 Row=F, genomic survey sequence.//1.7e-24:173:88//AQ243865

F-MAMMA1001760//Human DNA sequence from clone 354N19 on chromosome 6q22. Contains the 3' part of the gene for Mannosyl-Oligosaccharide Alpha-1,2-Mannosidase (Man(9)-alpha-mannosidase, EC 3.2.1.113), a Cytochrome C Oxidase Polypeptide I (EC 1.9.3.1) pseudogene and a pseudogene similar to 60S Ribosomal Protein L13A. Contains genomic markers D6S287 and D6S1696, ESTs, STSs, GSSs and two CA repeat polymorphisms, complete sequence //6.6e-76:349:87//AL022722

F-MAMMA1001764//Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds./0.23:633:57//M97514

F-MAMMA1001768//Bovine herpesvirus 1 complete genome.//2.3e-11:547:60//AJ004801

F-MAMMA1001769//Homo sapiens 12q13.1 PAC RPC11-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.1e-76:509:78//AC004801

F-MAMMA1001771//M.musculus mRNA for semaphorin BJ/2.7e-106:744:82//X85991

F-MAMMA1001783//Human PAC clone 127H14 from 12q, complete sequence//6.0e-20:228:75//AC002563

F-MAMMA1001785

F-MAMMA1001788//Human DNA sequence from clone 425C14 on chromosome 6q22 Contains the HSF2 gene for Heat Shock Factor 2 (Heat Shock Transcription Factor 2, HSTF 2) and an unknown gene similar to the placental protein D15F33 gene. Contains ESTs, STSs and GSS. cDNA sequence: 15,36,35,153,34,799,133.

COMMUNICATIONS TO THE EDITOR OF POLYMER LETTERS

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- F-MAMMA1001806//Homo sapiens chromosome 19, cosmid R29368, complete sequence.//1.0:131:67//AC004262
- F-MAMMA1001812//Human Chromosome X clone bWXD187, complete sequence.//3.0e-34:257:83//AC004383
- 5 F-MAMMA1001815//Homo sapiens PAC clone DJ0850G01 from 7q21.2-q22, complete sequence.//5.2e-61:516:79//AC004128
- F-MAMMA1001817//Homo sapiens 12q24 PAC RPCI1-261P5 (Roswell Park Cancer Institute Human PAC library) complete sequence.//3.1e-32:295:78//AC004031
- F-MAMMA1001818//Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1.333303.//0.71:179:67//AJ011930
- 10 F-MAMMA1001820//Rattus norvegicus mRNA for PAG608 gene.//3.0e-91:726:79//Y13148
- F-MAMMA1001824//HS_3108_A1_G12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3108 Col=23 Row=M, genomic survey sequence.//3.4e-05:119:74//AQ107508
- F-MAMMA1001836//Homo sapiens chromosome 18, clone hRPK.537_E_1, complete sequence.//3.4e-45:312:85//AC006211
- 15 F-MAMMA1001837//Rattus norvegicus zinc finger protein Y1 (RLZF-Y) mRNA, complete cds.//4.5e-51:480:75//AF052042
- F-MAMMA1001848//CITBI-E1-2516P17.TF CITBI-E1 Homo sapiens genomic clone 2516P17, genomic survey sequence.//1.0e-100:486:98//AQ279620
- F-MAMMA1001851//Human DNA from overlapping chromosome 19-specific cosmids R30072 and R28588, genomic sequence, complete sequence.//5.1e-07:197:67//AC002390
- 20 F-MAMMA1001854
- F-MAMMA1001858//RPCI11-11L22.TP RPCI-11 Homo sapiens genomic clone RPCI-11-11L22, genomic survey sequence.//0.091:161:65//B75631
- F-MAMMA1001864//Human PAC clone DJ0205E24 from Xq23, complete sequence.//2.6e-09:397:61//AC003013
- 25 F-MAMMA1001868//HS_2196_B2_A12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2196 Col=24 Row=B, genomic survey sequence.//5.8e-13:86:100//AQ032455
- F-MAMMA1001874//H.sapiens CpG island DNA genomic Mse1 fragment, clone 63h5, reverse read cpg63h5.rta.//1.0:127:63//Z62129
- F-MAMMA1001878//Human DNA sequence from BAC 999D10 on chromosome 22q13.3. Contains two BAC end-sequences (GSSs).//1.7e-19:372:67//Z94802
- 30 F-MAMMA1001880//RPCI11-90K3.TJ RPCI11 Homo sapiens genomic clone R-90K3, genomic survey sequence.//6.6e-11:362:62//AQ283465
- F-MAMMA1001890//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 508I15, WORKING DRAFT SEQUENCE.//1.8e-45:317:86//AL021707
- 35 F-MAMMA1001907//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 424J12, WORKING DRAFT SEQUENCE.//2.7e-23:255:77//Z82207
- F-MAMMA1001908//HS_2225_A1_A03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2225 Col=5 Row=A, genomic survey sequence.//5.4e-08:264:62//AQ301597
- F-MAMMA1001931//HS_3049_B2_D09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3049 Col=18 Row=H, genomic survey sequence.//1.7e-47:295:90//AQ100157
- 40 F-MAMMA1001956//H.sapiens DNA sequence.//0.056:233:66//Z22493
- F-MAMMA1001963//Homo sapiens adenylosuccinate lyase gene, complete cds.//0.99:173:68//AF106656
- F-MAMMA1001969//Human DNA sequence from cosmid 232L22, between markers DXS366 and DXS87 on chromosome X contains ESTs glycerol kinase pseudogene.//5.3e-63:479:78//Z73986
- 45 F-MAMMA1001970//Homo Sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//1.4e-126:699:93//AC003071
- F-MAMMA1001992//HS_3078_A1_A09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3078 Col=17 Row=A, genomic survey sequence.//3.3e-08:257:65//AQ143646
- F-MAMMA1002009//Homo sapiens chromosome 17, clone hRPK.214_O_I, complete sequence.//1.5e-07:244:62//AC005224
- 50 F-MAMMA1002011//HS_3252_B1_B05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=9 Row=D, genomic survey sequence.//1.3e-07:170:69//AQ304711
- F-MAMMA1002032//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 37 unordered pieces.//2.1e-34:315:79//AC004803
- 55 F-MAMMA1002033//HS_3023_A2_G04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3023 Col=8 Row=M, genomic survey sequence.//4.3e-69:366:94//AQ105497
- F-MAMMA1002041//Genomic sequence from human HBB- complete sequence.//5.3e-85:439:82//AC000121
- F-MAMMA1002042//Homo sapiens chromosome 21, clone hRPK.155_E_1, complete sequence.//1.4e-20:314:70

AC005669

F-MAMMA1002047//Homo sapiens 12p13.3 BAC RPC11-429A20 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//6.8e-14:526:62//AC005906

F-MAMMA1002056//Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs, an STS and GSSs, complete sequence.//1.1e-47:648:71//AL030996

F-MAMMA1002058//Homo sapiens PAC clone DJ0732C22 from 7p11.2-p13, complete sequence.//2.4e-19:256:74//AC004869

F-MAMMA1002068//Homo sapiens, clone hRPK.2_A_1, complete sequence.//5.4e-41:407:78//AC006197

F-MAMMA1002078//Human DNA sequence from PAC 106I20 on chromosome 22q12 Contains ESTs and STS, complete sequence.//0.021:333:64//Z81313

F-MAMMA1002082

F-MAMMA1002084//Caenorhabditis elegans cosmid F28C12, complete sequence.//0.032:469:58//Z93380

F-MAMMA1002093//HS_3050_B1_F06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3050 Col=11 Row=L, genomic survey sequence.//1.0:77:71//AQ105997

F-MAMMA1002108//Homo sapiens anion exchanger 3 gene, exons 1 and 2 and complete 5'UTR.//8.3e-10:464:60//AF017308

F-MAMMA1002118

F-MAMMA1002125//Homo sapiens chromosome 17, clone HCIT217L10, complete sequence.//1.0e-35:619:68//AC003962

F-MAMMA1002132//RPC11-78F11.TJ RPC11 Homo sapiens genomic clone R-78F11, genomic survey sequence.//1.0e-90:357:97//AQ286460

F-MAMMA1002140//Homo sapiens 12q24 PAC RPC11-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.6e-45:583:64//AC004216

F-MAMMA1002143//Human serum constituent protein (MSE55) mRNA, complete cds.//6.0e-11:192:70//M88338

F-MAMMA1002145//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 102D24, WORKING DRAFT SEQUENCE.//0.0028:570:59//AL021391

F-MAMMA1002153//HS_3005_A1_D04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3005 Col=7 Row=G, genomic survey sequence.//4.9e-41:213:99//AQ132213

F-MAMMA1002155//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 462O23, WORKING DRAFT SEQUENCE.//1.2e-45:303:78//AL031431

F-MAMMA1002156

F-MAMMA1002158//CITBI-E1-2508P18.TR CITBI-E1 Homo sapiens genomic clone 2508P18, genomic survey sequence.//7.1e-42:255:92//AQ266165

F-MAMMA1002170//Homo sapiens chromosome 17, clone HCIT187M2, complete sequence.//2.0e-81:604:81//AC004448

F-MAMMA1002174//Homo sapiens clone UWGC:y67c126 from 6p21, complete sequence.//3.2e-43:333:83//AC004212

F-MAMMA1002198//H.sapiens thiol-specific antioxidant protein mRNA.//1.0e-34:121:98//Z22548

F-MAMMA1002209//HS_2197_B1_E07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2197 Col=13 Row=J, genomic survey sequence.//9.6e-18:163:84//AQ210058

F-MAMMA1002215//Homo sapiens anion exchanger 3 gene, exons 1 and 2 and complete 5'UTR.//6.3e-08:435:60//AF017308

F-MAMMA1002219//Rattus norvegicus rexo70 mRNA, complete cds.//1.8e-124:752:87//AF032667

F-MAMMA1002230//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.67:356:59//AC004710

F-MAMMA1002236//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds.//9.3e-140:836:87//U38253

F-MAMMA1002243//Homo sapiens chromosome 17, clone hRPK.112_H_10, complete sequence.//1.4e-145:691:98//AC005666

F-MAMMA1002250//Homo sapiens chromosome 16, P1 clone 109-9G (LANL), complete sequence.//6.0e-138:660:98//AC005600

F-MAMMA1002267//Homo sapiens chromosome 2, P1 clone 777H5 (LBNL H27), complete sequence.//0.066:333:114//AC003675

F-MAMMA1002269//Homo sapiens chromosome 17, clone hRPK.112_H_10, complete sequence.//1.4e-145:691:98//AC005666

F-MAMMA1002269//HS_2197_B1_E07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2197 Col=13 Row=J, genomic survey sequence.//9.6e-18:163:84//AQ210058

nomie clone Plate=3163 Col=5 Row=H, genomic survey sequence.//1.0:150:63//AQ171576

F-MAMMA1002282//Human Chromosome 16 BAC clone CIT987SK-327O24, complete sequence.//1.5e-22:315:67//AC003108

F-MAMMA1002292//B.garinii (strain Tis1) p83/100 gene (partial).//0.73:200:64//X81533

F-MAMMA1002293//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//1.6e-56:408:75//AC006023

F-MAMMA1002294//Sequence 2 from Patent WO9516779.//1.8e-06:401:62//A45258

F-MAMMA1002297

F-MAMMA1002298//Homo sapiens DNA from chromosome 19, cosmid R29144, complete sequence.//0.0056:525:61//AC004221

F-MAMMA1002299//CIT-HSP-2345B2.TR CIT-HSP Homo sapiens genomic clone 2345B2, genomic survey sequence.//1.2e-90:446:98//AQ053994

F-MAMMA1002308//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 850H21, WORKING DRAFT SEQUENCE.//1.3e-35:329:78//AL031680

F-MAMMA1002310//Human gastric (H+ + K+)-ATPase gene, complete cds.//0.0060:301:60//J05451

F-MAMMA1002311//Human Chromosome 15q11-q13 clone pDJ276c12 from the Prader-Willi/Angelman syndrome region, WORKING DRAFT SEQUENCE, 3 unordered pieces.//8.6e-50:327:69//AC004737

F-MAMMA1002312//Homo sapiens DNA sequence from PAC 435D1 on chromosome Xq25. Contains ESTs and STS.//1.3e-09:741:58//Z86064

F-MAMMA1002317

F-MAMMA1002319//Homo sapiens chromosome 19, fosmid 39347, complete sequence.//1.9e-158:746:99//AC005756

F-MAMMA1002322//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g4, complete sequence.//5.3e-52:817:70//AC004796

F-MAMMA1002329//Homo sapiens RaP2 interacting protein 8 (RPIP8) mRNA, complete cds.//0.22:143:67//U93871

F-MAMMA1002332//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 30G7, WORKING DRAFT SEQUENCE.//1.6e-31:287:74//AL034402

F-MAMMA1002333//Mycobacterium tuberculosis H37Rv complete genome; segment 148/162.//2.5e-09:674:59//AL022022

F-MAMMA1002339//Homo sapiens chromosome 21q22.3, cosmid clone Q4H9 complete sequence bases 1.41604.//2.1e-57:522:77//AJ011932

F-MAMMA1002347//Homo sapiens BAC clone RG136N17 from 7p15-p21, complete sequence.//2.0e-14:258:69//AC004129

F-MAMMA1002351//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1059H15, WORKING DRAFT SEQUENCE.//7.8e-132:723:91//AL022100

F-MAMMA1002352//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 128O3, WORKING DRAFT SEQUENCE.//5.8e-17:326:70//Z98742

F-MAMMA1002353//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.1e-14:399:63//AC004825

F-MAMMA1002355//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 109G6, WORKING DRAFT SEQUENCE.//3.7e-43:420:75//AL023879

F-MAMMA1002356//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0022:534:59//AC004153

F-MAMMA1002359//Homo sapiens 12p13.3 PAC RPCI5-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//5.3e-18:156:75//AC005831

F-MAMMA1002360//Human DNA sequence from cosmid L21F12B, Huntington's Disease Region, chromosome 4p16.3, contains EST.//4.9e-43:353:69//Z68885

F-MAMMA1002361//Human DNA sequence from clone 342B11 on chromosome 22q12.1-12.3. Contains ESTs and a GSS, complete sequence.//1.8e-22:282:74//AL008719

F-MAMMA1002362//Platymys spixii CR1-like LINE, partial sequence.//0.00058:83:79//D82938

F-MAMMA1002380//CIT-HSP-2383K24.TF CIT-HSP Homo sapiens genomic clone 2383K24, genomic survey sequence.//4.4e-10:85:92//AQ196889

F-MAMMA1002384//RPCI11-80J20.TV RPCI11 Homo sapiens genomic clone R-80J20, genomic survey sequence.//2.7e-56:286:98//AQ284134

F-MAMMA1002385//CIT-HSP-2383K24

F-MAMMA1002386//CIT-HSP-2383K24

F-MAMMA1002387//CIT-HSP-2383K24

F-MAMMA1002388//CIT-HSP-2383K24

F-MAMMA1002389//CIT-HSP-2383K24

F-MAMMA1002390//CIT-HSP-2383K24

F-MAMMA1002391//CIT-HSP-2383K24

F-MAMMA1002392//CIT-HSP-2383K24

F-MAMMA1002393//CIT-HSP-2383K24

F-MAMMA1002394//CIT-HSP-2383K24

F-MAMMA1002395//CIT-HSP-2383K24

F-MAMMA1002396//CIT-HSP-2383K24

F-MAMMA1002397//CIT-HSP-2383K24

F-MAMMA1002398//CIT-HSP-2383K24

F-MAMMA1002399//CIT-HSP-2383K24

F-MAMMA1002400//CIT-HSP-2383K24

AC004888

F-MAMMA1002411//Human DNA sequence from clone 1044017 on chromosome Xp11.3-11.4 Contains GSS and STS, complete sequence//8.2e-09:287:63//AL023 875

F-MAMMA1002413//Plasmodium falciparum (strain Dd2) variant-specific surface protein (var1) gene, complete cds//9.6e-08:730:57//L40608

F-MAMMA1002417//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 30G7, WORKING DRAFT SEQUENCE//4.1e-06:181:72//AL034402

F-MAMMA1002427//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces//1.3e-51:593:72//AC004604

F-MAMMA1002428

F-MAMMA1002434//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island//7.3e-56:388:81//Z93023

F-MAMMA1002446//CIT-HSP-2324O22.TR CIT-HSP Homo sapiens genomic clone 2324O22, genomic survey sequence//2.3e-56:302:95//AQ027479

F-MAMMA1002454//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete sequence//1.1e-54:190:94//AC005229

F-MAMMA1002461//Rattus norvegicus calcium channel alpha-1 subunit gene, partial cds//0.00045:457:60//U14005

F-MAMMA1002470//Saccharomyces cerevisiae chromosome VIII cosmid 9205//9.7e-33:709:60//U10556

F-MAMMA1002475//Homo sapiens 12p13.3 PAC RPCI3-340I3 (Roswell Park Cancer Institute Human PAC Library) complete sequence//0.092:506:58//AC004671

F-MAMMA1002480//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2-unordered pieces//0.025:100:76//AC005077

F-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds//2.9e-118:560:98//AF055460

F-MAMMA1002494//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library) complete sequence//1.5e-22:297:73//AC005913

F-MAMMA1002498//Human PAC clone DJ327A19 from Xq25-q26, complete sequence//7.2e-10:330:64//AC002477

F-MAMMA1002524//Homo sapiens huntingtin gene, partial exon//0.0080:124:72//L49359

F-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds//1.4e-160:775:97//AF065214

F-MAMMA1002545//Homo sapiens chromosome 17, clone hRPK.74_E_22 complete sequence//1.9e-41:345:80//AC005696

F-MAMMA1002554

F-MAMMA1002556

F-MAMMA1002566

F-MAMMA1002571//CIT-HSP-2296N17.TR CIT-HSP Homo sapiens genomic clone 2296N17, genomic survey sequence//1.7e-07:76:90//AQ006579

F-MAMMA1002573//Homo sapiens DNA, trinucleotide repeats region, clone GAA C27//2.7e-08:195:70//AB018507

F-MAMMA1002585

F-MAMMA1002590//Homo sapiens BAC clone GS250A16 from 7p21-p22, complete sequence//2.1e-26:361:69//AC005019

F-MAMMA1002597//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1103G7, WORKING DRAFT SEQUENCE//1.3e-34:550:69//AL034548

F-MAMMA1002598//H.sapiens mRNA for ribosomal protein L7//1.1e-21:123:100//X57958

F-MAMMA1002603//Homo sapiens chromosome 20, BAC clone 99 (LBNL H80), complete sequence//0.0018:358:61//AC005220

F-MAMMA1002612//Homo sapiens PAC clone DJ0696N01 from 7p21-p22, complete sequence//2.1e-13:336:63//AC004861

F-MAMMA1002617//Homo sapiens clone DJ1070G24, WORKING DRAFT SEQUENCE, 12 unordered pieces//0.14:229:64//AC005486

F-MAMMA1002618

F-MAMMA1002619//Homo sapiens chromosome 21 PAC RPCIP704E14135Q2//9.5e-71:319:85//AJ010598

F-MAMMA1002622//Homo sapiens advillin mRNA, complete cds//1.5e-20:157:90//AF041449

F-MAMMA1002623//Homo sapiens T cell receptor alpha delta gene from T cell clone 10.10.1

F-MAMMA1002624//Homo sapiens T cell receptor alpha delta gene from T cell clone 10.10.1

F-MAMMA1002625//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 10025, WORKING

DRAFT SEQUENCE.//1.9e-171:819:98//AL031727

F-MAMMA1002629//Human BAC clone RG385F02 from 7p15, complete sequence.//4.8e-85:478:78//AC003093

F-MAMMA1002636//Human POU domain factor (Brn-3a) gene, exon 2, complete cds.//5.6e-09:499:62//U10063

F-MAMMA1002637//Mus musculus kinesin light chain 2 (Klc2) mRNA, complete cds.//3.6e-115:785:82//AF055666

5 F-MAMMA1002646//Homo sapiens chromosome 2 clone 101B6 map 2p11, complete sequence.//1.5e-45:291:90//AC002038

F-MAMMA1002650//Homo sapiens candidate tumor suppressor HIC-1 (HIC-1) gene, complete cds.//6.6e-06:661:59//L41919

10 F-MAMMA1002655//HS_2003_A2_A11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2003 Col=22 Row=A, genomic survey sequence.//9.0e-15:198:74//AQ224233

F-MAMMA1002662

F-MAMMA1002665//Homo sapiens BAC clone GS588G18 from 7p12-p14, complete sequence.//1.4e-37:235:84//AC005029

15 F-MAMMA1002671//Human Cdk-inhibitor p57KIP2 (KIP2) mRNA, complete cds.//0.00027:272:64//U22398

F-MAMMA1002673

F-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds.//3.7e-161:752:99//D86987

F-MAMMA1002685//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 39417, WORKING

DRAFT SEQUENCE.//6.2e-45:510:70//AL023585

20 F-MAMMA1002698//HS_3024_B1_C06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3024 Col=11 Row=F, genomic survey sequence.//1.7e-10:155:75//AQ072214

F-MAMMA1002699//Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds.//5.9e-75:509:83//AF018261

F-MAMMA1002701//Homo sapiens gene for AF-6, complete cds.//1.2e-159:749:99//AB011399

25 F-MAMMA1002708//Human DNA sequence from clone 267M20 on chromosome Xq22.2-22.3. Contains part of the DIAPH2 gene and a pseudogene, ESTs, STSs and GSSs, complete sequence.//3.0e-57:347:79//AL031053

F-MAMMA1002711//Homo sapiens BAC clone GS589P19 from 7p13-p14, complete sequence.//3.4e-31:484:69//AC005030

F-MAMMA1002721//CIT-HSP-2350M5.TR CIT-HSP Homo sapiens genomic clone 2350M5, genomic survey sequence.//1.4e-06:265:63//AQ061245

30 F-MAMMA1002727//Human DNA sequence from clone 67K17 on chromosome 6q24.1-24.3. Contains the HIVP2 (Schnurri-2) gene for HIV type 1 Enhancer-binding Protein 2, and a possible pseudogene in an intron of this gene. Contains STSs and GSSs and an AAAT repeat polymorphism, complete sequence.//0.18:386:58//AL023584

F-MAMMA1002728//Human DNA sequence from PAC 296K21 on chromosome X contains cytochrome c oxidase, delta-aminolevulinic acid synthase (erythroid); 5-aminolevulinic acid synthase (EC 2.3.1.37). 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (EC 2.7.1.105, EC 3.1.3.46), ESTs and STS.//3.2e-05:362:63//Z83821

35 F-MAMMA1002744//Plasmodium falciparum chromosome 2, section 5 of 73 of the complete sequence.//0.00010:535:58//AE001368

F-MAMMA1002746//Homo sapiens chromosome 17, clone hRPK.136_H_19, complete sequence.//1.2e-182:880:97//AC005856

40 F-MAMMA1002748//Homo sapiens 3p22 Contig 7 PAC RPCI4-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.7e-175:829:98//AC006055

F-MAMMA1002754//Homo Sapiens Chromosome X clone bWDX171, WORKING DRAFT SEQUENCE, 1 ordered pieces.//3.1e-31:372:75//AC004676

F-MAMMA1002758//Homo sapiens KIAA0442 mRNA, partial cds.//3.3e-26:151:98//AB007902

45 F-MAMMA1002764//Human Chromosome 11 Cosmid cSRL166a1, complete sequence.//5.2e-49:355:81//U73636

F-MAMMA1002765//RPCI11-20A22.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-20A22, genomic survey sequence.//6.7e-13:155:76//B92153

F-MAMMA1002769//CIT-HSP-2323G1.TF CIT-HSP Homo sapiens genomic clone 2323G1, genomic survey sequence.//9.7e-21:151:90//AQ028244

50 F-MAMMA1002775//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds.//5.6e-105:179:99//U07561

F-MAMMA1002780//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-08, complete sequence.//0.071:277:58//Z98546

F-MAMMA1002782//HS_3213_B2_B08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=16 Row=D, genomic survey sequence.//0.00018:219:63//AQ175845

55 F-MAMMA1002796

F-MAMMA1002796//Homo sapiens chromosome 17, clone hRPK.136_H_19, complete sequence.//1.2e-182:880:97//AC005856

F-MAMMA1002820//Homo sapiens Xp22 bins 87-93 PAC RPCI1-122K4 (Roswell Park Cancer Institute Human PAC Library) complete sequence//5.9e-11:483:62//AC003035

F-MAMMA1002830//Homo sapiens chromosome 17, clone hCIT529I10, complete sequence//1.0e-64:320:83//AC002553

5 F-MAMMA1002833//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence//2.8e-47:413:80//AC004875

F-MAMMA1002835

F-MAMMA1002838//A-916H10.TP CIT978SK Homo sapiens genomic clone A-916H10, genomic survey sequence//1.1e-39:164:83//B14462

10 F-MAMMA1002842//Mus musculus c-Cbl associated protein CAP mRNA, complete cds//1.9e-62:373:81//U58883

F-MAMMA1002843//Homo sapiens mRNA for KIAA0810 protein, partial cds//1.7e-135:635:99//AB018353

F-MAMMA1002844//F1707-T7 IGF Arabidopsis thaliana genomic clone F1707, genomic survey sequence//6.7e-17:383:66//B11616

F-MAMMA1002858

15 F-MAMMA1002868//RPCI11-54F9.TJ RPCI11 Homo sapiens genomic clone R-54F9, genomic survey sequence//8.3e-81:392:99//AQ081566

F-MAMMA1002869//Sequence 1 from patent US 5552529//2.2e-86:696:78//I25863

F-MAMMA1002871//Lupinus angustifolius nodulin-45 gene, complete cds//0.029:370:59//L12388

F-MAMMA1002880//RPCI11-23M23.TV RPCI-11 Homo sapiens genomic clone RPCI-11-23M23, genomic survey sequence//1.8e-20:271:74//B86518

20 F-MAMMA1002881//Homo sapiens mRNA for 25 kDa trypsin inhibitor, complete cds//1.2e-28:680:61//D45027

F-MAMMA1002886//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 380A1, WORKING DRAFT SEQUENCE//0.00040:505:57//Z97653

F-MAMMA1002887//HS_3238_B2_G08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=16 Row=N, genomic survey sequence//5.5e-79:401:97//AQ219814

25 F-MAMMA1002890//Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC70t, and smRNP genes, complete cds; G7A gene, partial cds; and unknown genes//4.6e-35:136:73//AF109906

F-MAMMA1002892//Mouse Cosmid ma66a100 from 14D1-D2, complete sequence//5.7e-14:450:60//AC004096

30 F-MAMMA1002895//H.sapiens CpG island DNA genomic MseI fragment, clone 46b6, forward read cpg46b6.ft1a//3.7e-36:190:100//Z58616

F-MAMMA1002908//Penaues monodon microsatellite locus Pmo27//1.1e-05:195:62//AF068828

F-MAMMA1002909//Human Chromosome 11 pac pDJ205d23, complete sequence//1.0e-13:457:61//AC002402

F-MAMMA1002930//Homo sapiens Xp22 BAC GSHB-512P14 (Genome Systems Human BAC library) complete sequence//0.25:260:62//AC004467

35 F-MAMMA1002937//H.sapiens ZNF74-1 mRNA//6.3e-13:577:59//X71623

F-MAMMA1002938//Homo sapiens mRNA for KIAA0698 protein, complete cds//5.1e-193:910:98//AB014598

F-MAMMA1002941//Homo sapiens Chromosome 22q11.2 BAC Clone b437g10 In BCRL2-GGT Region, complete sequence//2.7e-23:174:77//AC004032

40 F-MAMMA1002947//Rhodobacter capsulatus strain SB1003, partial genome//1.3e-09:475:61//AF010496

F-MAMMA1002964//Human thiopurine methyltransferase (TPMT) gene, exon 5//0.0029:314:60//AF019366

F-MAMMA1002970//Human DNA sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked, juvenile) 1 (XLR51). Contains ESTs, an STS and GSSs, complete sequence//4.0e-10:194:71//Z94056

45 F-MAMMA1002972//H.sapiens CpG island DNA genomic MseI fragment, clone 2g10, forward read cpg2g10.ft1aa//0.38:156:66//Z55272

F-MAMMA1002973//Homo sapiens chromosome 17, clone hRPK.142_H_19, complete sequence//2.9e-41:234:79//AC005919

F-MAMMA1002982//Homo sapiens DNA sequence from PAC 510L9 on chromosome 6p24.1-p25.3//1.7e-05:322:63//AL022098

50 F-MAMMA1002987//CITBI-E1-2514J12.TR CITBI-E1 Homo sapiens genomic clone 2514J12, genomic survey sequence//0.0064:135:66//AQ275871

F-MAMMA1003003//cSRL-145D12-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-145D12, genomic survey sequence//2.8e-31:201:89//B01998

55 F-MAMMA1003004//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y237C10, WORKING DRAFT SEQUENCE //1.6e-10:180:73//A1031601

F-MAMMA1003005//Homo sapiens

1.6e-10:180:73//A1031601

F-MAMMA1003011//Rattus norvegicus histone macroH2A1.2 mRNA, complete cds.//2.3e-50:734:67//U79139
 F-MAMMA1003013//Mus musculus chromosome 19, clone CIT282B21, complete sequence.//1.2e-86:341:79//AC003694
 F-MAMMA1003015//Homo sapiens Chromosome 16 BAC clone CIT987SK-591M7, complete sequence.//2.6e-13:443:61//AC003661
 5 F-MAMMA1003019//HS_3221_A1_A01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3221 Col=1 Row=A, genomic survey sequence.//2.8e-51:299:92//AQ184271
 F-MAMMA1003026
 F-MAMMA1003031//Homo sapiens chromosome 5, BAC clone 319C17 (LBNL H159), complete sequence.//0.0037:134:73//AC005214
 10 F-MAMMA1003035//RPCI11-11P4.TP RPCI-11 Homo sapiens genomic clone RPCI-11-11P4, genomic survey sequence.//1.1e-07:66:100//B74936
 F-MAMMA1003039//Homo sapiens 12p13.3 PAC RPCI3-340I3 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.1e-19:220:76//AC004671
 15 F-MAMMA1003040//Human DNA sequence from PAC 340N1 on chromosome 1p35-36.2. Contains ESTs, polymorphic CA repeat, trna and endogenous retrovirus.//9.5e-91:469:78//Z98257
 F-MAMMA1003044//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS, complete sequence.//0.21:289:61//AL031321
 F-MAMMA1003047//Homo sapiens protein inhibitor of activated STAT protein PIASy mRNA, complete cds.//1.7e-139:663:98//AF077952
 20 F-MAMMA1003049
 F-MAMMA1003055//HS_3014_B2_F10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3014 Col=20 Row=L, genomic survey sequence.//4.2e-05:215:64//AQ164940
 F-MAMMA1003056//HS_3221_B2_D12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3221 Col=24 Row=H, genomic survey sequence.//1.4e-16:206:74//AQ302772
 25 F-MAMMA1003057//M.domesticus MD6 mRNA.//8.5e-128:654:94//X54352
 F-MAMMA1003066//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 273F20, WORKING DRAFT SEQUENCE.//1.0:142:71//AL034371
 F-MAMMA1003089//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g4, complete sequence.//1.7e-42:373:78//AC004796
 30 F-MAMMA1003099//Homo sapiens beta-filamin mRNA, complete cds.//2.6e-42:288:88//AF042166
 F-MAMMA1003104//Mus musculus rostral cerebellar malformation protein (rcm) mRNA, complete cds.//1.6e-12:477:64//U72634
 F-MAMMA1003113//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds.//3.4e-121:789:85//AF071316
 35 F-MAMMA1003127//R.norvegicus MYR1 mRNA for myosin I heavy chain.//9.4e-58:423:83//X68199
 F-MAMMA1003135//Mus musculus dentin sialophosphoprotein precursor (DSPP) mRNA, complete cds.//0.62:676:58//J67916
 F-MAMMA1003140
 40 F-MAMMA1003146//Homo sapiens mRNA for GalT3 protein.//2.2e-80:397:97//Y15062
 F-MAMMA1003150//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 598F2, WORKING DRAFT SEQUENCE.//7.3e-123:266:88//AL021579
 F-MAMMA1003166//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 250D10, WORKING DRAFT SEQUENCE.//1.6e-33:143:82//Z99716
 45 F-NT2RM1000001//Human DNA sequence from clone 393P23 on chromosome Xq21.1-21.33. Contains GSSs, complete sequence.//0.50:216:61//Z95400
 F-NT2RM1000018//Human mRNA for KIAA0066 gene, partial cds.//4.8e-65:385:92//D31886
 F-NT2RM1000032
 F-NT2RM1000035//Cricetulus griseus SREBP cleavage activating protein (SCAP) mRNA, complete cds.//6.3e-135:565:84//U67060
 50 F-NT2RM1000037//Homo sapiens mRNA for KIAA0690 protein, partial cds.//1.1 e-106:542:95//AB014590
 F-NT2RM1000039//Mouse genetic suppressor element mRNA.//0.080:239:60//L27155
 F-NT2RM1000055//Rattus norvegicus mRNA for TIP120, complete cds.//8.4e-96:535:91//D87671
 F-NT2RM1000059//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600
 55 F-NT2RM1000062//Nephila clavipes dragline silk protein gene, partial cds.//1.1e-106:542:95//AB014590
 F-NT2RM1000063//Human DNA sequence from clone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600
 F-NT2RM1000064//Human DNA sequence from clone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600
 F-NT2RM1000065//Human DNA sequence from clone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600
 F-NT2RM1000066//Human DNA sequence from clone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600
 F-NT2RM1000067//Human DNA sequence from clone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600
 F-NT2RM1000068//Human DNA sequence from clone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600
 F-NT2RM1000069//Human DNA sequence from clone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600
 F-NT2RM1000070//Human DNA sequence from clone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600
 F-NT2RM1000071//Human DNA sequence from clone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600
 F-NT2RM1000072//Human DNA sequence from clone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600
 F-NT2RM1000073//Human DNA sequence from clone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600
 F-NT2RM1000074//Human DNA sequence from clone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600
 F-NT2RM1000075//Human DNA sequence from clone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600
 F-NT2RM1000076//Human DNA sequence from clone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600
 F-NT2RM1000077//Human DNA sequence from clone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600
 F-NT2RM1000078//Human DNA sequence from clone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600
 F-NT2RM1000079//Human DNA sequence from clone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600
 F-NT2RM1000080//Human DNA sequence from clone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600
 F-NT2RM1000081//Human DNA sequence from clone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600
 F-NT2RM1000082//Human DNA sequence from clone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600
 F-NT2RM1000083//Human DNA sequence from clone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600
 F-NT2RM1000084//Human DNA sequence from clone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600
 F-NT2RM1000085//Human DNA sequence from clone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600
 F-NT2RM1000086//Human DNA sequence from clone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600
 F-NT2RM1000087//Human DNA sequence from clone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600
 F-NT2RM1000088//Human DNA sequence from clone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600
 F-NT2RM1000089//Human DNA sequence from clone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600
 F-NT2RM1000090//Human DNA sequence from clone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600
 F-NT2RM1000091//Human DNA sequence from clone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600
 F-NT2RM1000092//Human DNA sequence from clone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600
 F-NT2RM1000093//Human DNA sequence from clone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600
 F-NT2RM1000094//Human DNA sequence from clone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600
 F-NT2RM1000095//Human DNA sequence from clone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600
 F-NT2RM1000096//Human DNA sequence from clone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600
 F-NT2RM1000097//Human DNA sequence from clone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600
 F-NT2RM1000098//Human DNA sequence from clone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600
 F-NT2RM1000099//Human DNA sequence from clone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600
 F-NT2RM1000100//Human DNA sequence from clone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600

F-NT2RM1000092//Homo sapiens chromosome 19, cosmid R26894, complete sequence.//0.63:180:65//AC005594

F-NT2RM1000118//Homo sapiens clone 23763 unknown mRNA, partial cds.//0.027:126:70//AF007155

F-NT2RM1000119//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 466N1, WORKING DRAFT SEQUENCE.//0.022:644:58//Z97630

F-NT2RM1000127//RPCI11-44E5.TJ RPCI11 Homo sapiens genomic clone R-44E5, genomic survey sequence.//1.6e-45:254:94//AQ195884

F-NT2RM1000131//Homo sapiens mRNA for KIAA0792 protein, complete cds.//5.5e-153:778:95//AB018335

F-NT2RM1000132//Homo sapiens NADH:ubiquinone oxidoreductase NDUFS6 subunit mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.1e-90:448:97//AF044959

F-NT2RM1000153//Human NotI linking clone 924A081D, genomic survey sequence.//5.9e-07:66:96//U49890

F-NT2RM1000186//Homo sapiens clone 23763 unknown mRNA, partial cds.//0.025:126:70//AF007155

F-NT2RM1000187//CITBI-E1-2510J4.TR CITBI-E1 Homo sapiens genomic clone 2510J4, genomic survey sequence.//1.1e-05:56:98//AQ261184

F-NT2RM1000199//Mouse mRNA for seizure-related gene product 6 type 2 precursor, complete cds.//1.6e-38:711:65//D64009

F-NT2RM1000242

F-NT2RM1000244//HS_2229_A1_C04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2229 Col=7 Row=E, genomic survey sequence.//2.0e-13:95:95//AQ298474

F-NT2RM1000252//Homo sapiens chromosome 17, clone hRPK.206_C_20, complete sequence.//0.023:225:61//AC006070

F-NT2RM1000256//Caenorhabditis elegans cosmid F22B3, complete sequence.//8.5e-24:473:64//Z68336

F-NT2RM1000257//Homo sapiens MAGOH mRNA, complete cds.//6.4e-69:455:85//AF035940

F-NT2RM1000260//Human mRNA for KIAA0130 gene, complete cds.//6.5e-57:460:80//D50920

F-NT2RM1000271

F-NT2RM1000272

F-NT2RM1000280//Bos gaurus vacuolar H-ATPase subunit D (VATD) mRNA, complete cds.//6.7e-97:430:92//U11927

F-NT2RM1000300//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 92N15, WORKING DRAFT SEQUENCE.//2.1e-96:170:100//Z93097

F-NT2RM1000314//Human mRNA for KIAA0159 gene, complete cds.//8.1e-127:708:92//D63880

F-NT2RM1000318//Homo sapiens mRNA for ribosomal protein L39, complete cds.//5.7e-34:182:99//D79205

F-NT2RM1000341//Homo sapiens full-length insert cDNA clone YP11F06//1.3e-100:504:97//AF085879

F-NT2RM1000354//HS_2001_B1_E06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2001 Col=11 Row=J, genomic survey sequence.//1.6e-11:201:73//AQ218494

F-NT2RM1000355//Mus musculus E25B protein mRNA, complete cds.//1.8e-77:578:82//U76253

F-NT2RM1000365//Homo sapiens clone DJ0098022, WORKING DRAFT SEQUENCE, 5 unordered pieces.//9.4e-113:367:97//AC004821

F-NT2RM1000377//H.sapiens mRNA for MAP kinase phosphatase 4.//6.1e-14:362:62//Y08302

F-NT2RM1000388//Azospirillum brasilense lateral flagellin (laf1) gene, complete cds.//1.0:482:58//U26679

F-NT2RM1000394//M.musculus mRNA for histone H3.3A.//1.7e-94:549:89//Z85979

F-NT2RM1000399

F-NT2RM1000421//HS_2213_B1_E01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2213 Col=1 Row=J, genomic survey sequence.//3.6e-08:195:72//AQ032737

F-NT2RM1000430//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//3.7e-84:418:97//AF084928

F-NT2RM1000499//Human mRNA for KIAA0167 gene, complete cds.//1.3e-35:525:69//D79989

F-NT2RM1000539//Homo sapiens PAC clone DJ1194E14 from 7p21, complete sequence.//4.6e-73:533:83//AC004993

F-NT2RM1000553

F-NT2RM1000555//Homo sapiens clone 24514 unknown mRNA.//2.3e-110:555:97//AF070542

F-NT2RM1000563//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.3e-123:477:100//AC004873

F-NT2RM1000623//HS_2213_B1_E01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2213 Col=1 Row=J, genomic survey sequence.//8.2e-06:75:89//AQ032737

F-NT2RM1000648//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.3e-123:477:100//AC004873

F-NT2RM1000651

F-NT2RM1000651//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.3e-123:477:100//AC004873

F-NT2RM1000666//HS_2016_B2_H08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2016 Col=16 Row=P, genomic survey sequence.//5.7e-13:199:73//AQ227865

F-NT2RM1000669//Human DNA sequence from clone 281H8 on chromosome 6q25.1-25.3. Contains up to four novel genes, one with similarity to KIAA0323 and worm C30F12.1 and another with Ubiquitin-Like protein gene SMT3 (the latter in an intron of a novel gene). Contains ESTs, STSs, GSSs, a putative CpG island and genomic marker D6S1553, complete sequence.//2.7e-94:499:94//AL031133

F-NT2RM1000672

F-NT2RM1000691//Homo sapiens HRIHFB2060 mRNA, partial cds.//2.2e-119:582:98//AB015348

F-NT2RM1000699//Caenorhabditis elegans cosmid Y41C4A, complete sequence.//0.95:284:61//AL032627

F-NT2RM1000702//HS_3005_A1_A02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3005 Col=3 Row=A, genomic survey sequence.//0.073:290:58//AQ089514

F-NT2RM1000725//Homo sapiens mRNA for neuropathy target esterase.//4.8e-65:435:85//AJ004832

F-NT2RM1000741//Homo sapiens mRNA for KIAA0567 protein, partial cds.//8.0e-126:690:92//AB011139

F-NT2RM1000742//Homo sapiens AC133 antigen mRNA, complete cds.//2.5e-66:524:83//AF027208

F-NT2RM1000746//Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1.333303.//0.92:395:58//AJ011930

F-NT2RM1000770//Homo sapiens inosine monophosphate dehydrogenase type II gene, complete cds.//2.1e-70:407:92//L39210

F-NT2RM1000772//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//6.6e-36:98:93//AC000380

F-NT2RM1000780//Human DNA for 5' terminal region of LINE-1 transposable element clone CGL1-4.//9.3e-22:126:99//X52233

F-NT2RM1000781//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//7.1e-09:540:59//AC004153

F-NT2RM1000800//Mus musculus mRNA for B-IND1 protein.//4.0e-81:497:88//Z97207

F-NT2RM1000802

F-NT2RM1000811//Homo sapiens AC133 antigen mRNA, complete cds.//3.7e-63:490:84//AF027208

F-NT2RM1000826//Homo sapiens clone 24514 unknown mRNA.//7.2e-153:749:96//AF070542

F-NT2RM1000829//HS_3047_A1_A05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=9 Row=A, genomic survey sequence.//0.74:215:67//AQ099134

F-NT2RM1000833//Canis familiaris sec61 homologue mRNA, complete cds.//5.1e-114:683:88//M96629

F-NT2RM1000850//F.rubripes GSS sequence, clone 163A22aF11, genomic survey sequence.//1.1e-26:279:74//AL018762

F-NT2RM1000852//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//9.3e-148:726:97//AJ010840

F-NT2RM1000857//Rattus norvegicus gene for cytochrome P450/6 beta B, exon 2.//0.97:124:65//AB008378

F-NT2RM1000867//H.sapiens DNA sequence surrounding NotI site, clone NRLA143D.//1.2e-31:172:98//K95834

F-NT2RM1000874//Homo sapiens KE05 protein mRNA, complete cds.//2.8e-131:632:97//AF064605

F-NT2RM1000882//Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin heavy chain (FTH), complete sequence.//1.2e-98:214:99//AC004228

F-NT2RM1000883//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//2.7e-156:762:97//AF082516

F-NT2RM1000885//Homo sapiens mRNA for KIAA0661 protein, complete cds.//2.0e-17:310:67//AB014561

F-NT2RM1000894//Mus musculus second largest subunit of RNA polymerase I (RPA2) mRNA, complete cds.//3.2e-95:469:83//U58280

F-NT2RM1000898

F-NT2RM1000905//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 466N1, WORKING DRAFT SEQUENCE.//1.8e-74:188:98//Z97630

F-NT2RM1000924//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces.//5.7e-148:601:98//AC004873

F-NT2RM1000927//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//0.071:392:60//AC004846

F-NT2RM1000962//H.sapiens CpG island DNA genomic MseI fragment, clone 140d1, forward read cpg140d1.ft1a.//4.1e-35:187:99//Z56803

F-NT2RM1000978//Homo sapiens Chromosome 15q22.3-23 PAC 88m3, WORKING DRAFT SEQUENCE, 2 ordered pieces.//1.1e-23:266:77//AC005959

F-NT2RM1001003//Homo sapiens alpha subunit of RNA polymerase I (RPA1) mRNA, complete cds.//3.2e-95:469:83//U58280

F-NT2RM1001004//Homo sapiens alpha subunit of RNA polymerase I (RPA1) mRNA, complete cds.//3.2e-95:469:83//U58280

F-NT2RM1001005//Homo sapiens alpha subunit of RNA polymerase I (RPA1) mRNA, complete cds.//3.2e-95:469:83//U58280

F-NT2RM1001043//Human DNA sequence from PAC 27K14 on chromosome Xp11.3-Xp11.4. Contains monoamine oxidase B (MAOB), ESTs and polymorphic CA repeats.//3.9e-93:645:86//Z95125

F-NT2RM1001044//S.pombe chromosome III cosmid c320//0.90:128:66//AL022245

F-NT2RM1001059//Homo sapiens chromosome 5, Bac clone 58g14 (LBNL H76), complete sequence.//3.8e-53:261:80//AC005915

F-NT2RM1001066//CIT-HSP-2172N17.TF CIT-HSP Homo sapiens genomic clone 2172N17, genomic survey sequence.//0.64:285:59//B94391

F-NT2RM1001072//HS_3115_B1_D07_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3115 Col=13 Row=H, genomic survey sequence.//7.3e-23:140:95//AQ147905

F-NT2RM1001074//Homo sapiens chromosome 19, cosmid F20489, complete sequence.//5.0e-50:186:98//AC005263

F-NT2RM1001082//Sequence 1 from Patent WO9718303//2.1e-144:736:95//A62731

F-NT2RM1001085//CIT-HSP-2310F21.TR CIT-HSP Homo sapiens genomic clone 2310F21, genomic survey sequence.//8.8e-45:235:97//AQ020757

F-NT2RM1001092//HS_3055_B1_G05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=9 Row=N, genomic survey sequence.//1.1e-89:471:95//AQ155489

F-NT2RM1001102//Human HEM45 mRNA, complete cds.//1.2e-28:482:63//U88964

F-NT2RM1001105//Homo sapiens hRED1 gene, exon 1 (5'UTR)//0.0014:349:61//Z95973

F-NT2RM1001112//Homo sapiens chromosome 19, cosmid R34094, complete sequence.//0.060:429:58//AC004678

F-NT2RM1001115//Plasmodium falciparum merozoite surface protein 3 (MSP-3) gene, partial cds.//0.93:156:62//AF024624

F-NT2RM1001139//Homo sapiens chromosome 19, fosmid 37502, complete sequence.//1.2e-10:466:59//AC004755

F-NT2RM2000006//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 796F18, WORKING DRAFT SEQUENCE.//5.3e-150:724:98//AL031291

F-NT2RM2000013//D.melanogaster DmRP128 gene for RNA polymerase III second-largest subunit.//1.5e-58:749:69//X58826

F-NT2RM2000030//Homo sapiens clone DJ0708P22, WORKING DRAFT SEQUENCE, 11 unordered pieces.//2.1e-97:270:77//AC004863

F-NT2RM2000032//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE.//1.9e-25:172:76//AL034379

F-NT2RM2000042//Human DNA sequence from cosmid U55E4, between markers DXS6791 and DXS8038 on chromosome X contains ESTs.//5.0e-05:325:65//Z73418

F-NT2RM2000092//Homo sapiens (D8S321 locus) DNA sequence, tetranucleotide repeat polymorphism.//0.63:117:68//L12269

F-NT2RM2000093//Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; sm-RNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes.//0.38:312:62//AF109905

F-NT2RM2000101

F-NT2RM2000124//Mouse cAMP-dependent protein kinase catalytic subunit mRNA, complete cds.//3.8e-58:297:97//M12303

F-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A2 (PDE9A) mRNA, complete cds.//3.8e-138:653:98//AF067224

F-NT2RM2000192//CIT-HSP-2172B3.TF CIT-HSP Homo sapiens genomic clone 2172B3, genomic survey sequence.//2.2e-33:191:95//B93289

F-NT2RM2000239//F. rubripes GSS sequence, clone 156P04aG12, genomic survey sequence.//8.9e-44:445:69//AL018549

F-nnnnnnnnnnnn//Homo sapiens fibroblast growth factor 18 (FGF18) mRNA, complete cds.//0.00020:380:61//AF075292

F-NT2RM2000250//Homo sapiens mRNA for KIAA0590 protein, complete cds.//3.1e-128:615:98//AB011162

F-NT2RM2000259//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 310O13, WORKING DRAFT SEQUENCE.//0.0013:305:63//AL031658

F-NT2RM2000260//Mus musculus WW domain binding protein 15 mRNA, partial sequence.//3.0e-14:645:61//AF073934

F-NT2RM2000287//*** SEQUENCING IN PROGRESS *** from clone 310O13, WORKING DRAFT SEQUENCE

NOTE: This sequence has been determined by the Human Genome Center, Washington University School of Medicine, St. Louis, MO. It is a preliminary sequence and may contain errors. It is not for publication without the approval of the Human Genome Center.

QUENCE, 50 unordered pieces.//1.3e-11:96:86//AC003656

F-NT2RM2000322//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//8.5e-115:233:97//AL031864

5 F-NT2RM2000359//Homo sapiens mRNA for KIAA0560 protein, complete cds.//8.8e-175:805:99//AB011132

F-NT2RM2000363//RPCI11-90B10.TJ RPCI11 Homo sapiens genomic clone R-90B10, genomic survey sequence.//6.7e-15:96:98//AQ285300

F-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK7 mRNA, partial cds.//1.2e-94:599:86//U48251

10 F-NT2RM2000371//RPCI11-57I4.TJ RPCI11 Homo sapiens genomic clone R-57I4, genomic survey sequence.//1.1e-52:312:91//AQ083343

F-NT2RM2000374//M. musculus nodal gene, a TGF-beta-like gene.//6.7e-31:196:91//X70514

F-NT2RM2000395//Leishmania major chromosome 1, complete sequence.//0.99:345:58//AE001274

F-NT2RM2000402//Arabidopsis thaliana BAC T19D16 genomic sequence.//2.1e-23:414:63//U95973

15 F-NT2RM2000407//Mus musculus semaphorin VIa mRNA, complete cds.//1.4e-131:439:88//AF030430

F-NT2RM2000420//HS_3063_B2_F11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3063 Col=22 Row=L, genomic survey sequence.//3.2e-25:154:95//AQ103204

F-NT2RM2000422//Rat orphan transporter v7-3 (NTT73) mRNA, complete cds.//1.7e-128:782:86//L22022

F-NT2RM2000452//HS_3009_B2_D05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3009 Col=10 Row=H, genomic survey sequence.//1.2e-16:122:90//AQ130794

20 F-NT2RM2000469//HS_2019_A1_G02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2019 Col=3 Row=M, genomic survey sequence.//9.6e-22:176:85//AQ229041

F-NT2RM2000490//Homo sapiens mRNA for KIAA0747 protein, partial cds.//7.5e-15:386:63//AB018290

F-NT2RM2000502

25 F-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//5.1e-171:824:97//AF061243

F-NT2RM2000522

F-NT2RM2000540

F-NT2RM2000556//Homo sapiens 12q13.1 PAC RPCI5-1057I20 (Roswell Park Cancer Institute Human PAC library) complete sequence.//2.9e-42:344:82//AC004466

30 F-NT2RM2000566//Homo sapiens integrin alpha-7 mRNA, complete cds.//2.8e-154:751:97//AF072132

F-NT2RM2000567//Pseudomonas aeruginosa enoyl-CoA hydratase gene, partial cds; pilin biosynthetic protein (fimL) gene, complete cds; and unknown gene.//3.0e-06:664:58//AF083252

F-NT2RM2000569//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 862K6, WORKING DRAFT SEQUENCE.//1.3e-15:348:67//AL031681

35 F-NT2RM2000577//RPCI11-43G22.TJ RPCI11 Homo sapiens genomic clone R-43G22, genomic survey sequence.//1.6e-14:155:80//AQ199391

F-NT2RM2000581//Homo sapiens mRNA for KIAA0214 protein, complete cds.//5.4e-174:820:98//D86987

F-NT2RM2000588//Homo sapiens 12q13.1 PAC RPCI5-1057I20 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.1e-60:344:82//AC004466

40 F-NT2RM2000594//Mus musculus DNA cytosine-5 methyltransferase 3B1 (Dnmt3b) mRNA, alternatively spliced, complete cds.//4.9e-118:761:85//AF068626

F-NT2RM2000599//O.sativa osr40g3 gene.//0.30:585:56//Y08988

F-NT2RM2000609

F-NT2RM2000612//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//7.8e-102:709:83//U35776

45 F-NT2RM2000623//Homo sapiens chromosome 19, cosmid F19847, complete sequence.//3.4e-17:450:65//AC005952

F-NT2RM2000624

2.9e-06:231:64//Z82061

50 F-NT2RM2000635//Homo sapiens mRNA for KIAA0729 protein, partial cds.//6.3e-142:664:98//AB018272

F-NT2RM2000636//Homo sapiens mRNA for KIAA0658 protein, partial cds.//7.4e-138:664:98//AB014558

F-NT2RM2000639//RPCI11-69E5.TJ RPCI11 Homo sapiens genomic clone R-69E5, genomic survey sequence.//3.7e-14:97:97//AQ267491

F-NT2RM2000649//Homo sapiens mRNA for KIAA0676 protein, partial cds.//1.1e-167:518:99//AB014576

55 F-NT2RM2000669

F-NT2RM2000681

AC002001

F-NT2RM2000711//Homo sapiens mRNA for KIAA0621 protein, partial cds.//1.4e-04:140:94//L86984

F-NT2RM2000718//Homo sapiens HRIHFB2436 mRNA, partial cds.//2.4e-124:594:98//AB015342
 F-NT2RM2000735//Human ZNF43 mRNA.//8.4e-111:756:82//X59244
 F-NT2RM2000740//Mus musculus lymphocyte specific helicase mRNA, complete cds.//1.3e-141:815:89//U25691
 F-NT2RM2000795//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 439F8, WORKING
 5 DRAFT SEQUENCE.//1.0e-78:723:76//AL021392
 F-NT2RM2000821//Rat mRNA for beta COP.//2.0e-150:879:88//X57228
 F-NT2RM2000837//Homo sapiens BAC clone GS214N13 from 7p14-p15, complete sequence.//1.1e-05:361:62//
 AC005017
 F-NT2RM2000951//Homo sapiens XYLB mRNA for xylulokinase, complete cds.//8.7e-184:847:99//AB015046
 10 F-NT2RM2000952
 F-NT2RM2000984//Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; sm-
 RNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes.//
 7.6e-41:239:76//AF109905
 F-NT2RM2001004//CIT-HSP-2333N18.TR CIT-HSP Homo sapiens genomic clone 2333N18, genomic survey se-
 15 quence.//1.1e-11:298:66//AQ035862
 F-NT2RM2001035//Mus musculus mCAF1 protein mRNA, complete cds.//1.4e-120:627:91//U21855
 F-NT2RM2001065//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, complete cds.//6.8e-118:690:88//
 AF071314
 F-NT2RM2001100//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.3e-
 20 145:614:99//AC004873
 F-NT2RM2001105//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50O24, WORKING
 DRAFT SEQUENCE.//2.7e-95:461:99//AL034380
 F-NT2RM2001131//Kaposi's sarcoma-associated herpes-like virus ORF73 homolog gene, complete cds.//7 2e-
 24:726:62//U52064
 25 F-NT2RM2001141
 F-NT2RM2001152//Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the
 CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase com-
 ponent A 1, Choroideraemia protein, Tapetochoroidal Dystrophy (TCD) protein). Contains ESTs and an STS, com-
 plete sequence.//0.98:300:62//AL022401
 30 F-NT2RM2001177//Homo sapiens clone NH0313P13, WORKING DRAFT SEQUENCE, 15 unordered pieces.//
 1.2e-147:741:96//AC005488
 F-NT2RM2001194//Suid herpesvirus 1 UL5 gene, partial cds, UL6 and UL7 genes, complete cds, UL8 gene, partial
 cds.//0.026:408:59//U66829
 F-NT2RM2001196//Homo sapiens clone DJ1173I20, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.2e-
 35 135:627:98//AC004987
 F-NT2RM2001201//Mus musculus clone OST431, genomic survey sequence.//6.1e-80:503:86//AF046700
 F-NT2RM2001221//Chimpanzee (P.paniscus) involucrin, complete cds.//0.53:670:55//M26514
 F-NT2RM2001238//Rat glutaminase mRNA, complete cds.//3.4e-128:719:90//M65150
 F-NT2RM2001243
 40 F-NT2RM2001247//CITBI-E1-2521M18.TR CITBI-E1 Homo sapiens genomic clone 2521M18, genomic survey
 sequence.//0.0011:274:59//AQ276184
 F-NT2RM2001256//M.musculus mRNA for 200 kD protein.//2.3e-129:742:90//X80169
 F-NT2RM2001291//CIT-HSP-2010I15.TR CIT-HSP Homo sapiens genomic clone 2010I15, genomic survey se-
 quence.//4.6e-09:156:72//B57734
 45 F-NT2RM2001306//RPCI11-28I5.TP RPCI-11 Homo sapiens genomic clone RPCI-11-28I5, genomic survey se-
 quence.//0.069:234:64//B84850
 F-NT2RM2001312//Homo sapiens chromosome 17, clone hRPK.142_H_19, complete sequence.//1.1e-22:111:
 81//AC005919
 F-NT2RM2001319//Borrelia burgdorferi (section 4 of 70) of the complete genome.//0.99:340:58//AE001118
 50 F-NT2RM2001324//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 209H1, WORKING
 DRAFT SEQUENCE.//3.7e-44:340:85//Z84465
 F-NT2RM2001345//HS_3005_A1_A02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3005 Col=3 Row=A, genomic survey sequence.//0.042:290:58//AQ089514
 F-NT2RM2001360//Human HeLa mRNA isolated as a false positive in a two-hybrid-screen.//5.0e-60:365:87//
 55 U56429
 F-NT2RM2001393//Homo sapiens chromosome 22q11.2 PAC clone p.m11 in BCRL2-GGT Region, complete

sequence.//4.0e-54:394:75//AC004033

F-NT2RM2001420//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 349A12, WORKING DRAFT SEQUENCE.//2.8e-169:789:99//AL033520

F-NT2RM2001424//Homo sapiens mRNA for E1B-55kDa-associated protein.//7.1e-96:453:99//AJ007509

F-NT2RM2001499//Rattus norvegicus mRNA for cationic amino acid transporter 3, complete cds.//7.1e-91:601:83//AB000113

F-NT2RM2001504//Homo sapiens chromosome 19, cosmid R30017, complete sequence.//0.81:200:69//AC005624

F-NT2RM2001524//Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No. 2.//3.8e-16:316:65//Z99708

F-NT2RM2001544

F-NT2RM2001547//Caenorhabditis elegans cosmid Y47H9C, complete sequence.//3.3e-24:318:67//AL032657

F-NT2RM2001575//Human 52-kD ribonucleoprotein Ro/SSA mRNA, complete cds.//2.1e-26:582:64//M34551

F-NT2RM2001582//M.musculus red-1 gene.//1.4e-102:581:90//X92750

F-NT2RM2001588//Homo sapiens KIAA0442 mRNA, partial cds.//7.0e-10:282:65//AB007902

F-NT2RM2001592//Rattus norvegicus rexo70 mRNA, complete cds.//9.6e-131:736:90//AF032667

F-NT2RM2001605//RBP2=retinoblastoma binding protein 2 [human, Nalm-6 pre-B cell leukemia, mRNA, 6455 nt].//2.3e-85:749:75//S66431

F-NT2RM2001613//Rattus rattus sec61 homologue mRNA, complete cds.//8.6e-118:779:85//M96630

F-NT2RM2001632//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.//1.5e-50:561:71//AC004691

F-NT2RM2001635//Homo sapiens mRNA for KIAA0618 protein, complete cds.//9.2e-153:740:98//AB014518

F-NT2RM2001637//F.rubripes GSS sequence, clone 155D22bD8, genomic survey sequence.//2.5e-13:224:64//Z91020

F-NT2RM2001641//CIT-HSP-2347F23.TF CIT-HSP Homo sapiens genomic clone 2347F23, genomic survey sequence.//1.3e-67:340:98//AQ060913

F-NT2RM2001648//Canis familiaris sec61 homologue mRNA, complete cds.//1.4e-110:459:89//M96629

F-NT2RM2001652//Bos taurus guanine nucleotide-exchange protein (ARF-GEP1) mRNA, complete cds.//1.2e-153:807:93//AF023451

F-NT2RM2001659//nbxb0002cE07f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0002J13f, genomic survey sequence.//1.0:485:56//AQ051653

F-NT2RM2001664//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//3.7e-172:802:99//AF044195

F-NT2RM2001668

F-NT2RM2001670//Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease.//3.2e-18:279:70//AJ003147

F-NT2RM2001671//Oryctolagus cuniculus sarcolemmal associated protein-3 mRNA; complete cds.//1.6e-137:683:94//U21157

F-NT2RM2001675//RPC111-51J16.TJ RPC111 Homo sapiens genomic clone R-51J16, genomic survey sequence.//1.0:394:58//AQ053677

F-NT2RM2001681//Arabidopsis thaliana DNA chromosome 4, BAC clone T8O5 (ESSAII project).//0.87:220:61//AL021890

F-NT2RM2001688//B.parapertussis bvg locus (transcription regulators of virulence factors) with bvgA and bvgS genes.//1.0:286:62//X52948

F-NT2RM2001695//CIT-HSP-345H13.TVB CIT-HSP Homo sapiens genomic clone 345H13, genomic survey sequence.//3.2e-53:241:82//B59854

F-NT2RM2001696//Mouse DNA with homology to EBV IR3 repeat, segment 2, clone Mu2.//1.2e-05:306:58//M10668

F-NT2RM2001698//Homo sapiens DNA sequence from PAC 163M9 on chromosome 1p35.1-p36.21. Contains protein synthesis factor (eIF-4C), D1F15S1A pseudogene, ESTs, STS, GSS, complete sequence.//6.0e-06:548:59//AL021920

F-NT2RM2001699//HS_3195_8B2_DO1_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3195 Col=2 Row=H, genomic survey sequence.//2.7e-07:322:61//AQ189056

F-NT2RM2001700//Mycobacterium tuberculosis H37Rv complete genome; segment 109/162.//7.8e-05:354:58//Z95556

F-NT2RM2001718//Drosophila melanogaster DNA sequence (P1 DS04106 (D172)), complete sequence//4.2e-08:536:58//AC004290

F-NT2RM2001723//Homo sapiens clone 23770 mRNA sequence//1.4e-26:163:95//AF052123

F-NT2RM2001727//Homo sapiens mRNA for KIAA0462 protein, partial cds//6.2e-111:530:98//AB007931

F-NT2RM2001730//Homo sapiens chromosome 21 PAC RPCIP704E14135Q2//3.1e-102:248:95//AJ010598

F-NT2RM2001743

F-NT2RM2001753//Caenorhabditis elegans cosmid F45E6, complete sequence//0.11:138:66//Z68117

F-NT2RM2001760//Canis familiaris sec61 homologue mRNA, complete cds//9.4e100:418:88//M96629

F-NT2RM2001768//HS_3064_B2_A04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, genomic survey sequence//3.1e-28:153:100//AQ136993

F-NT2RM2001771//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence//1.3e-66:680:72//AC006116

F-NT2RM2001782

F-NT2RM2001784//Bovine herpesvirus type 1 (Cooper) DNA (30 kb)//0.027:384:60//Z48053

F-NT2RM2001785//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence//1.6e-18:229:65//AC004770

F-NT2RM2001797//HS_3045_AT_D01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3045 Col=1 Row=G, genomic survey sequence//1.4e-74:381:97//AQ129456

F-NT2RM2001800

F-NT2RM2001803//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//8.3e-178:827:99//AF044195

F-NT2RM2001805//Malus domestica leucine-rich receptor-like protein kinase (LRPKm1) gene, 5' flanking region and 5' UTR//1.0:290:58//AF053126

F-NT2RM2001813//CIT-HSP-2169F21.TR CIT-HSP Homo sapiens genomic clone 2169F21, genomic survey sequence//3.3e-16:109:95//B89870

F-NT2RM2001823//Drosophila melanogaster DNA sequence (P1 DS07049 (D133)), complete sequence//5.8e-62:819:68//AC004274

F-NT2RM2001839//Homo sapiens calumein (Calu) mRNA, complete cds//3.6e-131:738:90//AF013759

F-NT2RM2001840//Homo sapiens chromosome 17, clone 297N7, complete sequence//1.1e-57:422:79//AC002347

F-NT2RM2001855//HS_3224_A1_H07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3224 Col=13 Row=O, genomic survey sequence//0.00012:68:91//AQ205285

F-NT2RM2001867//Human DNA sequence from clone 889N15 on chromosome Xq22.1-22.3. Contains part of the gene for a novel protein similar to X. laevis Cortical Thymocyte Marker CTX, the possibly alternatively spliced gene for 26S Proteasome subunit p28 (Ankyrin repeat protein), a novel gene and exons 36 through 45 of the COL4A6 for Collagen Alpha 6(IV). Contains ESTs, STSs, GSSs and a putative CpG island, complete sequence//0.068:102:70//AL031177

F-NT2RM2001879//Human DNA sequence from cosmid cU72E5, between markers DXS366 and DXS87 on chromosome X//0.0029:500:59//Z68328

F-NT2RM2001886//Homo sapiens mRNA for KIAA0710 protein, complete cds//1.9e-187:866:97//AB014610

F-NT2RM2001896//S.cerevisiae chromosome III complete DNA sequence//8.6e-30:613:63//X59720

F-NT2RM2001903//Homo sapiens mRNA for KIAA0462 protein, partial cds//2.9e-176:859:97//AB007931

F-NT2RM2001930//M.musculus mRNA for semaphorin G//4.7e-117:730:85//X97818

F-NT2RM2001935//Sequence 11 from Patent WO9610637//1.0:356:60//A50028

F-NT2RM2001936//Homo sapiens clone 614 unknown mRNA, complete sequence//6.9e-138:653:98//AF091080

F-NT2RM2001950//RPCI11-24L12.TP RPCI-11 Homo sapiens genomic clone RPCI-11-24L12, genomic survey sequence//2.7e-19:188:81//B86700

F-NT2RM2001982//Arabidopsis thaliana chromosome II BAC T24I21 genomic sequence, complete sequence//0.42:179:65//AC005825

F-NT2RM2001983//Homo sapiens RGS-GAIP interacting protein GIPC mRNA, complete cds//3.8e-20:123:98//AF089816

F-NT2RM2001989//Sequence 3 from patent US 5747317//1.9e-167:786:98//AR004981

F-NT2RM2001997//Human HepG2 partial cDNA, clone hmd1b08m5//9.6e-25:160:95//D16955

F-NT2RM2001998//Homo sapiens DNA, chromosome 21q22.2, PAC clone 25P16 complete sequence, encoding carbonyl reductase and carbonyl reductase 3 (complete cds)//0.88:380:60//AB003151

F-NT2RM2002004

F-NT2RM2002011

F-NT2RM2002030//Mus musculus glutamine fructose-6-phosphate amidotransferase mRNA, complete cds//

1.5e-89:822:74//U00932

F-NT2RM2002049//Bovine elastin mRNA, partial cds.//8.8e-11:125:81//M26132

F-NT2RM2002055

F-NT2RM2002088//Mus musculus WW domain binding protein 17 mRNA, partial sequence.//1.4e-15:421:63//AF073936

F-NT2RM2002091//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50O24, WORKING DRAFT SEQUENCE.//4.6e-160:771:98//AL034380

F-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//7.7e-164:776:98//AJ010840

F-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds.//2.4e-143:684:98//AF030435

F-NT2RM2002128//Mesocricetus auratus guanine nucleotide-binding protein beta 5 (Gnb5) mRNA, complete cds.//7.0e-27:330:73//U13152

F-NT2RM2002142//Danio rerio gastrulation specific (G12) mRNA, complete cds.//6.3e-10:135:80//U27121

F-NT2RM2002145//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//4.2e-143:800:92//AF084928

F-NT2RM2002178//Homo sapiens mRNA for KIAA0467 protein, partial cds.//5.2e-164:787:97//AB007936

F-NT2RM2002580//Drosophila melanogaster DNA sequence (P1 DS02110 (D147)), complete sequence.//7.4e-13:337:62//AC004423

F-NT2RM4000024//D.melanogaster DmRP128 gene for RNA polymerase III second-largest subunit.//1.2e-62:801:70//X58826

F-NT2RM4000027//Caenorhabditis elegans cosmid F09E5.//0.36:336:60//U37429

F-NT2RM4000030//H.sapiens CpG island DNA genomic MseI fragment, clone 56h10, forward read cpg56h10.ft1a.//9.3e-22:127:100//Z55685

F-NT2RM4000046//Curcubita maxima 25S - 18S rDNA intergenic spacer.//4.1e-05:386:60//X13059

F-NT2RM4000061

F-NT2RM4000085//B.taurus mRNA for nuclear DNA helicase II.//1.9e-10:485:59//X82829

F-NT2RM4000086

F-NT2RM4000104//Homo sapiens chromosome 16 zinc finger protein ZNF210 (ZNF210) mRNA, complete cds.//4.2e-23:345:69//AF060865

F-NT2RM4000139//R.norvegicus trg mRNA.//1.4e-56:708:69//X68101

F-NT2RM4000155//CIT-HSP-2282N15.TR CIT-HSP Homo sapiens genomic clone 2282N15, genomic survey sequence.//3.0e-09:88:90//AQ000070

F-NT2RM4000156//H.sapiens HPBR11-7 gene.//2.0e-21:586:60//X67336

F-NT2RM4000167//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//2.7e-143:810:90//D12646

F-NT2RM4000169//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0054:746:57//AC004157

F-NT2RM4000191//Mus musculus cathepsin S (CatS) gene, promoter region and exons 1 and 2.//0.00018:468:60//AF051726

F-NT2RM4000197

F-NT2RM4000199//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 620E11, WORKING DRAFT SEQUENCE.//0.67:461:60//AL031667

F-NT2RM4000200

F-NT2RM4000202//H.sapiens CpG island DNA genomic MseI fragment, clone 34c2, forward read cpg34c2.ft1a.//1.7e-27:190:90//Z65361

F-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds.//1.4e-182:856:98//AB018255

F-NT2RM4000215//S.cerevisiae MAK16 protein gene, complete cds, and LTE1 protein gene, 3' end.//3.1e-31:731:62//J03852

F-NT2RM4000229//Homo sapiens chromosome 10 clone CIT987SK-1144G6 map 10q25.1, complete sequence.//4.6e-102:233:94//AC005383

F-NT2RM4000233//Mus musculus semaphorin VIa mRNA, complete cds.//1.6e-135:835:86//AF030430

F-NT2RM4000244//RPCI11-24P15.TV RPCI-11 Homo sapiens genomic clone RPCI-11-24P15, genomic survey sequence.//5.5e-08:422:62//B86757

F-NT2RM4000251//Mus musculus clone UWGC:mbac92 from 14D1-D2 (T-Cell Receptor Alpha Locus), complete sequence.//0.98:207:60//AC005855

F-NT2RM4000265//H.sapiens

glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA, complete sequence.//1.2e-11:165:60//AC003684

F-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, complete cds.//7.9e-153:609:93//

M99438

F-NT2RM4000324

F-NT2RM4000327//Rattus norvegicus guanine nucleotide binding protein beta 4 subunit mRNA, partial cds//3.9e-44:727:68//AF022085

5 F-NT2RM4000344//Mus musculus ATP-dependent metalloprotease FtsH1 mRNA, complete cds//1.0e-143:801:90//AF090430

F-NT2RM4000349//Mus musculus clone OST431, genomic survey sequence//6.1e-80:503:86//AF046700

F-NT2RM4000354//HS_2221_A2_C07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2221 Col=14 Row=E, genomic survey sequence//1.0e-20:180:83//AQ253449

10 F-NT2RM4000356

F-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cds//1.6e-133:628:99//AB014542

F-NT2RM4000368//RPC111-91B5.TJ RPC111 Homo sapiens genomic clone R-91B5, genomic survey sequence//5.0e-12:431:61//AQ283217

F-NT2RM4000386//Mus musculus DOC4 (Doc4) mRNA, complete cds//7.4e-86:845:72//AF059485

15 F-NT2RM4000395//Saccharomyces cerevisiae chromosome VI cosmid 9965//2.5e-34:767:61//D44597

F-NT2RM4000414//Homo sapiens XYLB mRNA for xylulokinase, complete cds//1.5e-15:114:94//AB015046

F-NT2RM4000421

F-NT2RM4000425//Homo sapiens chromosome 17, clone hRPK.294_J_22, complete sequence//1.5e-37:295:82//AC005921

20 F-NT2RM4000433//Mus musculus retinoic acid-responsive protein (Stra6) mRNA, complete cds//3.9e-94:740:78//AF062476

F-NT2RM4000457//CIT-HSP-2346B17.TR CIT-HSP Homo sapiens genomic clone 2346B17, genomic survey sequence//1.5e-22:149:92//AQ062111

F-NT2RM4000471//Homo sapiens mRNA for putative tRNA splicing protein, partial//1.3e-76:386:97//AJ010952

25 F-NT2RM4000486//Homo sapiens mRNA, complete cds, clone:RES4-22A, //1.1e-22:356:67//AB000459

F-NT2RM4000496//Homo sapiens 12p13.3 BAC RPC111-476M19 (Roswell Park Cancer Institute Human BAC Library) complete sequence//0.53:198:70//AC005908

F-NT2RM4000511

F-NT2RM4000514

30 F-NT2RM4000515//CIT-HSP-2285L3.TR CIT-HSP Homo sapiens genomic clone 2285L3, genomic survey sequence//0.0012:200:66//AQ000113

F-NT2RM4000520

F-NT2RM4000531//Human zinc finger protein 42 (MZF-1) mRNA, complete cds//2.9e-31:732:64//M58297

35 F-NT2RM4000532//HS_3231_B1_C05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3231 Col=9 Row=F, genomic survey sequence//1.3e-59:362:90//AQ192093

F-NT2RM4000534

F-NT2RM4000585//CITBI-E1-2508I18.TR CITBI-E1 Homo sapiens genomic clone 2508I18, genomic survey sequence//1.1e-34:208:93//AQ260706

40 F-NT2RM4000590//CIT-HSP-2291M14.TF CIT-HSP Homo sapiens genomic clone 2291M14, genomic survey sequence//8.3e-34:180:99//AQ004125

F-NT2RM4000595//Homo sapiens chromosome 17, clone hCIT.131_K_11, complete sequence//1.2e-09:203:66//AC005288

F-NT2RM4000603//Human mRNA for KIAA0392 gene, partial cds//5.3e-14:305:68//AB002390

45 F-NT2RM4000611//CIT-HSP-2169F21.TR CIT-HSP Homo sapiens genomic clone 2169F21, genomic survey sequence//8.4e-16:109:94//B89870

F-NT2RM4000616//D.melanogaster mRNA for acetyl-CoA synthetase//2.3e-59:721:68//Z46786

F-NT2RM4000674

F-NT2RM4000689//CIT-HSP-2381O13.TF CIT-HSP Homo sapiens genomic clone 2381O13, genomic survey sequence//2.6e-31:174:97//AQ110303

50 F-NT2RM4000698

F-NT2RM4000700

F-NT2RM4000712//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//1.1e-89:744:77//AF022789

F-NT2RM4000717

55 F-NT2RM4000733//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423R22. WORKING
AF1 SEQUENCING IN PROGRESS

F-NT2RM4000734//Homo sapiens mRNA for KIAA0642 protein, partial cds//1.6e-133:628:99//AB014542

F-NT2RM4000741

F-NT2RM4000751//Human zinc finger protein 20 (ZNF20) pentanucleotide repeat polymorphism.//7.1e-95:754:77//M99593

F-NT2RM4000764

F-NT2RM4000778//Caenorhabditis elegans cosmid F36H12.//0.30:523:60//AF078790

5 F-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds.//5.5e-172:810:98//AB007920

F-NT2RM4000787//Human DNA sequence from PAC 370M22 on chromosome 22q12-qter. contains GRB2 ADAP-TOR LIKE PROTEIN, UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT PRECURSOR (UQCRRS1) exon, ESTs, STS, CA repeat and CpG island.//0.0057:163:69//Z82206

10 F-NT2RM4000790//Homo sapiens chromosome 19, cosmid R27216, complete sequence.//6.9e-39:237:94//AC005306

F-NT2RM4000795//Rattus norvegicus neuroligin 3 mRNA, complete cds.//5.9e-97:857:74//U41663

F-NT2RM4000796//HS_3214_B1_F11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3214 Col=21 Row=L, genomic survey sequence.//1.1e-14:254:68//AQ175988

15 F-NT2RM4000798//Bos taurus guanine nucleotide-exchange protein (ARF-GEP1) mRNA, complete cds.//6.2e-78:816:72//AF023451

F-NT2RM4000813//Leishmania major glycoprotein 96-92 (GP 96-92) gene, partial cds.//0.33:276:63//M63109

F-NT2RM4000820//, complete sequence.//2.6e-142:450:97//AC005406

F-NT2RM4000833//Drosophila melanogaster DNA sequence (P1 DS05273 (D80)), complete sequence.//1.9e-52:501:71//AC004373

20 F-NT2RM4000848//Homo sapiens chromosome 17, clone hRPK.167_N_20, complete sequence.//1.0:477:56//AC005940

F-NT2RM4000852

F-NT2RM4000855//Homo sapiens chromosome 17, clone hCIT.457_I_16, complete sequence.//3.4e-29:229:83//AC003957

25 F-NT2RM4000887

F-NT2RM4000895//Homo sapiens HuUAP1 mRNA for UDP-N-acetylglucosamine pyrophosphorylase, complete cds.//2.1e-20:407:64//AB011004

F-NT2RM4000950//Homo sapiens clone DJ0917G04, WORKING DRAFT SEQUENCE, 35 unordered pieces.//0.41:311:64//AC004929

30 F-NT2RM4000971//RPCI11-53H3.TJ RPCI11 Homo sapiens genomic clone R-53H3, genomic survey sequence.//1.0:208:64//AQ053735

F-NT2RM4000979//Homo sapiens chromosome 17, clone hRPK.642_C_21, complete sequence.//1.3e-19:207:78//AC005245

35 F-NT2RM4000996//CITBI-E1-2506B10.TF CITBI-E1 Homo sapiens genomic clone 2506B10, genomic survey sequence.//1.4e-73:361:98//AQ263651

F-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds.//5.1e-170:803:98//AB018272

F-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds.//3.3e-125:584:99//AB014539

F-NT2RM4001032//Gallus gallus chicken brain factor-2 (CBF-2) mRNA, complete cds.//0.00034:777:58//U47276

F-NT2RM4001047//MO25 gene [mice, embryos, mRNA, 2322 nt].//2.5e-92:776:74//S51858

40 F-NT2RM4001054//Canis familiaris sec61 homologue mRNA, complete cds.//3.1e-102:859:76//M96629

F-NT2RM4001084//CIT-HSP-2330F9.TR CIT-HSP Homo sapiens genomic clone 2330F9, genomic survey sequence.//4.6e-78:379:99//AQ044479

F-NT2RM4001092//cSRL-71b1-u cSRL flow sorted Chromosome 11 specific cosmid Homosapiens genomic clone cSRL-71b1, genomic survey sequence.//1.1e-12:152:75//B05776

45 F-NT2RM4001116

F-NT2RM4001140//Homo sapiens PAC clone DJ0964C11 from 7p14-p15, complete sequence.//1.9e-136:717:93//AC004593

F-NT2RM4001151//Streptomyces antibioticus ATP-binding protein and membrane protein (oleC-ORF1, oleC-ORF2, oleC-ORF3, oleC-ORF4, and oleC-PRF5) genes, complete cds; 3427 base-pairs.//0.0083:368:60//L06249

50 F-NT2RM4001155//Bos taurus 50 kDa protein (adp50) mRNA, complete cds.//3.9e-120:764:85//U04706

F-NT2RM4001160

F-NT2RM4001187

F-NT2RM4001191//CIT-HSP-2010E7.TF CIT-HSP Homo sapiens genomic clone 2010E7, genomic survey sequence.//6.2e-12:181:72//B53378

55 F-NT2RM4001200//H sapiens HZF10 mRNA for zinc finger protein //1.3e-66:799:69//X78933

F-NT2RM4001201

F-NT2RM4001202

F-NT2RM4001203

F-NT2RM4001217//Homo sapiens ectoderm-neural cortex-1 protein (ENC-1) mRNA, complete cds//1.6e-62:715:70//AF005381

F-NT2RM4001256//Human NotI linking clone 924A058R, genomic survey sequence//7.6e-14:109:90//U49884

5 F-NT2RM4001258//HS_3171_B2_G09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3171 Col=18 Row=N, genomic survey sequence//2.5e-18:215:77//AQ149676

F-NT2RM4001309//Human DNA sequence from clone 551E13 on chromosome Xp11.2-11.3 Contains farnesyl pyrophosphate synthetase pseudogene, VT4 protein pseudogene, EST, GSS, complete sequence//4.9e-28:526:66//AL022163

10 F-NT2RM4001313//H.sapiens mRNA for phosphatidylinositol 3-kinase//2.5e-77:474:89//Z46973

F-NT2RM4001316//Caenorhabditis elegans cosmid K09H11//1.2e-16:230:73//U97002

F-NT2RM4001320//Homo sapiens mRNA for Neuroblastoma, complete cds//1.1e-41:642:66//D89016

F-NT2RM4001340//EP(3)0614 Drosophila melanogaster EP line Drosophila melanogaster genomic Sequence recovered from 5' end of P element, genomic survey sequence//0.0040:141:68//AQ025127

15 F-NT2RM4001344//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y1E3, WORKING DRAFT SEQUENCE//5.5e-06:469:60//AL021388

F-NT2RM4001347

F-NT2RM4001371//Arabidopsis thaliana chromosome II BAC T20K9 genomic sequence, complete sequence//0.10:400:61//AC004786

20 F-NT2RM4001382//Homo sapiens RanBP7/importin 7 mRNA, complete cds//2.2e-167:790:98//AF098799

F-NT2RM4001384//Homo sapiens DNA sequence from BAC 747E2 on chromosome 22q12.1. Contains ESTs, STSs and GSSs and genomic marker D22S56, complete sequence//0.99:255:59//AL021393

F-NT2RM4001410//Homo sapiens genomic DNA, chromosome 21q11.1, segment 1/5, WORKING DRAFT SEQUENCE//0.027:336:58//AP000023

25 F-NT2RM4001411//Mus musculus Pro-rich, PH, SH2 domain-containing signaling mediator (PSM) mRNA, complete cds//5.9e-124:783:85//AF020526

F-NT2RM4001412//Rattus norvegicus GTPase activating protein SynGAP-c mRNA, complete cds//2.2e-34:418:71//AF050183

F-NT2RM4001414//Homo sapiens full-length insert cDNA clone ZE16C11//9.1e-76:363:100//AF086563

30 F-NT2RM4001437//Homo sapiens chromosome 5, BAC clone 313n8 (LBNL H146), complete sequence//2.0e-47:623:69//AC004226

F-NT2RM4001444//Streptococcus pneumoniae penicillin-binding protein 2b (pbp2b), RecM (recM), D-Ala-D-Ala ligase (ddl), D-Ala-D-Ala adding enzyme (murF), MutT (mutT), cell division protein FtsA (ftsA), cell division protein FtsZ (ftsZ), YlmE (ylmE), YlmF (ylmF), YlmG (ylmG), YlmH (ylmH), cell division protein DivIVA (divIVA), and isoleucine-tRNA synthetase (ileS) genes, complete cds; and unknown gene//3.6e-09:566:58//AF068901

35 F-NT2RM4001454

F-NT2RM4001455

F-NT2RM4001483//Human zinc finger protein ZNF136//3.2e-36:329:78//U09367

F-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds//1.2e-155:724:99//AB014585

40 F-NT2RM4001519//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces//0.00019:418:59//AC004688

F-NT2RM4001522//Human HepG2 3' region MboI cDNA, clone hmd6a08m3//1.4e-16:130:88//D17274

F-NT2RM4001557

F-NT2RM4001565

F-NT2RM4001566

45 F-NT2RM4001569//HS_2050_B1_C08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2050 Col=15 Row=F, genomic survey sequence//2.7e-09:109:84//AQ234720

F-NT2RM4001582//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds//1.2e-127:740:89//AF071317

50 F-NT2RM4001592//M.musculus mRNA of enhancer-trap-locus 1//7.3e-117:710:88//X69942

F-NT2RM4001594//Homo sapiens chromosome 9q34, clone 107G20, WORKING DRAFT SEQUENCE, 2 ordered pieces//0.34:388:59//AC002355

F-NT2RM4001597//M.musculus red-1 gene//6.2e-139:788:90//X92750

F-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds//3.3e-162:750:99//AB018334

55 F-NT2RM4001611//Synechocystis sp. PCC6803 complete genome, 12/27, 1430419-1576592//2.5e-05:490:58//D90910

F-NT2RM4001650//Homo sapiens chromosome 4, BAC clone 313n8 (LBNL H146), complete sequence//2.0e-47:623:69//AC004226

F-NT2RM4001650*** SEQUENCING IN PROGRESS *** from clone Y1E3, WORKING DRAFT SEQUENCE, 4 unordered pieces//0.99:422:59//AC004689

F-NT2RM4001662//Human mRNA for KIAA0322 gene, partial cds.//2.6e-81:449:93//AB002320

F-NT2RM4001666

F-NT2RM4001682//Mus musculus clone OST9187, genomic survey sequence.//3.2e-35:240:87//AF046699

F-NT2RM4001710//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 126A5, WORKING DRAFT SEQUENCE.//1.9e-151:564:97//AL031447

F-NT2RM4001714//Human mRNA for KIAA0202 gene, partial cds.//7.0e-85:748:74//D86957

F-NT2RM4001715//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs, complete sequence.//1.2e-91:488:94//AL034430

F-NT2RM4001731//Orang-utan in volucrin gene, complete cds.//0.40:530:59//M25312

F-NT2RM4001741//Mouse mRNA for talin.//1.1e-129:737:90//X56123

F-NT2RM4001746//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 316G12, WORKING DRAFT SEQUENCE.//2.3e-49:320:89//AL031709

F-NT2RM4001754//Homo sapiens 12p13.3 PAC RPCI5-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//6.3e-64:379:76//AC005831

F-NT2RM4001758//R.norvegicus mRNA for serine/threonine kinase MARK1.//3.7e-146:871:87//Z83868

F-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds.//2.3e-173:803:99//AB018270

F-NT2RM4001783//Homo sapiens clone DJ0981007, complete sequence.//2.0e-165:593:99//AC006017

F-NT2RM4001810

F-NT2RM4001813//Homo sapiens BAC clone NH0364H22 from 2, complete sequence.//7.1e-31:176:84//AC005036

F-NT2RM4001819//Human p58/GTA (galactosyltransferase associated protein kinase) mRNA, complete cds.//4.4e-34:195:95//M37712

F-NT2RM4001823//Mus musculus zinc finger protein (Zfp64) mRNA, complete cds.//3.3e-51:490:75//U49046

F-NT2RM4001828//Human zinc finger containing protein ZNF157 (ZNF157) mRNA, complete cds.//5.6e-74:688:72//U28687

F-NT2RM4001836//Homo sapiens Chromosome 22q11.2 Cosmid Clone 2h In DGCR Region, complete sequence.//1.0:406:60//AC000076

F-NT2RM4001841//Mus musculus A kinase anchor protein (AKAP-KL) mRNA, alternatively spliced isoform 2, complete cds.//1.6e-131:831:86//AF033275

F-NT2RM4001842//HS_3163_A2_G10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3163 Col=20 Row=M, genomic survey sequence.//1.5e-05:355:60//AQ168513

F-NT2RM4001856//Caenorhabditis elegans cosmid K08F11.//4.0e-23:823:60//U70855

F-NT2RM4001858//Notophthalmus viridescens NvTbox1 mRNA, partial cds.//6.4e-11:266:66//U64433

F-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC.//6.9e-149:704:98//Y17711

F-NT2RM4001876//F.rubripes GSS sequence, clone 060E22bA4, genomic survey sequence.//5.7e-48:600:68//Z88651

F-NT2RM4001880//CIT-HSP-2348J1.TF CIT-HSP Homo sapiens genomic clone 2348J1, genomic survey sequence.//0.0025:61:88//AQ060809

F-NT2RM4001905//R.norvegicus CYP3A1 gene, 5' flanking region.//2.5e-29:535:67//X98335

F-NT2RM4001922//HS_2237_A1_C10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=19 Row=E, genomic survey sequence.//2.2e-73:364:98//AQ033732

F-NT2RM4001930//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence.//4.9e-10:269:63//AB005248

F-NT2RM4001938//Homo sapiens chromosome 17, clone hRPC.1081_P_3, complete sequence.//7.6e-152:311:100//AC005207

F-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds.//1.1e-170:808:98//AF098162

F-NT2RM4001953//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone B13E4; HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//2.7e-45:310:86//AC004046

F-NT2RM4001965//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 11/11.//1.6e-107:622:90//AB020868

F-NT2RM4001969//R.norvegicus mRNA for IP63 protein.//3.9e-24:221:76//X99330

F-NT2RM4001979//Homo sapiens mRNA for KIAA0798 protein, complete cds.//1.0e-61:527:76//AB018341

F-NT2RM4001984//Human DNA sequence from cosmid U151E3, between markers on chromosome X.//5.8e-07:502:60//Z82253

F-NT2RM4001987//RPCI11-49L11.T1 RPCI11 Homo sapiens genomic clone B13E4, genomic survey sequence.//1.5e-05:355:60//AQ168513

F-NT2RM4002010//Homo sapiens chromosome 1, clone H11, genomic survey sequence.//1.5e-05:355:60//AQ168513

AC00592

F-NT2RM4002018//Human high molecular weight B cell growth factor mRNA sequence///1.0:527:57//L15344
 F-NT2RM4002034//Human DNA sequence from PAC 84F12 on chromosome Xq25-Xq26.3. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2), ESTs and CA repeat.//0.11:322:60//AL008712
 F-NT2RM4002044//Homo sapiens SS-A/Ro autoantigen 52 kda component gene, complete cds.//0.015:513:61//U01882
 5 F-NT2RM4002054//Homo sapiens clone DJ1039L24, WORKING DRAFT SEQUENCE, 3 unordered pieces//2.0e-44:473:76//AC005283
 F-NT2RM4002055//Homo sapiens mRNA for KIAA0640 protein, partial cds.//1.0e-171:803:98//AB014540
 F-NT2RM4002062//Drosophila melanogaster; Chromosome 2L; Region 36B1-36B3; P1 clone DS02528, WORKING DRAFT SEQUENCE, 8 unordered pieces//0.0031:298:59//AC005122
 10 F-NT2RM4002063//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//1.1e-147:705:98//U82267
 F-NT2RM4002066//Human mRNA for KIAA0192 gene, partial cds.//3.4e-73:889:69//D83783
 F-NT2RM4002067//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence//1.1e-53:295:76//AC005216
 15 F-NT2RM4002073//Mus musculus fatty acid transport protein 3 mRNA, partial cds.//7.8e-25:277:75//AF072758
 F-NT2RM4002075//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//9.0e-23:588:61//AF059569
 F-NT2RM4002093//Rat PYBP1 mRNA for pyrimidine binding protein 1.//3.1e-68:544:69//X60789
 20 F-NT2RM4002109//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//2.0e-121:762:86//D12646
 F-NT2RM4002128//HS_3084_A1_D04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3084 Col=7 Row=G, genomic survey sequence.//7.7e-18:117:95//AQ186312
 F-NT2RM4002140
 25 F-NT2RM4002145//Homo sapiens chromosome 19, fosmid 37308, complete sequence.//1.8e-49:736:65//AC004152
 F-NT2RM4002146//Homo sapiens MAGOH mRNA, complete cds.//6.5e-70:454:85//AF035940
 F-NT2RM4002161//Homo sapiens mRNA for LAFPTase, isoform 1, partial.//4.2e-151:763:96//AJ130763
 F-NT2RM4002174//Helicobacter pylori 26695 section 18 of 134 of the complete genome.//2.1e-16:580:60//AE000540
 30 F-NT2RM4002189//Homo sapiens DNA sequence from BAC 722E9 on chromosome 22q13.2-13.33. Contains ESTs.//1.0e-07:792:61//AL008636
 F-NT2RM4002194//Mus musculus semaphorin VIa mRNA, complete cds.//3.2e-132:782:87//AF030430
 F-NT2RM4002205//Rattus norvegicus nuclear-encoded mitochondrial elongation factor G mRNA, complete cds.//1.5e-40:292:84//L14684
 35 F-NT2RM4002213
 F-NT2RM4002226//Mus musculus p190-B gene, complete cds.//0.099:350:59//U67160
 F-NT2RM4002251//Homo sapiens chromosome 17, clone HCIT187M2, complete sequence.//1.0:428:58//AC004448
 40 F-NT2RM4002256//Mouse genomic DNA, chromosome 17, clone cosmid 49.1, genomic survey sequence.//9.4e-60:294:81//AB005959
 F-NT2RM4002266//Fugu rubripes GSS sequence, clone 006118aG12, genomic survey sequence.//3.3e-12:217:67//AL024779
 F-NT2RM4002278//HS_3089_A1_E05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3089 Col=9 Row=I, genomic survey sequence.//1.9e-64:381:92//AQ121653
 45 F-NT2RM4002281
 F-NT2RM4002287//CIT-HSP-2327E14.TF CIT-HSP Homo sapiens genomic clone 2327E14, genomic survey sequence.//9.0e-49:336:86//AQ042515
 F-NT2RM4002294//Human mRNA for KIAA0281 gene, complete cds.//2.1e-48:511:72//D87457
 50 F-NT2RM4002301//Human NotI linking clone 924A053D, genomic survey sequence.//8.9e-05:62:91//U49881
 F-NT2RM4002323//Human DNA sequence from clone 59B16 on chromosome 6p22.1-22.3. Contains a pseudo-gene similar to GPISG20 and other exonucleases). Contains ESTs, STSs, GSSs, genomic markers D6S1691 and D6S299 and a ca repeat polymorphism, complete sequence.//4.9e-115:729:87//AL032822
 F-NT2RM4002339//Homo sapiens PAC clone DJ0728D04, complete sequence.//1.1e-97:457:93//AC004865
 55 F-NT2RM4002344//Caenorhabditis elegans cosmid K04A8.//2.2e-06:190:69//U64849
 F-NT2RM4002375//Homo sapiens mRNA for KIAA0450 gene, partial cds.//1.0e-171:803:98//AB014540
 F-NT2RM4002374//Homo sapiens clone 2024 PAC 1336P3 (Research Park Cancer Institute Human Genomic Library), complete sequence.//6.00040:312:63//AC002978

F-NT2RM4002383//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 469D22, WORKING DRAFT SEQUENCE.//6.8e-29:378:66//AL031284

F-NT2RM4002390

F-NT2RM4002398//CIT-HSP-2288N22.TR CIT-HSP Homo sapiens genomic clone 2288N22, genomic survey sequence.//3.4e-35:184:100//AQ001110

F-NT2RM4002409//Archaeoglobus fulgidus section 15 of 172 of the complete genome.//2.0e-16:468:59//AE001092

F-NT2RM4002438//Human HLA class III region containing NOTCH4 gene, partial sequence, homeobox PBX2 (HPBX) gene, receptor for advanced glycosylation end products (RAGE) gene, complete cds, and 6 unidentified cds, complete sequence.//1.6e-16:123:91//U89336

F-NT2RM4002446//Human DNA sequence from cosmid 443D9 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contains ESTs, STS and CpG islands.//9.6e-64:467:84//Z92845

F-NT2RM4002452

F-NT2RM4002457//Human DNA sequence from PAC 151B14 on chromosome 22, complete sequence.//2.2e-24:201:86//Z85988

F-NT2RM4002460//Homo sapiens PAC clone DJ0630C24 from 7q31-q32, complete sequence.//1.3e-45:487:70//AC004690

F-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds.//2.7e-163:777:98//AF083255

F-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds.//2.3e-93:464:97//AB014591

F-NT2RM4002493

F-NT2RM4002499//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.5e-41:442:75//AC005484

F-NT2RM4002504//Human DNA sequence from clone 391O22 on chromosome 6p21.2-21.31 Contains pseudo-genes similar to ribosomal protein, ESTs, GSSs, complete sequence.//3.8e-31:233:87//AL031577

F-NT2RM4002527//Fugu rubripes GSS sequence, clone 096G17aC8, genomic survey sequence.//7.7e-08:274:62//AL027162

F-NT2RM4002532

F-NT2RM4002534

F-NT2RM4002558//Mus musculus fatty acid transport protein 4 mRNA, partial cds.//3.8e-53:394:81//AF072759

F-NT2RM4002565//Mus musculus Sec8 mRNA, complete cds.//6.4e-160:902:89//AF022962

F-NT2RM4002567//CITBI-E1-2503J7.TR CITBI-E1 Homo sapiens genomic clone 2503J7, genomic survey sequence.//8.5e-31:220:88//AQ263402

F-NT2RM4002571//Rattus norvegicus UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase T5 mRNA, complete cds.//5.2e-05:199:65//AF049344

F-NT2RM4002593//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//0.89:275:61//AC004875

F-NT2RM4002594//Drosophila melanogaster, chromosome 2R, region 31C1-31D6, P1 clone DS08879, complete sequence.//3.7e-44:768:64//AC005454

F-NT2RM4002623//Drosophila melanogaster; Chromosome 2L; Region 36B1-36B3; P1 clone DS02528, WORKING DRAFT SEQUENCE, 8 unordered pieces.//7.8e-34:574:65//AC005122

F-NT2RP1000018//Homo sapiens mRNA for NIK, partial cds.//3.9e-111:582:95//AB013385

F-NT2RP1000035//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//1.1e-153:747:96//AJ012449

F-NT2RP1000040//Homo sapiens genomic DNA, chromosome 21q11.1, segment 18/28, WORKING DRAFT SEQUENCE.//1.6e-125:243:88//AP000047

F-NT2RP1000063//Caenorhabditis elegans cosmid F31C3, complete sequence.//9.6e-09:414:59//Z92784

F-NT2RP1000086//H.sapiens mRNA for zinc finger protein, Hsa12.//2.8e-183:548:91//X98834

F-NT2RP1000101//H.sapiens CpG island DNA genomic MseI fragment, clone 28b4, forward read cpg28b4.ft1a.//6.0e-27:163:95//Z60555

F-NT2RP1000111//CIT-HSP-2307O14.TR CIT-HSP Homo sapiens genomic clone 2307O14, genomic survey sequence.//1.2e-11:128:81//AQ016069

F-NT2RP1000112//Human kinase (TTK) mRNA, complete cds.//1.0e-38:324:81//M86699

F-NT2RP1000124//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE.//0.59:476:59//AL034557

F-NT2RP1000130//DNA encoding human Hepatoma-derived Growth Factor.//2.7e-35:535:681//F08546

F-NT2RP1000170//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//

1.9e-20:431:64//AC006030

F-NT2RP1000174//Homo sapiens clone 24432 mRNA sequence//2.5e-138:679:97//AF070535

F-NT2RP1000191

F-NT2RP1000202//Porcine mRNA for M130 of smooth muscle myosin phosphatase, partial cds.//5.3e-05:220:61//D89496

F-NT2RP1000243//Drosophila melanogaster DNA sequence (P1 DS05273 (D80)), complete sequence//4.7e-51:508:69//AC004373

F-NT2RP1000259

F-NT2RP1000272//Mus musculus TLS-associated protein with SR repeats mRNA, complete cds//7.8e-142:866:88//AF042383

F-NT2RP1000324//RPC11-81O21.TJ RPC11 Homo sapiens genomic clone R-81O21, genomic survey sequence//2.8e-29:182:92//AQ285136

F-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds//4.2e-147:693:98//AF053551

F-NT2RP1000333//Caenorhabditis elegans cosmid C03D6, complete sequence//1.4e-08:281:61//Z75525

F-NT2RP1000348//H.sapiens CpG island DNA genomic MseI fragment, clone 12f1, reverse read cpg12f1.rt1c.//1.7e-09:71:100//Z56610

F-NT2RP1000357

F-NT2RP1000358 5.7e-16:403:61//AC005456

F-NT2RP1000363//Homo sapiens mRNA for KIAA0638 protein, partial cds.//9.8e-125:497:86//AB014538

F-NT2RP1000376//Homo sapiens calcium-independent phospholipase A2 mRNA, complete cds//1.8e-176:877:96//AF064594

F-NT2RP1000409//Homo sapiens repetitive sequences, alphoid DNA, 2482bp.//4.6e-106:700:84//AJ001558

F-NT2RP1000413//Homo sapiens mRNA for KIAA0587 protein, complete cds.//9.4e-178:710:98//AB011159

F-NT2RP1000416

F-NT2RP1000418//Oryctolagus cuniculus troponin T cardiac isoform mRNA, 3' end of cds//1.0:198:60//L40178

F-NT2RP1000439//HS_2182_A1_D06_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=11 Row=G, genomic survey sequence//2.1e-68:441:87//AQ024305

F-NT2RP1000443//Homo sapiens genomic DNA, chromosome 21q11.1, segment 18/28, WORKING DRAFT SEQUENCE//3.8e-57:185:88//AP000047

F-NT2RP1000460//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence//2.7e-132:204:99//AC004453

F-NT2RP1000470//Human DNA from chromosome 19-specific cosmid R27090, genomic sequence, complete sequence//4.9e-80:196:95//AC002985

F-NT2RP1000478//Human beta-tubulin class III isotype (beta-3) mRNA, complete cds//1.9e-55:440:80//U47634

F-NT2RP1000481//Homo sapiens DNA sequence from PAC 262D12 on chromosome 1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neuronectin, Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30S ribosomal protein S14-LIKE gene preceded by a CpG island. Contains ESTs, genomic marker D1S2691 and STSs.//2.6e-92:562:88//Z99297

F-NT2RP1000493//Homo sapiens mRNA for KIAA0017 protein, complete cds.//2.0e-130:622:98//D87686

F-NT2RP1000513//Xanthomonas campestris campestris xpsD, xpsM, and xpsN genes, complete cds's//0.11:360:58//M81648

F-NT2RP1000522//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces//4.9e-34:209:93//AC004895

F-NT2RP1000547//Cricetulus griseus COP-coated vesicle membrane protein CHOp24 mRNA, partial cds.//1.2e-08:331:63//U26264

F-NT2RP1000574//Homo sapiens homeobox protein MEIS2 (MEIS2) mRNA, partial cds.//4.4e-81:295:92//AF017418

F-NT2RP1000577//HS_2228_B2_C05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=10 Row=F, genomic survey sequence//1.9e-31:179:75//AQ185128

F-NT2RP1000581//Pan troglodytes von Willebrand factor (vWF) gene, partial cds.//4.7e-34:223:90//U31620

F-NT2RP1000609//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence//1.6e-18:229:65//AC004770

F-NT2RP1000629//Mouse clathrin-associated protein (AP47) mRNA, complete cds.//9.3e-89:584:84//M62419

F-NT2RP1000630//Human DNA sequence from PAC 151B14 on chromosome 22 Contains EST complete sequence//1.2e-09:100:100//AF005940

F-NT2RP1000631//Homo sapiens clone 24432 mRNA sequence//2.5e-138:679:97//AF070535

F-NT2RP1000688//H.sapiens gene for mitochondrial ATP synthase c subunit (P1 form)//5.2e-10:120:80//X69907
F-NT2RP1000695

F-NT2RP1000701//Sequence 1 from patent US 5580968//2.4e-99:624:86//I30536

F-NT2RP1000721//Homo sapiens clone DJ0943F02, WORKING DRAFT SEQUENCE, 3 unordered pieces//1.1e-19:188:81//AC004932

F-NT2RP1000730

F-NT2RP1000733//Human chromosome 16p13-1 BAC clone CIT987SK-551G9 complete sequence//1.3e-30:315:75//U95742

F-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete cds//8.0e-122:604:96//AF101434

F-NT2RP1000746//HS_3084_A1_H03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3084 Col=5 Row=O, genomic survey sequence//1.5e-83:466:92//AQ186344

F-NT2RP1000767//Homo sapiens full-length insert cDNA clone ZD81B04//2.8e-21:144:91//AF086442

F-NT2RP1000782//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds//2.1e-121:591:97//AF054840

F-NT2RP1000796//T.thermophilus phosphofructokinase 1 (PFK1) gene, complete cds//0.76:263:64//M71213

F-NT2RP1000825//Human DNA sequence from clone 116F5 on chromosome 22q13. Contains part of an unknown gene and part of a RhoGAP (CDC42 GTPase Activating Protein) LIKE gene. Contains ESTs, STSs, GSSs, genomic marker D22S1168 and a CA repeat polymorphism, complete sequence//1.5e-77:163:96//Z93244

F-NT2RP1000833//Homo sapiens cGMP-specific phosphodiesterase (PDE9A2) mRNA, complete cds//1.3e-147:424:96//AF048837

F-NT2RP1000834//Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds//1.9e-89:702:79//AF047020

F-NT2RP1000836//Homo sapiens DNA sequence from PAC 434O14 on chromosome 1q32.3.41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence//8.7e-169:842:96//AL022398

F-NT2RP1000846//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence//3.3e-15:196:76//U96629

F-NT2RP1000851//Homo sapiens PAC clone 267D11 from 12, complete sequence//1.6e-144:724:96//AC004812

F-NT2RP1000856//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds//2.1e-121:591:97//AF054840

F-NT2RP1000860//Homo sapiens KL04P mRNA, complete cds//6.7e-106:551:95//AF064094

F-NT2RP1000902//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 316D5, WORKING DRAFT SEQUENCE//0.0097:55:100//Z82199

F-NT2RP1000915//H.sapiens genomic DNA fragment (clone J32A032R)//1.3e-30:174:97//Z94761

F-NT2RP1000916

F-NT2RP1000943//Hylobates lar huntingtin gene, partial exon//0.19:103:72//L49362

F-NT2RP1000944//HS_2179_B2_C12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2179 Col=24 Row=F, genomic survey sequence//0.032:140:63//AQ065269

F-NT2RP1000947//Mus musculus ubiquitin conjugating enzyme (ubc4) mRNA, complete cds//3.7e-53:461:78//U62483

F-NT2RP1000954//cSRL-143G4-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-143G4, genomic survey sequence//0.030:89:78//B01950

F-NT2RP1000958//Caenorhabditis elegans cosmid K01C8, complete sequence//3.9e-11:445:61//Z49068

F-NT2RP1000959//Homo sapiens PAC clone 278C19 from 12q, complete sequence//3.3e-57:326:92//AC004263

F-NT2RP1000966//Human nucleolin gene, complete cds//3.4e-64:197:981//M60858

F-NT2RP1000980//CIT-HSP-2314B10.TF CIT-HSP Homo sapiens genomic clone 2314B10, genomic survey sequence//0.32:137:68//AQ017126

F-NT2RP1000988//Human chromosome 3p21.1 gene sequence//8.0e-72:665:80//L13435

F-NT2RP1001011//Drosophila melanogaster DNA repair protein (mei-41) gene, complete cds, and TH1 gene, partial cds//1.3e-31:497:65//U34925

F-NT2RP1001013//HS_3068_B1_809_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3068 Col=17 Row=D, genomic survey sequence//1.0e-24:414:66//AQ127667

F-NT2RP1001014//HS_3252_B1_B05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=5 Row=E, genomic survey sequence//1.1e-24:414:66//AQ127667

F-NT2RP1001033//Homo sapiens chromosome 10p15.1 BAC clone CIT987SK-2A8 complete sequence//3.3e-15:196:76//U96629

F-NT2RP1001073//Homo sapiens PAC clone DJ1194E14 from 7p21, complete sequence.//2.5e-59:451:83//AC004993

F-NT2RP1001079//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//4.5e-93:476:96//U82267

5 F-NT2RP1001080//Homo sapiens clone DJ0971C03, WORKING DRAFT SEQUENCE, 18 unordered pieces.//6.6e-54:217:89//AC004938

F-NT2RP1001113

F-NT2RP1001173

F-NT2RP1001177//Rattus norvegicus histone macroH2A1.2 mRNA, complete cds.//8.1e-26:373:681/U79139

10 F-NT2RP1001185//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.5e-32:388:73//AC006039

F-NT2RP1001199

F-NT2RP1001247//Homo sapiens signaling molecule LEFTY-A gene, exon 1 //2.0e-29:166:96//AF081508

15 F-NT2RP1001248//Homo sapiens Chromosome 11q23 PAC clone pDJ356d6, complete sequence.//7.3e-50:128:99//AC002036

F-NT2RP1001253//Homo sapiens oscillin (hLn) mRNA, complete cds.//4-3e-91:344:93//AF029914

F-NT2RP1001286//Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's-//0.54:292:63//L44140

F-NT2RP1001294

20 F-NT2RP1001302

F-NT2RP1001310//Rabbit skeletal muscle mRNA for ryanodine receptor.//1.5e-07:335:64//X15750

F-NT2RP1001311//RPC11-67O14.TK RPC11 Homo sapiens genomic clone R-67O14, genomic survey sequence.//0.26:80:75//AQ239291

25 F-NT2RP1001313//Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin heavy chain (FTH), complete sequence.//8.8e-75:304:98//AC004228

F-NT2RP1001361//B.taurus Cl-B14.5b mRNA for NADH dehydrogenase (ubiquinone).//2.7e-57:412:84//X68647

F-NT2RP1001385

30 F-NT2RP1001395//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds.//1.4e-72:535:83//AF071316

F-NT2RP1001410//Homo sapiens DNA sequence from PAC 257I20 on chromosome 22q13.1-13.2. Contains cytochrome P450 pseudogenes CYP2D7P, CYP2D8P, CYP2D6(D),TCF20, NADH ubiquinone oxidoreductase B14 subunit, ESTs, CA repeat, STS, GSS.//5.8e-105:570:94//AL021878

F-NT2RP1001424

35 F-NT2RP1001432

F-NT2RP1001449//Homo sapiens clone 24733 mRNA sequence.//1.7e-84:422:97//AF052149

F-NT2RP1001457//Xenopus laevis notchless (nle) mRNA, complete cds.//1.3e-47:471:73//AF069737

F-NT2RP1001466//HS_3006_A2_D08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3006 Col=16 Row=G, genomic survey sequence.//0.56:289:60//AQ154336

40 F-NT2RP1001475//H.sapiens genomic DNA fragment (clone NLMA194R).//0.00011:91:79//Z95375

F-NT2RP1001482//Mouse oncogene (ect2) mRNA, complete cds.1/4-0e-87:563:85//L11316

F-NT2RP1001494

F-NT2RP10015431/Drosophila melanogaster DNA sequence (P1 DS01142 (D148)), complete sequence.//1.9e-27:387:67//AC004280

45 F-NT2RP1001546//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds.//8.0e-63:314:98//AF054840

F-NT2RP1001569//Mus musculus signal recognition particle receptor beta subunit mRNA, complete cds.//1.2e-68:514:81//U17343

F-NT2RP100T616//Human clone 23665 mRNA sequence.//7.6e-40:496:74//U90913

50 F-NT2RP1001665//CIT-HSP-2059N5.TF CIT-HSP Homo sapiens genomic clone 2059N5, genomic survey sequence.//2.4e-45:305:88//B69912

F-NT2RP2000001//Homo sapiens clone 617 unknown mRNA, complete sequence.//1.5e-135:685:96//AF091081

F-NT2RP2000006//HS_3061_B2_C03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3061 Col=6 Row=F, genomic survey sequence.//1.9e-17:394:67//AQ178856

55 F-NT2RP2000007//Human mRNA for KIAA0392 gene, partial cds //3.5e-14:241:68//AB002390

DRAFT SEQUENCE: F-NT2RP1001997//AF034423

F-NT2RP2000027//Homo sapiens BAC clone RG118P15 from 8q21, complete sequence.//1.4e-32:345:75/

AC005066

F-NT2RP2000032//F.rubripes GSS sequence, clone 060E22aG10, genomic survey sequence.//5.0e-41:445:72//Z88655

F-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds.//1.9e-76:383:97//AB018290

F-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//2.4e-95:467:97//AF061749

F-NT2RP2000054//CIT-HSP-2328J24.TF CIT-HSP Homo sapiens genomic clone 2328J24, genomic survey sequence.//3.3e-39:236:91//AQ043092

F-NT2RP2000056//Rat mRNA for protein tyrosine phosphatase epsilon C, partial cds.//3.2e-50:311:90//D78610

F-NT2RP2000067//Mus musculus DOC4 (Doc4) mRNA, complete cds.//3.0e-55:766:66//AF059485

F-NT2RP2000070//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//2.0e-118:597:95//AC005754

F-NT2RP2000076//Homo sapiens clone NH0263G22, complete sequence.//0.0017:423:60//AC006037

F-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds.//2.1e-77:278:97//AF050079

F-NT2RP2000079//H.sapiens CpG island DNA genomic Mse1 fragment, clone 40c2, forward read cpg40c2.ft1k.//3.2e-33:197:95//Z55440

F-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds.//2.2e-158:752:98//AB018338

F-NT2RP2000091//HS_2228_A2_B02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=4 Row=C, genomic survey sequence.//0.26:55:90//AQ146363

F-NT2RP2000097

F-NT2RP2000098//Homo sapiens clone DJ1098J04, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.5e-05:482:60//AC004961

F-NT2RP2000108//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//1.0e-22:274:69//AC003973

F-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds.//4.9e-114:551:97//AB018356

F-NT2RP2000120//HS_3000_B1_E03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3000 Col=5 Row=J, genomic survey sequence.//1.8e-21:129:97//AQ090365

F-NT2RP2000126//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds.//4.2e-119:607:96//AF054177

F-NT2RP2000133//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.//1.3e-07:339:63//AC004827

F-NT2RP2000147//Mouse clathrin-associated protein (AP47) mRNA, complete cds.//9.0e-101:638:85//M62419

F-NT2RP2000153//Human DNA sequence from clone 218J18 on chromosome Xp11.3-11.4. Contains the NDP (Norrie Disease (Pseudoglioma)) gene and a CC1.3 Splicing Factor pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.45:377:58//AL034370

F-NT2RP2000157//Homo sapiens Chr.14 PAC RPCI4-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//4.0e-73:317:87//AC005924

F-NT2RP2000161//CIT-HSP-2353L5.TF.1 CIT-HSP Homo sapiens genomic clone 2353L5, genomic survey sequence.//3.0e-14:123:90//AQ263431

F-NT2RP2000173

F-NT2RP2000175

F-NT2RP2000183//F.rubripes GSS sequence, clone 168M02aC2, genomic survey sequence.//3.7e-06:152:66//AL007295

F-NT2RP2000195//Human DNA sequence from clone 45I4 on chromosome 6q24.1-24.3. Contains two putative unknown genes, ESTs, STSs and GSSs, complete sequence.//7.6e-62:170:99//AL023581

F-NT2RP2000205

F-NT2RP2000208//Homo sapiens chromosome 19, overlapping cosmids R29828 and F25496, complete sequence.//7.2e-80:170:90//AC003030

F-NT2RP2000224//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence.//5.5e-64:400:85//AC004382

F-NT2RP2000232//Human DNA sequence from PAC 196E23 on chromosome Xq26.1-27.2. Contains the TAT-SF1 (HIV-1 transcriptional elongation factor TAT cofactor TAT-SF1) gene, the BRS3 (Bombesin Receptor subtype-3 (Uterine Bombesin Receptor, BRS-3) gene, an unknown gene coding for two isoforms, a predicted CpG island, ESTs and STSs.//2.2e-07:280:66//Z97632

508 67 0884

F-NT2RP2000239//Homo sapiens chromosome 4 clone B353C18 map 4q25, complete sequence.//4.0e-79:504

87//AC004066

F-NT2RP2000248

F-NT2RP2000257//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y1E3, WORKING DRAFT SEQUENCE //0.0078:286:60//AL021388

5 F-NT2RP2000258//CIT-HSP-2349P21.TF CIT-HSP Homo sapiens genomic clone 2349P21, genomic survey sequence //5.7e-82:416:97//AQ059184

F-NT2RP2000270//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence //4.5e-29:310:73//AC006116

F-NT2RP2000274

10 F-NT2RP2000283//G.gallus mRNA for LRP/alpha-2-macroglobulin receptor //6.3e-20:260:73//X74904

F-NT2RP2000288

F-NT2RP2000289

F-NT2RP2000297//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9 //4.6e-69:744:70//M27877

15 F-NT2RP2000298//Streptomyces coelicolor cosmid 2E9 //4.4e-05:502:59//AL021530

F-NT2RP2000310//WORKING DRAFT SEQUENCE, 6 unordered pieces //2.1e-13:173:76//AC006082

F-NT2RP2000327//Homo sapiens DNA sequence from PAC 434O14 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence //8.3e-144:731:95//AL022398

20 F-NT2RP2000328//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs, complete sequence //1.9e-102:555:90//AL034430

F-NT2RP2000329//Bovine mitochondrial GTP:AMP phosphotransferase mRNA, complete cds //6 4e-105:639:87//M25757

25 F-NT2RP2000337//HS_2060_B1_E01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2060 Col=1 Row=J, genomic survey sequence //0.78:218:60//AQ243333

F-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds //3.6e-129:627:97//U83981

30 F-NT2RP2000369//HS_2182_B1_B11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=21 Row=D, genomic survey sequence //2.5e-87:421:99//AQ024835

F-NT2RP2000412//Human DNA sequence from PAC 124O9 on chromosome 6q21. Contains DNAJ2 (HDJ1) like pseudogene, ESTs, STSs and GSSs //0.72:170:65//AL021327

F-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds //5.0e-66:375:93//L28010

F-NT2RP2000420//Homo sapiens full-length insert cDNA YQ86E07 //9.2e-77:423:93//AF075093

35 F-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds //2.1e-126:609:96//AF102265

F-NT2RP2000438//CITBI-E1-2519O19.TR CITBI-E1 Homo sapiens genomic clone 2519O19, genomic survey sequence //0.96:61:78//AQ276878

40 F-NT2RP2000448//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence //7.1e-17:341:67//AC004691

F-NT2RP2000459//H.sapiens mRNA for imogen 38 //5.7e-21:158:87//Z68747

F-NT2RP2000498//Human DNA sequence from PAC 435C23 on chromosome X. Contains ESTs //3.2e-11:160:73//Z92844

F-NT2RP2000503//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete sequence //0.0031:187:66//AC005229

45 F-NT2RP2000510//Fugu rubripes GSS sequence, clone 066G04aC1, genomic survey sequence //8.8e-07:179:64//AL026277

F-NT2RP2000516//Mus musculus t complex testis-specific protein (Tctex2) gene, wild type, promoter sequence //0.19:72:81//U21671

50 F-NT2RP2000523//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 150C2, WORKING DRAFT SEQUENCE //5.0e-115:570:96//AL022318

F-NT2RP2000603//Homo sapiens mRNA for MCM3 import factor, complete cds //8.4e-37:196:98//AB005543

F-NT2RP2000617//Homo sapiens chromosome 19, cosmid R27377, complete sequence //0.81:354:60//AC005321

55 F-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein partial cds //1 3e-149:732:97//AB014514

F-NT2RP2000644//Homo sapiens DNA sequence from PAC 435C23 on chromosome X. Contains ESTs, STSs and GSSs //0.72:170:65//AL021327
 F-NT2RP2000656//Homo sapiens DNA sequence from PAC 435C23 on chromosome X. Contains ESTs, STSs and GSSs //0.72:170:65//AL021327

F-NT2RP2000658//CITBI-E1-2518N15.TF CITBI-E1 Homo sapiens genomic clone 2518N15, genomic survey sequence.//0.57:141:66//AQ278386

F-NT2RP2000668

F-NT2RP2000678//Homo sapiens clone DJ0891L14, WORKING DRAFT SEQUENCE, 12 unordered pieces.//4.3e-22:433:62//AC004916

F-NT2RP2000704//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library) complete sequence.//2.7e-22:270:75//AC005913

F-NT2RP2000710//Drosophila melanogaster; Chromosome 2L; Region 36B1-36B3; P1 clone DS02528, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.4e-32:574:64//AC005122

F-NT2RP2000715//Homo sapiens PAC clone DJ1066K24 from 7p15, complete sequence.//4.8e-113:546:98//AC004540

F-NT2RP2000731//Homo sapiens clone DJ1106H14, WORKING DRAFT SEQUENCE, 42 unordered pieces.//0.97:115:70//AC004965

F-NT2RP2000758//Human LIM-kinase1 and alternatively spliced LIM-kinase1 (LIMK1) gene, complete cds.//9.7e-16:162:77//U62293

F-NT2RP2000764//HS_2254_B2_D07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2254 Col=14 Row=H, genomic survey sequence.//0.071:45:95//AQ068887

F-NT2RP2000809

F-NT2RP2000812//Egernia stokesii clone EST3 microsatellite.//0.040:158:64//AF069698

F-NT2RP2000814

F-NT2RP2000816

F-NT2RP2000819

F-NT2RP2000841//Human mRNA for KIAA0294 gene, complete cds.//1.1e-26:390:70//AB002292

F-NT2RP2000842//H.sapiens mRNA for G protein-coupled receptor Edg-2.//1.2e-44:255:93//Y09479

F-NT2RP2000845

F-NT2RP2000863//Human partial cDNA sequence, clone x874.//5.9e-29:173:94//Z47045

F-NT2RP2000880//Homo sapiens mRNA for KIAA0741 protein, complete cds.//2.4e-140:732:94//AB018284

F-NT2RP2000892

F-NT2RP2000931//Homo sapiens mRNA for KIAA0723 protein, complete cds.//3.4e-129:610:98//AB018266

F-NT2RP2000932//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//1.8e-37:212:84//AC005014

F-NT2RP2000938//Human DNA sequence from cosmid RJ14 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs and CpG island.//1.6e-126:682:93//Z69890

F-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds.//5.8e-112:533:98//AB018298

F-NT2RP2000965

F-NT2RP2000970//Homo sapiens DNA sequence from BAC 747E2 on chromosome 22q12.1. Contains ESTs, STSs and GSSs and genomic marker D22S56, complete sequence.//9.2e-101:505:96//AL021393

F-NT2RP2000985//Homo sapiens chromosome 17, clone hRPK.597_M_12, complete sequence.//1.6e-72:498:82//AC005277

F-NT2RP2000987//Human Chromosome 16 BAC clone CIT987SK-A-211C6, complete sequence.//7.4e-12:171:77//AC002394

F-NT2RP2001036//Homo sapiens chromosome 17, clone HRPC1096F1, complete sequence.//1.2e-37:390:76//AC004167

F-NT2RP2001044//HS_2253_B1_G01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2253 Col=1 Row=N, genomic survey sequence.//0.21:276:61//AQ069224

F-NT2RP2001056//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488.//3.2e-144:696:97//AB007957

F-NT2RP2001065

F-NT2RP2001070//Rattus norvegicus pyridoxine 5'-phosphate oxidase mRNA, complete cds.//4.3e-104:775:81//U91561

F-NT2RP2001081//Rattus norvegicus synaptotagmin XI mRNA, complete cds.//3.7e-69:488:82//AF000423

F-NT2RP2001094//Human DNA sequence from PAC 410B11 on chromosome X contains STS.//7.4e-11:490:61//Z86063

F-NT2RP2001119//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 745C22, WORKING DRAFT SEQUENCE.//5.1e-30:316:76//AL031596

F-NT2RP2001141//HS_2253_B1_G01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2253 Col=1 Row=N, genomic survey sequence.//0.21:276:61//AQ069224

F-NT2RP2001142//HS_2253_B1_G01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2193 Col=24 Row=H, genomic survey sequence.//1.8e-11:136:78//AQ032187

F-NT2RP2001149//Homo sapiens Chromosome 22q11.2 Cosmid Clone 2h In DGCR Region, complete sequence.//6.2e-29:247:78//AC000076

F-NT2RP2001168//Human DNA sequence from clone 431P23 on chromosome 6q27. Contains the first coding exon of the MLLT4 gene for myeloid/lymphoid or mixed-lineage leukemia (trithorax (*Drosophila*) homolog); translocated to, 4 (AF-6, Afadin, MLLT-4, ALL-1 fusion partner), and a Serine Palmitoyltransferase 2 (EC 2.3.1.50, Long Chain Base Biosynthesis protein 2, LCB-2, SPT-2) pseudogene. Contains ESTs, STss, GSSs, and a putative CpG island, complete sequence.//0.23:207:66//AL009178

F-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds.//2.3e-112:567:96//AB007949

F-NT2RP2001174//RPC111-58L2.TK RPC111 Homo sapiens genomic clone R-58L2, genomic survey sequence.//7.6e-07:196:64//AQ237306

F-NT2RP2001196

F-NT2RP2001218

F-NT2RP2001226//Homo sapiens LERK-6 (EPLG6) gene, exon 1.//1.1e-09:320:65//U92893

F-NT2RP2001233//Human ZFP-36 mRNA for a zinc finger protein.//6.1e-71:681:72//X51760

F-NT2RP2001245//HS_3062_B1_F07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3062 Col=13 Row=L, genomic survey sequence.//1.5e-05:268:63//AQ143177

F-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds.//2.5e-106:514:97//AB018353

F-NT2RP2001277//Plasmodium falciparum chromosome 2, section 67 of 73 of the complete sequence.//0.32:183:64//AE001430

F-NT2RP2001290//M.musculus mRNA for l47 clone.//8.6e-102:641:86//X61455

F-NT2RP2001295//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y105E8, WORKING DRAFT SEQUENCE.//0.20:171:63//AL022594

F-NT2RP2001312//Bovine synaptophysin mRNA, complete cds.//0.98:253:58//M22967

F-NT2RP2001327//Human B12 protein mRNA, complete cds.//5.8e-29:359:71//M80783

F-NT2RP2001328//CIT-HSP-2335A5.TF CIT-HSP Homo sapiens genomic clone 2335A5, genomic survey sequence.//1.3e-65:366:94//AQ038539

F-NT2RP2001347//Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease.//3.8e-31:325:77//AJ003147

F-NT2RP2001366//H.sapiens CpG island DNA genomic MseI fragment, clone 4e11, forward read cpg4e11.f1a.//1.7e-12:98:92//Z61305

F-NT2RP2001378//HS_3054_B2_A03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=6 Row=B, genomic survey sequence.//9.8e-17:131:89//AQ100721

F-NT2RP2001381//Arabidopsis thaliana BAC T2L5.//0.080:434:59//AF096371

F-NT2RP2001392//S.pristinaespiralis snbC gene & snbDE gene.//0.019:267:59//Y11548

F-NT2RP2001394//Human DNA sequence from PAC 389A20 on chromosome X contains ESTs STS, CpG islands and polymorphic CA repeat.//1.9e-16:133:78//Z93242

F-NT2RP2001397//Bos taurus cyclin B2 (CYCB2) mRNA, complete cds.//1.3e-63:419:84//AF080219

F-NT2RP2001420//Mus musculus nuclear protein NIP45 mRNA, complete cds.//3.1e-98:747:79//U76759

F-NT2RP2001423//Xenopus laevis ER1 mRNA, complete cds.//3.7e-34:269:85//AF015454

F-NT2RP2001427//Homo sapiens Chromosome 2p13 BAC Clone h173, complete sequence.//3.2e-13:164:78//AC003065

F-NT2RP2001436//Mus musculus clone OST1784, genomic survey sequence.//3.0e-06:136:71//AF046702

F-NT2RP2001440//cDNA sequence coding for gamma protein.//7.9e-83:553:86//E02350

F-NT2RP2001445//P.falciparum complete gene map of plastid-like DNA (IR-A).//1.5e-09:829:57//X95275

F-NT2RP2001449//B.taurus mRNA for cleavage and polyadenylation specificity factor.//1.3e-136:766:90//X75931

F-NT2RP2001450

F-NT2RP2001467

F-NT2RP2001506//CIT-HSP-2374H21.TF CIT-HSP Homo sapiens genomic clone 2374H21, genomic survey sequence.//7.9e-14:151:80//AQ109561

F-NT2RP2001511//Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds.//2.6e-22:462:64//AF005355

F-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1.//2.0e-136:657:97//Y14494

F-NT2RP2001526//Homo sapiens chromosome 17, clone hCIT.175_E_5, complete sequence.//1.2e-37:357:64//AC004596

F-NT2RP2001536//Homo sapiens X ray repair cross complementing protein 3 (XRCC3) mRNA, complete cds.//

F-NT2RP2001566

F-NT2RP2001569//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488.//4.4e-123:590:98//

AB007957

F-NT2RP2001576//Schistocerca americana Antennapedia homeotic protein (Antp) mRNA, complete cds//0.038:580:58//U32943

F-NT2RP2001581//Mus musculus semaphorin VIa mRNA, complete cds//6.5e-09:222:66//AF030430

5 F-NT2RP2001597//Homo sapiens alpha2-C4-adrenergic receptor gene, complete cds//0.0057:361:60//U72648

F-NT2RP2001601//Homo sapiens mRNA for KIAA0797 protein, partial cds//7.2e-137:647:98//AB018340

F-NT2RP2001613

F-NT2RP2001628//H.sapiens (xs128) mRNA, 380bp//1.7e-15:279:68//Z36784

10 F-NT2RP2001634//Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA, complete cds//5.4e-123:606:96//AF030233

F-NT2RP2001660//Homo sapiens putative 13 S Golgi transport complex 90kD subunit brain-specific isoform mRNA, complete cds//4.2e-144:687:97//AF058718

F-NT2RP2001663//H.sapiens mRNA for 2-phosphopyruvate-hydratase-alpha-enolase//1.0e-36:372:74//X84907

F-NT2RP2001675//S.pombe chromosome I cosmid c2G11//0.070:507:59//Z54354

15 F-NT2RP2001677//Mouse BAC CitbCJ7 219m7, genomic sequence, complete sequence//2.0e-60:232:96//AC005259

F-NT2RP2001678//HS_2007_A2_A04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2007 Col=8 Row=A, genomic survey sequence//7.3e-62:370:91//AQ269699

20 F-NT2RP2001699//RPCI11-57B17.TK RPCI11 Homo sapiens genomic clone R-57B17, genomic survey sequence//0.99:141:63//AQ115592

F-NT2RP2001720//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence//9.4e-117:604:95//AC004079

25 F-NT2RP2001721//Homo sapiens DNA sequence from clone 46618 on chromosome Xq11.1-13.2. Contains an unknown gene similar to Coagulation Factor V (Activated Protein C Cofactor), Coagulation Factor VIII (Procoagulant Component) and Ceruloplasmin (EC 1.16.3.1, Ferroxidase). Contains ESTs and an STS, complete sequence//1.0:273:61//AL030998

F-NT2RP2001740//Homo sapiens Chromosome 22q11.2 Cosmid Clone 8c In DGCR Region, complete sequence//1.0:356:62//AC000090

F-NT2RP2001748//Human mRNA for KIAA0003 gene, complete cds//3.7e-18:151:86//D14697

30 F-NT2RP2001762//Homo sapiens chromosome 1, BAC CIT-HSP-292g8 (BC262482), complete sequence//6.0e-145:715:97//AC004783

F-NT2RP2001813//Plasmodium falciparum chromosome 2, section 15 of 73 of the complete sequence//0.38:340:60//AE001378

35 F-NT2RP2001839//HS_3000_B1_C07_MR CIT Approved Human Genomic Sperm Library D_ Homo sapiens genomic clone Plate=3000 Col=13 Row=F, genomic survey sequence//0.026:253:60//AQ090347

F-NT2RP2001861//Homo sapiens mRNA for paraplegin//0.89:146:71//Y16610

F-NT2RP2001869//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds//0.040:174:62//AF027219

F-NT2RP2001876//Cyprinus carpio mRNA for allograft inflammatory factor-1, complete cds//2.8e-44:483:71//AB012309

40 F-NT2RP2001883//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence//1.8e-87:496:92//AL031864

F-NT2RP2001898//Human inositol polyphosphate 5-phosphatase (5ptase) mRNA, 3' end//9.2e-112:633:90//M74161

45 F-NT2RP2001900//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone R08A5, WORKING DRAFT SEQUENCE//0.0026:360:62//Z82281

F-NT2RP2001907//H.sapiens CpG island DNA genomic Mse1 fragment, clone 97f11, forward read cpg97f11.ft1a//4.2e-26:206:84//Z64125

50 F-NT2RP2001926//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces//5.5e-06:621:59//AC004688

F-NT2RP2001936//cSRL-47D9-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-47D9, genomic survey sequence//3.1e-50:282:93//B04856

F-NT2RP2001943//Drosophila melanogaster cosmid 25E8//0.00036:248:60//AL009196

F-NT2RP2001946//Homo sapiens clone NH0140K04, complete sequence//3.8e-78:232:99//AC005033

55 F-NT2RP2001947//Homo sapiens full-length insert cDNA clone ZD81B04 //2.0e-28:172:94//AF086442

1015248 111a 112a 113a 114a 115a 116a 117a 118a 119a 120a

NT2RP2001976

F-NT2RP2001985//Homo sapiens mRNA for KIAA0545 protein, partial cds.//0.0023:235:62//AB011117
 F-NT2RP2001991//Rat orphan transporter v7-3 (NTT73) mRNA, complete cds.//3.1e-35:180:80//L22022
 F-NT2RP2002025//Homo sapiens mRNA for KIAA0756 protein, partial cds.//9.8e-61:314:97//AB018299
 F-NT2RP2002032//Homo sapiens chromosome 5, Bac clone 5m9 (LBNL H220), complete sequence//0.76:189:
 5 65//AC005895
 F-NT2RP2002033//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.9e-
 12:160:79//AC004825
 F-NT2RP2002041//Human BAC clone RG035E18 from 7q31, complete sequence.//0.0014:123:73//AC004029
 F-NT2RP2002046//Homo sapiens Xp22 BAC GSHB-184P14 (Genome Systems Human BAC library) complete
 10 sequence.//2.2e-86:722:77//AC004552
 F-NT2RP2002047//Human DNA sequence from clone 21F7 on chromosome 6q16.1-21. Contains part of an exon
 of a putative new gene and STSs and GSSs, complete sequence.//0.13:350:61//AL033375
 F-NT2RP2002058//S.cerevisiae chromosome XII reading frame ORF YLR129w.//9.7e-11:480:60//Z73301
 F-NT2RP2002066//Rattus norvegicus transmembrane receptor Unc5H2 mRNA, complete cds.//6.5e-97:610:86//
 15 U87306
 F-NT2RP2002070//beta -ADD=adducin beta subunit 63 kda isoform/membrane skeleton protein, beta -ADD=add-
 ducin beta subunit 63 kda isoform/membrane skeleton protein [alternatively spliced, exon 10 to 13 region] [human,
 Genomic, 1851 nt, segment 3 of 3].//0.0059:107:73//S81083
 F-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence.//1.0e-127:643:96//AF052183
 20 F-NT2RP2002078//F12O16-T7.1 IGF Arabidopsis thaliana genomic clone F12016, genomic survey sequence.//
 0.14:191:64//AQ249805
 F-NT2RP2002079//Homo sapiens clone DJ0892G19, complete sequence.//0.0094:325:60//AC004917
 F-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein.//9.8e-111:533:97//AJ007509
 F-NT2RP2002105//H.sapiens CpG island DNA genomic MseI fragment, clone 10h8, forward read cpg10h8.ft1a.//
 25 2.4e-29:178:94//Z58857
 F-NT2RP2002124//CIT-HSP-2023E9.TF CIT-HSP Homo sapiens genomic clone 2023E9, genomic survey se-
 quence.//2.5e-32:202:92//B64468
 F-NT2RP2002137//Human plasma membrane calcium ATPase (hPMCA4) mRNA, complete cds.//0.095:319:59//
 M25874
 30 F-NT2RP2002154//Mus musculus mRNA for myosin, complete cds.//1.0:258:63//D85923
 F-NT2RP2002172//HS_3020_B1_H02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3020 Col=3 Row=P, genomic survey sequence.//1.2e-11:124:82//AQ093169
 F-NT2RP2002185//RPCI11-67B15.TJ RPCI11 Homo sapiens genomic clone R-67B15, genomic survey se-
 quence.//2.8e-18:109:100//AQ201833
 35 F-NT2RP2002192//Human PM-Scl-75 autoantigen (PM-scl1) mRNA, complete cds.//2.7e-36:363:78//U09215
 F-NT2RP2002193//Rattus norvegicus potassium channel regulatory protein KChAP mRNA, complete cds.//9.5e-
 82:477:89//AF032872
 F-NT2RP2002208
 F-NT2RP2002219//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING
 40 DRAFT SEQUENCE.//1.0:378:58//AL034557
 F-NT2RP2002231//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING
 DRAFT SEQUENCE, 5 unordered pieces.//0.60:560:56//AC005308
 F-NT2RP2002235//P.falciparum glutamic acid-rich protein gnen, complete cds.//0.59:341:60//J03998
 F-NT2RP2002252//Mus musculus mSin3A (sin3A) mRNA, complete cds.//3.5e-81:398:87//U22394
 45 F-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds.//6.6e-50:315:89//AF005418
 F-NT2RP2002259//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 118J21, WORKING
 DRAFT SEQUENCE.//9.7e-67:340:89//AL033527
 F-NT2RP2002270//RPCI11-77C23.TV RPCI11 Homo sapiens genomic clone R-77C23, genomic survey se-
 quence.//2.9e-18:79:93//AQ268098
 50 F-NT2RP2002292//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 321D2, WORKING
 DRAFT SEQUENCE.//1.0:290:60//AL031033
 F-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds.//1.5e-93:467:96//
 AF069532
 F-NT2RP2002316//HS_2171_B2_D11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 55 nomic clone Plate=2171 Col=22 Row=H, genomic survey sequence.//7.3e-94:463:97//AQ119673
 F-NT2RP2002325//Homo sapiens CYP11B1 mRNA, complete cds.//1.0e-100:100:100//U00000
 F-NT2RP2002330//Homo sapiens CYP11B1 mRNA, complete cds.//1.0e-100:100:100//U00000
 F-NT2RP2002373//Homo sapiens CYP11B1 mRNA, complete cds.//1.0e-100:100:100//U00000

Z87330

F-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds.//9.4e-138:673:97//AF038958

F-NT2RP2002394//P.falciparum complete gene map of plastid-like DNA (IR-A).//0.79:421:56//X95275

F-NT2RP2002408//F.rubripes GSS sequence, clone 080G11aA8, genomic survey sequence.//5.7e-15:220:71//AL015615

F-NT2RP2002426//Sus scrofa SCAMP1 gene, exon 9//7.1e-71:582:80//AJ223742

F-NT2RP2002439//Caenorhabditis elegans cosmid T07D3.//0.0018:210:67//AF016682

F-NT2RP2002442//Caenorhabditis elegans cosmid T03F1.//2.8e-18:295:67//U88169

F-NT2RP2002457//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence.//1.9e-06:281:66//AC004381

F-NT2RP2002464//Human mRNA for KIAA0086 gene, complete cds.//0.039:207:63//D42045

F-NT2RP2002475

F-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds.//2.4e-123:607:96//AB005289

F-NT2RP2002498//Arabidopsis thaliana BAC F3D13.//0.73:395:57//AF069300

F-NT2RP2002503//Homo sapiens, clone hRPK.15_A_1, complete sequence.//7.2e-18:134:90//AC006213

F-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds.//1.2e-157:761:97//AB018334

F-NT2RP2002520

F-NT2RP2002537

F-NT2RP2002546//Homo sapiens Chromosome 11q12 pac pDJ741n15, WORKING DRAFT SEQUENCE, 7 un-ordered pieces.//0.83:252:60//AC004127

F-NT2RP2002549//Human Chromosome 15q26.1 PAC clone pDJ457j11 containing DNA polymerase gamma (polg) gene, complete sequence.//5.9e-93:186:99//AC005317

F-NT2RP2002591//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 54B20, WORKING DRAFT SEQUENCE.//4.0e-38:175:78//Z98304

F-NT2RP2002595//Sequence 2 from patent US 5763220.//1.5e-84:430:95//AR012155

F-NT2RP2002606//Rattus norvegicus Rabin3 mRNA, complete cds.//1.9e-43:282:87//U19181

F-NT2RP2002609//Mus musculus defender against death 1 (DAD1) gene, partial cds.//1.5e-11:99:90//AF051310

F-NT2RP2002618//H.sapiens mRNA for arginine methyltransferase, splice variant, 1316 bp.//5.6e-27:460:63//Y10806

F-NT2RP2002621

F-NT2RP2002643//Rat calmodulin III gene for calmodulin, promoter region and exon 1.//0.023:322:60//D90397

F-NT2RP2002672//Homo sapiens chromosome 10 clone CIT-HSP-1326H7 map 10q24.3-10q25.1, complete sequence.//3.9e-149:794:94//AC005384

F-NT2RP2002701//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50O24, WORKING DRAFT SEQUENCE.//9.2e-10:129:75//AL034380

F-NT2RP2002706//S.griseus secA gene.//1.3e-05:311:63//Y10980

F-NT2RP2002710//Homo sapiens mRNA for KIAA0672 protein, complete cds.//2.5e-40:631:65//AB014572

F-NT2RP2002727//Rattus norvegicus tulip 2 mRNA, complete cds.//4.8e-65:600:73//AF041107

F-NT2RP2002736//S.pombe chromosome II cosmid c887.//0.17:352:58//AL033388

F-NT2RP2002740//Absidia glauca ORF, 3' end; (+) mating type surface protein (PSSP15) gene, complete cds; ORF, 5' end.//0.0073:274:66//M94861

F-NT2RP2002741//Homo sapiens mRNA for Neuroblastoma, complete cds.//7.5e-29:628:62//D89016

F-NT2RP2002750//Homo sapiens Xp22 Bins 35-37 BAC GSHB-214D18 (Genome Systems Human BAC Library) complete sequence.//3.6e-31:568:67//AC005296

F-NT2RP2002752//Human BAC clone RG317M02 from 7p15-p21, complete sequence.//1.7e-08:206:63//AC002433

F-NT2RP2002753//Human DNA sequence from cosmid B11B7 on chromosome 22 contains ESTs.//2.8e-71:195:89//Z82171

F-NT2RP2002769//Streptomyces fradiae ty lactone synthase, starter module and modules 1-7, (tylG) gene, complete cds.//0.0016:412:60//U78289

F-NT2RP2002778//CIT-HSP-2059C5.TF CIT-HSP Homo sapiens genomic clone 2059C5, genomic survey sequence.//6.8e-18:186:79//B69837

F-NT2RP2002800

F-NT2RP2002800

WORKING DRAFT SEQUENCE, 7 un-ordered pieces.//0.83:252:60//AC004127

F-NT2RP2002857//Rat T-cell receptor active beta-chain V-region (V-beta6-J-beta2.5) mRNA, partial cds, clone

TRB-4 //0.85:93:68//M18845

F-NT2RP2002862//HS_3084_A1_H03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3084 Col=5 Row=O, genomic survey sequence.//5.0e-67:390:91//AQ186344

F-NT2RP2002880

5 F-NT2RP2002891//CIT-HSP-2310O14.TF CIT-HSP Homo sapiens genomic clone 2310O14, genomic survey sequence.//0.11:53:90//AQ019792

F-NT2RP2002925//Pig mRNA for carbonyl reductase, complete cds.//0.66:194:65//D16511

F-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds.//2.3e-135:628:99//AF038392

10 F-NT2RP2002929//F.rubripes GSS sequence, clone 123l23aA1, genomic survey sequence.//3.9e-06:66:83//AL017246

F-NT2RP2002939

F-NT2RP2002954

15 F-NT2RP2002959//Mus musculus ubiquitin conjugating enzyme (ubc4) mRNA, complete cds.//1.3e-47:411:79//U62483

F-NT2RP2002979//CIT-HSP-2340D12.TF CIT-HSP Homo sapiens genomic clone 2340D12, genomic survey sequence.//4.6e-96:476:97//AQ057233

F-NT2RP2002980//Sequence 20 from Patent EP0705842.//4.0e-13:100:94//A52230

20 F-NT2RP2002986//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//2.4e-09:272:61//AF059569

F-NT2RP2002987//Homo sapiens (subclone 6_d9 from P1 H21) DNA sequence, complete sequence.//1.0e-22:293:67//AC000958

F-NT2RP2002993//Rattus norvegicus RNA polymerase I 127 kDa subunit mRNA, complete cds.//4.0e-74:502:84//AF025424

25 F-NT2RP2003000//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 21 unordered pieces.//2.3e-46:474:76//AC004765

F-NT2RP2003034//Homo sapiens chromosome 17, clone hRPK.849_N_15, complete sequence.//4.2e-23:202:82//AC005703

30 F-NT2RP2003073//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.//3.4e-59:330:82//Z83822

F-NT2RP2003099//HS_3008_B2_C09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3008 Col=18 Row=F, genomic survey sequence.//1.4e-71:362:96//AQ089786

F-NT2RP2003108//Sequence 59 from patent US 5773577.//0.95:123:69//AR014362

35 F-NT2RP2003117//HS_2034_B2_D12_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2034 Col=24 Row=H, genomic survey sequence.//1.5e-88:461:96//AQ230797

F-NT2RP2003121//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//4.3e-46:470:72//AF079765

F-NT2RP2003125//Homo sapiens chromosome 19, cosmid R34382, complete sequence.//5.7e-10:436:61//AC005329

40 F-NT2RP2003129//P.thunbergii cab gene.//0.00044:541:60//X61915

F-NT2RP2003137//CIT-HSP-2300J6.TR CIT-HSP Homo sapiens genomic clone 2300J6, genomic survey sequence.//5.0e-78:393:97//AQ012976

F-NT2RP2003157//Human DNA sequence from cDNA 16pHQG;16 from chromosome 16p13.3.//5.4e-07:137:71//Z84716

45 F-NT2RP2003158//Homo sapiens mRNA for proteasome subunit p58, complete cds.//1.8e-111:581:93//D67025

F-NT2RP2003161//CITBI-E1-2506E20.TR CITBI-E1 Homo sapiens genomic clone 2506E20, genomic survey sequence.//0.0025:156:67//AQ262657

F-NT2RP2003164

50 F-NT2RP2003165//Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds.//1.4e-43:334:79//U91328

F-NT2RP2003177//Human signaling inositol polyphosphate 5 phosphatase SIP-110 mRNA, complete cds.//0.91:346:62//U50040

55 F-NT2RP2003194//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 996D20, WORKING DRAFT SEQUENCE.//1.7e-108:511:90//AL031597

F-NT2RP2003206

F-NT2RP2003228//Homo sapiens chromosome 17, clone hRPK.849_N_15, complete sequence.//1.0e-22:293:67//AC000958

F-NT2RP2003230//Rattus norvegicus endo-alpha-D-mannosidase (Enman) mRNA, complete cds.//2.6e-51:348:72//AF025424

86//AF023657

F-NT2RP2003237//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 126A5, WORKING DRAFT SEQUENCE.//2.6e-56:415:83//AL031447

F-NT2RP2003243//RPCI11-36J1.TP RPCI-11 Homo sapiens genomic clone RPCI-11-36J1, genomic survey sequence.//2.1e-16:112:93//AQ047107

F-NT2RP2003265//Muridae sp. (mouse-rat, neuroblastoma-glioma hybrid cell line NGD5) mRNA, complete cds.//6.0e-114:696:87//L38481

F-NT2RP2003272//RPCI11-67B15.TJ RPCI11 Homo sapiens genomic clone R-67B15, genomic survey sequence.//3.8e-16:110:94//AQ201833

F-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds.//1.5e-145:714:96//AB014525

F-NT2RP2003280//RPCI11-14I2.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-14I2, genomic survey sequence.//6.4e-77:400:95//B85286

F-NT2RP2003286//CIT-HSP-2336D3.TF CIT-HSP Homo sapiens genomic clone 2336D3, genomic survey sequence.//5.3e-29:287:73//AQ041024

F-NT2RP2003293//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//1.5e-54:508:74//AC003973

F-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 meidating protein, complete cds.//6.1e-85:416:97//AB006572

F-NT2RP2003297//S.pombe pho2 gene for specific p-nitrophenylphosphatase.//0.60:309:64//X62722

F-NT2RP2003307//Mus musculus kinesin light chain 2 (Klc2) mRNA, complete cds.//1.0e-45:442:75//AF055666

F-NT2RP2003308//D.melanogaster cm mRNA.//1.1e-63:697:70//X58374

F-NT2RP2003329//Homo sapiens chromosome 17, clone hCIT.131_K_11, complete sequence.//0.040:145:64//AC005288

F-NT2RP2003339

F-NT2RP2003347//Plasmodium falciparum MAL3P7, complete sequence.//0.12:275:60//AL034559

F-NT2RP2003367//Homo sapiens chromosome 4 clone B368A9 map 4q25, complete sequence.//0.83:225:63//AC005510

F-NT2RP2003391

F-NT2RP2003393//HS_3218_A2_B09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=18 Row=C, genomic survey sequence.//0.021:93:79//AQ204356

F-NT2RP2003394

F-NT2RP2003401

F-NT2RP2003433//Rattus rattus sec61 homologue mRNA, complete cds.//4.2e-61:533:75//M96630

F-NT2RP2003445//Homo sapiens genomic DNA, chromosome 21q11.1, segment 1/5, WORKING DRAFT SEQUENCE.//2.1e-49:301:72//AP000023

F-NT2RP2003446

F-NT2RP2003456//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4.//0.0018:366:60//AJ235272

F-NT2RP2003466//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.//7.5e-16:189:68//AC004770

F-NT2RP2003480//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//1.9e-25:197:85//M21977

F-NT2RP2003499 2.1e-08:408:61//AB000826

F-NT2RP2003506//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces.//1.9e-33:192:96//AC005236

F-NT2RP2003511//Ceratopteris richardii mRNA for CRHB11, partial cds.//1.0:328:60//AB013801

F-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds.//7.3e-76:403:93//D87460

F-NT2RP2003517//Human osteosarcoma cell line U-2 OS mRNA fragment for PDGF-B chain (PDGF= platelet-derived growth factor).//1.5e-24:151:95//X03702

F-NT2RP2003522//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//1.3e-101:564:91//M21977

F-NT2RP2003533//Human DNA sequence from cosmid F1121 on chromosome 6.//2.0e-40:315:75//Z80899

F-NT2RP2003543

F-NT2RP2003559//H.sapiens CpG island DNA genomic Mse1 fragment, clone 90a5, reverse read cpg90a5.rt1a.//1.1e-20:122:99//Z56144

F-NT2RP2003564//Human 52-kD ribonucleoprotein Ro/SSA mRNA, complete cds.//8.8e-27:664:63//M34551

F-NT2RP2003567//Homo sapiens mRNA for KIAA0462 protein, partial cds.//4.1e-113:541:98//AB007931

F-NT2RP2003568

F-NT2RP2003569 // Homo sapiens genomic DNA sequence, clone 90a5, reverse read cpg90a5.rt1a.//1.1e-20:122:99//Z56144

F-NT2759

F-NT2RP2003604//Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA, complete cds./1.9e-123:587:
98//AF030233
F-NT2RP2003629
F-NT2RP2003643//Mus musculus mRNA for CMP-N-acetylneuraminic acid synthetase./7.8e-88:582:84/
AJ006215
F-NT2RP2003668//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces./.
5.6e-47:335:83//AC005081
F-NT2RP2003687//Homo sapiens Xp22 BAC GSHB-519E5 (Genome Systems Human BAC library) complete se-
quence./1.2e-06:133:74//AC003684
F-NT2RP2003691//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 525L6, WORKING
DRAFT SEQUENCE./1.7e-47:337:81//AL023807
F-NT2RP2003702//Rattus norvegicus ovarian-specific protein mRNA, complete cds./1.3e-65:458:82/U44803
F-NT2RP2003704//H.sapiens CpG island DNA genomic MseI fragment, clone 2a9, reverse read cpg2a9.rt1e./.
3.8e-17:170:84/Z60615
F-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds./2.6e-108:518:98//AB011097
F-NT2RP2003713//HS_2016_B1_B05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
nomic clone Plate=2016 Col=9 Row=D, genomic survey sequence./1.3e-11:102:90/AQ226895
F-NT2RP2003714//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence./1.4e-27:249:78/
AC003973
F-NT2RP2003727//RPC11-77119.TV RPC11 Homo sapiens genomic clone R-77119, genomic survey sequence./.
3.4e-26:294:74/AQ268303
F-NT2RP2003737//Homo sapiens clone DJ1022114, WORKING DRAFT SEQUENCE, 14 unordered pieces./2.6e-
74:194:91//AC004951
F-NT2RP2003751//Homo sapiens Chromosome 16 BAC clone CIt987SK-A-911E12, complete sequence./1.7e-
92:165:96//AC003964
F-NT2RP2003760//B.primigenius mRNA for coat protein gamma-cop./4.5e-76:696:73/X92987
F-NT2RP2003764//Homo sapiens gene for MTG16, exon 1b, partial sequence./1.0:109:69//AB013275
F-NT2RP2003769
F-NT2RP2003770//Homo sapiens chromosome 17, clone hRPC.1050_D_4, complete sequence./3.0e-96:467:
98//AC004771
F-NT2RP2003777
F-NT2RP2003781//tricarboxylate carrier [rats, liver, mRNA Partial, 2986 nt]./7.2e-107:731:82/S70011
F-NT2RP2003793//CIT-HSP-2326L12.TF CIT-HSP Homo sapiens genomic clone 2326L12, genomic survey se-
quence./7.0e-20:124:95/AQ038761
F-NT2RP2003825//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence./8.9e-06:151:74/
AC004491
F-NT2RP2003840//Arabidopsis thaliana chromosome II BAC F12A24 genomic sequence, complete sequence./.
0.018:145:69//AC005167
F-NT2RP2003857//HS_3227_A2_G04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
nomic clone Plate=3227 Col=8 Row=M, genomic survey sequence./0.96:257:61/AQ303467
F-NT2RP2003859
F-NT2RP2003871//Homo sapiens 12q24 PAC RPC11-74B13 (Roswell Park Cancer Institute Human PAC library)
complete sequence./2.0e-12:369:65//AC002375
F-NT2RP2003885//CITBI-E1-2514D6.TF CITBI-E1 Homo sapiens genomic clone 2514D6, genomic survey se-
quence./0.13:167:64/AQ265722
F-NT2RP2003912//nek1=s erine/threonine- and tyrosine-specific protein kinase [mice, erythro leukemia cells, mR-
NA, 4263 nt]/1.3e-136:838:86/S45828
F-NT2RP2003952
F-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds./2.1e-28:165:96/
AB014458
F-NT2RP2003976//Human DNA sequence from clone 283E3 on chromosome 1p36.21-36.33. Contains the alter-
natively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract MIFR1, -2, MMP21/22A, -B
and -C, a novel gene, the alternatively spliced CDC2L2 gene for Cell Division Cycle 2-Like 2 (PITS/LRE, p58/GTA,
Galactosyltransferase Associated Protein Kinase) beta 1, beta 2-1, beta 2-2 and alpha 2-4, a 40S Ribosomal
Protein S7 pseudogene, part of the KIAA0447 gene, a novel alternatively spliced gene similar to many (archaeo-
maltoxin A, maltoxin B, MalT, MalZ genes), PstII site, HindIII sites, EcoRV sites, Ets binding site, HNF1B bind-
ing site, TATA box, initiator element, poly(A) signal, transducin Beta chain contains putative Lys islands, ESTs, RTSS and GSSIs.
Complete sequence./2.6e-24:298:74//AL031282

F-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds.//9.9e-160:783:96//AB018347

F-NT2RP2003984

F-NT2RP2003986//Human Chromosome 11 pac pDJ197h17, WORKING DRAFT SEQUENCE, 11 unordered pieces.//1.7e-26:260:77//AC000382

5 F-NT2RP2003988//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 862K6, WORKING DRAFT SEQUENCE.//9.1e-61:701:70//AL031681

F-NT2RP2004013//Human DNA sequence from clone 372K1 on chromosome 6q24 Contains EST, STS, GSS and CpG Island, complete sequence.//3.0e-123:693:91//AL023580

F-NT2RP2004014

10 F-NT2RP2004041//Homo sapiens chromosome 19, cosmid F17127, complete sequence.//5.8e-83:427:87//AC004780

F-NT2RP2004042

F-NT2RP2004066//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 134O19, WORKING DRAFT SEQUENCE.//5.6e-110:528:98//AL034555

15 F-NT2RP2004081

F-NT2RP2004098//HS_2216_A1_B12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2216 Col=23 Row=C, genomic survey sequence.//1.0e-07:86:84//AQ145694

F-NT2RP2004124//HS_3064_B2_A04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, genomic survey sequence.//3.0e-25:155:94//AQ136993

20 F-NT2RP2004142//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K8K14, complete sequence.//1.0:220:62//AB007645

F-NT2RP2004152//Drosophila melanogaster DNA sequence (P1 DS02252 (D97)), complete sequence.//0.93:480:56//AC002493

25 F-NT2RP2004165//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.051:265:61//AC005140

F-NT2RP2004170//Homo sapiens distal-less homeobox protein (DLX7) gene, complete cds.//1.0:162:66//AF028235

F-NT2RP2004172//S.pombe chromosome II cosmid c24E9.//1.7e-06:466:59//AL021816

F-NT2RP2004187//Homo sapiens full-length insert cDNA YQ86E07.//3.5e-17:354:64//AF075093

30 F-NT2RP2004194//Rattus norvegicus Golgi SNARE GS15 mRNA, complete cds.//9.4e-53:397:82//AF003998

F-NT2RP2004196

F-NT2RP2004207//Human von Willebrand factor pseudogene corresponding to exons 23 through 34.//0.0023:386:61//M60676

35 F-NT2RP2004226//HS_2186_A1_D03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2186 Col=5 Row=G, genomic survey sequence.//7.8e-58:370:87//AQ063813

F-NT2RP2004232//H.sapiens mRNA for protein kinase C mu.//1.2e-34:448:67//X75756

F-NT2RP2004239//Homo sapiens lok mRNA for protein kinase, complete cds.//5.2e-108:510:99//AB015718

F-NT2RP2004240//Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt. position (6/7).//1.1e-12:489:61//AP000006

40 F-NT2RP2004242

F-NT2RP2004245

F-NT2RP2004270//Streptomyces coelicolor cosmid 1A9.//7.5e-07:462:62//AL034446

F-NT2RP2004300//Homo sapiens chromosome 19, cosmid R33632, complete sequence.//3.5e-11:299:64//AC005781

45 F-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete cds.//4.5e-150:735:97//AF000416

F-NT2RP2004321//Drosophila melanogaster DNA sequence (P1 DS02110 (D147)), complete sequence.//0.98:267:59//AC004423

F-NT2RP2004339//Human Chromosome 16 BAC clone CIT987SK-A-355G7, complete sequence.//1.6e-40:419:75//AC002519

50 F-NT2RP2004347//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018D12, WORKING DRAFT SEQUENCE.//1.2e-72:439:82//AL031650

F-NT2RP2004364

F-NT2RP2004365

55 F-NT2RP2004366//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs STS GSS CpG Island

pathway map: <http://www.ncbi.nlm.nih.gov/Pathway/>

F-NT2RP2004373//Homo sapiens cosmid 12-11-114486 from Xg1.1 complete sequence.//1.0e-114:144:144//AF035397

F-NT2RP2004389//HS_2183_B2_H04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=8 Row=P, genomic survey sequence.//2.9e-11:83:96//AQ063969

F-NT2RP2004392

F-NT2RP2004396//Homo sapiens BAC clone RG135C18 from 7q21, complete sequence.//1.1e-171:875:95//AC005164

F-NT2RP2004399//Homo sapiens SYBL1 gene.//1.4e-24:467:64//AJ004799

F-NT2RP2004400//Arabidopsis thaliana BAC T19B17 from chromosome IV, near 19.3 cM, complete sequence.//0.00074:455:59//AF069441

F-NT2RP2004412//H.sapiens CpG island DNA genomic MseI fragment, clone 34g4, reverse read cpg34g4.rt1a.//5.0e-27:154:98//Z65369

F-NT2RP2004425

F-NT2RP2004463//Streptomyces coelicolor cosmid 2E9.//0.0053:196:65//AL021530

F-NT2RP2004476//Drosophila melanogaster cosmid 67A9.//5.2e-15:377:63//AL034388

F-NT2RP2004490//Homo sapiens chromosome 16, P1 clone 94-10H (LANL), complete sequence.//4.3e-100:497:97//AC005591

F-NT2RP2004512//Plasmodium falciparum MAL3P5, complete sequence.//2.3e-07:815:57//AL034556

F-NT2RP2004523//Homo sapiens clone DJ0800G07, complete sequence.//8.5e-138:718:95//AC004890

F-NT2RP2004538//Homo sapiens mRNA for KIAA0591 protein, partial cds.//1.4e-137:687:96//AB011163

F-NT2RP2004551//CIT-HSP-2387G7.TF.1 CIT-HSP Homo sapiens genomic clone 2387G7, genomic survey sequence.//2.1e-85:484:91//AQ239555

F-NT2RP2004568//H.vulgare GAA-satellite DNA.//2.0e-07:292:62//Z50100

F-NT2RP2004580//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 968D22, WORKING DRAFT SEQUENCE.//4.5e-44:512:72//AL023755

F-NT2RP2004587//Candida albicans cytoskeleton assembly control protein (SLA2) gene, partial cds.//1.0:344:56//AF092908

F-NT2RP2004594//nbxb0019H13r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0019H13r, genomic survey sequence.//0.053:324:60//AQ258020

F-NT2RP2004600

F-NT2RP2004602//Homo sapiens chromosome 19, cosmid F21431, complete sequence.//0.12:109:73//AC005176

F-NT2RP2004614

F-NT2RP2004655//Homo sapiens mRNA for leucine rich protein.//2.6e-102:496:98//AJ006291

F-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds.//1.6e-153:728:98//AB007929

F-NT2RP2004675//Homo sapiens chromosome 12q24.1, WORKING DRAFT SEQUENCE, 33 unordered pieces.//0.092:239:61//AC005805

F-NT2RP2004681//Human DNA sequence from clone 51J23 on chromosome Xq26.3-27.3. Contains an EST and GSSs, complete sequence.//1.0:236:61//AL031312

F-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds.//1.3e-59:327:94//AB014525

F-NT2RP2004709//HS_2033_B2_E04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2033 Col=8 Row=J, genomic survey sequence.//1.9e-15:187:74//AQ230714

F-NT2RP2004710//HS_3185_82_D07_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3185 Col=14 Row=H, genomic survey sequence.//9.9e-10:110:84//AQ172885

F-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds.//6.4e-117:582:96//AB007947

F-NT2RP2004743//Human DNA sequence from PAC 37M17 chromosome X.//0.14:138:71//Z78022

F-NT2RP2004767//H.sapiens CpG island DNA genomic MseI fragment, clone 65c11, reverse read cpg65c11.rt1a.//1.3e-24:217:81//Z62210

F-NT2RP2004768//Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds.//1.6e-45:541:71//AF024636

F-NT2RP2004775//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//5.8e-13:697:59//AE001398

F-NT2RP2004791//Human HeLa mRNA isolated as a false positive in a two-hybrid screen.//5.0e-53:353:84//U56252

F-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//1.5e-116:594:95//AF058953 F-NT2RP2004802

F-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds.//2.1e-101:495:97//AF054179

F-NT2RP2004841//Human DNA sequence from cosmid J138O17 between markers DXS6791 and DXS8038 on chromosome 12p13.3, genomic survey sequence.//1.1e-11:111:74//AL025645

F-NT2RP2004861//Homo sapiens GSS sequence from clone 34V117bA, genomic survey sequence.//1.1e-11:111:74//AL025645

F-NT2RP2004897//Human Chromosome X clone BWXD187, complete sequence.//4.8e-142:710:96//AC004383
F-NT2RP2004933//Homo sapiens mRNA for ZIP-kinase, complete cds.//2.0e-82:418:95//AB007144
F-NT2RP2004936
F-NT2RP2004959//HS_3197_A2_G11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
nomic clone Plate=3197 Col=22 Row=M, genomic survey sequence.//3.5e-25:218:83//AQ150183
F-NT2RP2004961//Rattus norvegicus KRAB/zinc finger suppressor protein 1 (KS1) mRNA, complete cds.//2.5e-
59:339:79//U56732
F-NT2RP2004962//Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemo-
chromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds.//3.6e-
19:187:72//U91328
F-NT2RP2004967//Plasmodium falciparum MAL3P6, complete sequence.//0.0020:297:61//Z98551
F-NT2RP2004978//Chlamydomonas reinhardtii VSP-3 mRNA, complete cds.//0.22:162:69//L29029
F-NT2RP2004982//F26D4-Sp6 IGF Arabidopsis thaliana genomic clone F26D4, genomic survey sequence.//0.13:
273:61//B12642
F-NT2RP2004985//Human mRNA for KIAA0144 gene, complete cds.//1.5e-20:431:65//D63478
F-NT2RP2004999
F-NT2RP2005000//R.rattus gene for beta-1 subunit of Na,K-ATPase.//0.019:240:63//X63375
F-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds.//6.0e-159:782:97//AB014515
F-NT2RP2005003//H.sapiens Staf50 mRNA.//3.1e-42:430:75//X82200
F-NT2RP2005012//Homo sapiens SEC63 (SEC63) mRNA, complete cds.//1.4e-98:501:96//AF100141
F-NT2RP2005018//Homo sapiens PAC clone DJ0659J06 from 7q33-q35, complete sequence.//1.0:209:63//
AC004849
F-NT2RP2005020
F-NT2RP2005022//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//
3.0e-43:98:93//AC000380
F-NT2RP2005031//HS_2052_B2_G10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
nomic clone Plate=2052 Col=20 Row=N, genomic survey sequence.//0.019:363:61//AQ231464
F-NT2RP2005037//Human 3' of immunoglobulin heavy chain locus (IGHA2) gene.//0.70:174:65//U64454
F-NT2RP2005038//Homo sapiens chromosome 17, clone hRPK.74_E_22, complete sequence.//0.20:519:57//
AC005696
F-NT2RP2005108
F-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds.//2.0e-103:495:98//AB014564
F-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein).//2.9e-27:157:98//
X98743
F-NT2RP2005139//Amycolatopsis mediterranei genes encoding rifamycin polyketide synthases, ORFs 1 to 5.//
0.00024:547:59//AJ223012
F-NT2RP2005140//Homo sapiens chromosome 21, Neurofibromatosis 1 (NF1) related locus, complete se-
quence.//0.95:191:62//AC004527
F-NT2RP2005144//Homo sapiens tubby like protein 3 (TULP3) mRNA, complete cds.//2.6e-89:447:96//AF045583
F-NT2RP2005147//HS_3184_A1_E01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
nomic clone Plate=3184 Col=1 Row=I, genomic survey sequence.//0.10:294:60//AQ252226
F-NT2RP2005159//H.sapiens CpG island DNA genomic MseI fragment, clone 132g6, forward read
cpg132g6.ft1a.//1.1e-13:93:97//Z59162
F-NT2RP2005162//Caenorhabditis elegans cosmid F01F1.//2.6e-20:394:64//U13070
F-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein.//1.4e-125:633:96//AJ007509
F-NT2RP2005204//Arabidopsis thaliana ubiquitin activating enzyme (UBA1) gene, complete cds.//0.00016:316:
60//U80808
F-NT2RP2005227//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//0.51:52:92//
AC005189
F-NT2RP2005239//S.pombe chromosome II cosmid c21D10.//1.3e-22:356:67//AL031536
F-NT2RP2005254
F-NT2RP2005270//H.sapiens genomic DNA (chromosome 3; clone NL197R).//0.58:132:65//X87513
F-NT2RP2005276//Rat mRNA for brain acyl-CoA synthetase II, complete cds.//9.0e-103:656:85//D30666
F-NT2RP2005287//Cavia porcellus zinc finger protein (zfoC1) mRNA, complete cds.//3.4e-37:302:84//L26335
F-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.//7.1e-122:604:96//
AF060219

[illegible]

omic clone Plate=3245 Col=19 Row=J, genomic survey sequence.//8.2e-37:223:92//AQ217454
 F-NT2RP2005315//Homo sapiens mRNA for KIAA0676 protein, partial cds.//1.1e-95:483:96//AB014576
 F-NT2RP2005325//Human LIM-homeobox domain protein (hLH-2) mRNA, complete cds.//8.2e-22:166:90//
 U11701

5 F-NT2RP2005336//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete
 cds.//0.39:353:62//AF032387

F-NT2RP2005344//Homo sapiens mRNA for KIAA0566 protein, partial cds.//8.8e-29:456:66//AB011138

F-NT2RP2005354//Human DNA sequence from PAC 435C23 on chromosome X. Contains ESTs.//0.72:431:61//
 Z92844

10 F-NT2RP2005358//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds.//4.7e-99:489:
 96//AF072247

F-NT2RP2005360//Pan troglodytes huntingtin gene, partial exon.//0.93:105:67//L49358

F-NT2RP2005393//Rat parathyroid hormone receptor mRNA, complete cds.//2.4e-08:97:83//M77184

F-NT2RP2005407

15 F-NT2RP2005436//Homo sapiens chromosome 16, cosmid clone 2H2 (LANL), complete sequence.//0.014:235:
 62//AC005346

F-NT2RP2005441//CIT-HSP-2338P5.TR CIT-HSP Homo sapiens genomic clone 2338P5, genomic survey se-
 quence.//4.0e-107:532:97//AQ055548

20 F-NT2RP2005453//F21C16TFC IGF Arabidopsis thaliana genomic clone F21C16, genomic survey sequence.//
 1.0:239:61//B97865

F-NT2RP2005457//B.taurus Cl-B14.5b mRNA for NADH dehydrogenase (ubiquinone).//4.7e-25:245:79//X68647

F-NT2RP2005464//Human DNA sequence from clone 836E8 on chromosome 20p12 Contains EST, CA repeat,
 STS, GSS, retroviral sequence, complete sequence.//4.6e-111:724:86//AL031679

25 F-NT2RP2005465//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//6.5e-
 18:152:75//AC006116

F-NT2RP2005472//Human DNA sequence from clone 1118D24 on chromosome 1p36.11-36.33. Contains part of
 a novel gene similar to worm genes T08G11.1 and C25H3.9, part of a 60S Ribosomal Protein L10 LIKE (pseudo)
 gene and two 3' exons of the TNFR2 gene for Tumor Necrosis Factor Receptor 2 (75 kD) (TNF Binding Protein 2,
 TBPII, TNF-R2, CD120B, TNFR). Contains ESTs, STSs, GSSs, genomic marker D1S434 and a ca repeat poly-
 morphism, complete sequence.//4.4e-12:89:97//AL031276

30 F-NT2RP2005476//Homo sapiens BAC clone RG293F17 from 7p15-p21, complete sequence.//4.3e-40:463:73//
 AC004130

F-NT2RP2005490//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//
 3.2e-115:228:99//AC006030

35 F-NT2RP2005491//HS_2253_A2_G10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=2253 Col=20 Row=M, genomic survey sequence.//4.6e-23:234:80//AQ116847

F-NT2RP2005495

F-NT2RP2005496//HS_3064_A1_F08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3064 Col=15 Row=K, genomic survey sequence.//5.3e-90:436:98//AQ143097

40 F-NT2RP2005498//Rabbit protein phosphatase 2A beta subunit mRNA, complete cds.//1.4e-63:503:78//M64931

F-NT2RP2005501//Homo sapiens chromosome 10 clone CIT987SK-1143A11 map 10q25, complete sequence.//
 0.86:183:63//AC005880

F-NT2RP2005509//Homo sapiens cosmid LM1937 from Xq28.//1.0:160:65//U82695

45 F-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//3.9e-81:
 444:92//AF092563

F-NT2RP2005525//Homo sapiens mRNA for KIAA0764 protein, complete cds.//6.9e-18:112:99//AB018307

F-NT2RP2005531//Human structural protein 4.1 mRNA, complete cds.//1.1e-06:282:60//M14993

F-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//2.9e-153:747:97//AJ012449

F-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds.//5.9e-130:618:98//AB007963

50 F-NT2RP2005549//Mus musculus clone OST142, genomic survey sequence.//3.1e-43:277:89//AF046734

F-NT2RP2005555//HS_2188_A2_D04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=2188 Col=8 Row=G, genomic survey sequence.//8.0e-05:195:65//AQ086723

F-NT2RP2005557//Homo sapiens clone 486790 diphosphoinositol polyphosphate phosphohydrolase mRNA,
 complete cds.//2.5e-44:473:71//AF062529

55 F-NT2RP2005581//Homo sapiens BAC clone GS180J15 from 7q31, complete sequence.//0.99:213:65//AC005016

F-NT2RP2005600//H sapiens CpG island DNA genomic Map1 fragment clone 170410

F-NT2RP2005601

F-NT2RP2005620//Homo sapiens epsin 2a mRNA, complete cds.//9.8e-91:447:97//AF062085

F-NT2RP2005622

F-NT2RP2005635//Saccharomyces cerevisiae chromosome VIII cosmid 9205.//8.6e-17:411:61//U10556

F-NT2RP2005637//NATI (NATI*10)=acetyltransferase 1 {3' region, polyadenylation polymorphism} [human, unrelated Caucasians, mRNA Partial Mutant, 300 nt]//0.22:156:65//S78829

F-NT2RP2005640//Mouse U6 RNA gene.//5.5e-19:249:76//X06980

F-NT2RP2005645//HS_2201_B2_D07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2201 Col=14 Row=H, genomic survey sequence.//0.30:159:65//AQ066763

F-NT2RP2005651//H.sapiens DNA sequence.//0.00037:150:66//Z22493

F-NT2RP2005654//Homo sapiens mRNA for KIAA0288 gene, complete cds.//4.7e-07:351:62//AB006626

F-NT2RP2005669//Homo sapiens KE05 protein mRNA, complete cds.//8.2e-98:472:98//AF064605

F-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//2.4e-94:462:98//AF089814

F-NT2RP2005683//HS-1024-B1-H05-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 803 Col=9 Row=P, genomic survey sequence.//0.99:156:64//B34405

F-NT2RP2005690//Human pyrroline 5-carboxylate reductase mRNA, complete cds.//7.7e-10:328:61//M77836

F-NT2RP2005694

F-NT2RP2005701//Homo sapiens 12p13.3 BAC RPC111-288K12 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.72:160:65//AC005183

F-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds.//1.6e-124:599:97//AB018342

F-NT2RP2005719//R.norvegicus mRNA for metallothionein-III.//0.86:117:64//X89603

F-NT2RP2005722//Human zinc finger protein ZNF136.//2.6e-44:415:77//U09367

F-NT2RP2005723//Human BAC clone GS542D18 from 7q31-q32, complete sequence.//6.9e-15:153:81//AC002528

F-NT2RP2005726//Homo sapiens clone DJ0577P23, WORKING DRAFT SEQUENCE, 28 unordered pieces.//5.1e-41:138:95//AC005627

F-NT2RP2005732//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 291J10, WORKING DRAFT SEQUENCE.//0.61:303:60//Z93017

F-NT2RP2005741//Homo sapiens PALM gene, exon 1 and joined CDS.//0.52:116:67//Y16270

F-NT2RP2005748//Human Kox11 mRNA for zinc finger protein, partial.//0.11:136:66//X52342

F-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds.//7.8e-22:134:96//AF068868

F-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//1.2e-100:486:98//AF082516

F-NT2RP2005763//Human mRNA for KIAA0111 gene, complete cds.//0.00073:425:56//D21853

F-NT2RP2005767//G.gallus PB1 gene.//2.1e-73:544:80//X90849

F-NT2RP2005773//Human pyrroline 5-carboxylate reductase mRNA, complete cds.//6.2e-15:153:82//M77836

F-NT2RP2005775//Sus scrofa mRNA for soluble angiotensin-binding protein, complete cds.//1.2e-121:649:88//D11336

F-NT2RP2005781//Pseudomonas aeruginosa gene for MexX and MexY, complete cds.//0.96:184:60//AB015853

F-NT2RP2005784//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1185N5, WORKING DRAFT SEQUENCE.//1.9e-63:222:96//AL034423

F-NT2RP2005804//Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete cds.//2.6e-07:232:64//AF010579

F-NT2RP2005812

F-NT2RP2005815//Streptomyces sp. gene for alkaline serine protease I.//0.031:358:59//X74103

F-NT2RP2005835//Rattus norvegicus mRNA for p47, complete cds.//2.5e-107:449:91//AB002086

F-NT2RP2005841//Human DNA sequence from cosmid U209G1 on chromosome X.//5.1e-05:144:73//Z68873

F-NT2RP2005853//RPC111-24D4.TKBF RPC111 Homo sapiens genomic clone RPC111-24D4, genomic survey sequence.//6.4e-13:130:85//AQ013490

F-NT2RP2005857//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds.//1.7e-174:829:98//AF092564

F-NT2RP2005859//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 914P20, WORKING DRAFT SEQUENCE.//0.25:174:62//AL034553

F-NT2RP2005868//Fugu rubripes GSS sequence, clone 103I24aF4, genomic survey sequence.//7.8e-06:92:79//AF027276

F-NT2RP2005890//Mouse oncostome (ect2) mRNA, complete cds.//2.7e-32:660:66//L11316
F-NT2RP2005901//H.sapiens CpG island DNA genomic Mse1 fragment, clone 15b5, reverse read cpG15b5.rt1a.//0.0026:66:84//Z54729
F-NT2RP2005908//Homo sapiens 12q13.1 PAC RPCI3-197B17 (Roswell Park Cancer Institute Human PAC library) complete sequence.//6.4e-49:481:75//AC004241
F-NT2RP2005933//Rattus norvegicus nucleoporin p54 mRNA, complete cds.//6.6e-61:657:73//U63840
F-NT2RP2005942//H.sapiens PAP mRNA.//1.6e-46:618:67//X76770
F-NT2RP2005980//Homo sapiens chromosome 17, clone hRPC.1081_P_3, complete sequence.//1.0e-48:533:71//AC005207
F-NT2RP2006023//HS_3048_A1_A11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3048 Col=21 Row=A, genomic survey sequence.//2.1e-25:167:91//AQ126553
F-NT2RP2006038//CIT-HSP-384K4.TR CIT-HSP Homo sapiens genomic clone 384K4, genomic survey sequence.//3.9e-06:102:74//B51912
F-NT2RP2006043//Human intercrine-alpha (hIRH) mRNA, complete cds.//1.9e-05:418:59//U19495
F-NT2RP2006052//Peromyscus polionotus ammobates dinucleotide microsatellite Ppa55.//0.0035:226:65//AF016861
F-NT2RP2006069//Human HepG2 partial cDNA, clone hmd3g02m5.//3.9e-11:121:85//D17047
F-NT2RP2006071
F-NT2RP2006098//Homo sapiens chromosome 21q22.2, cosmid D13C2, complete sequence.//0.46:264:59//AF027207
F-NT2RP2006100//Human Chromosome X, complete sequence.//3.2e-94:488:95//AC004073
F-NT2RP2006103//HS_2254_A2_D02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2254 Col=4 Row=G, genomic survey sequence.//5.7e-27:156:96//AQ129602
F-NT2RP2006106//Human Chromosome 11 pac pDJ1173a5, complete sequence.//1.2e-62:655:71//AC000378
F-NT2RP2006141//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 537K23, WORKING DRAFT SEQUENCE.//1.2e-69:316:98//AL034405
F-NT2RP2006166//Homo sapiens chromosome 4 clone B32I8, complete sequence.//3.1e-45:387:81//AC004063
F-NT2RP2006184//Cricetulus griseus beta-1,6-N-acetylglucosaminyltransferase Lec4A cell line point mutant mRNA, complete cds.//0.99:111:73//U62587
F-NT2RP2006186//Homo Sapiens mRNA for KIAA0654 protein, partial cds.//7.8e-113:567:96//AB014554
F-NT2RP2006196//Homo sapiens clone DJ1189D06, complete sequence.//2.8e-28:718:62//AC005232
F-NT2RP2006200//Homo sapiens chromosome 12p13.3 clone RPCI1-96H9, WORKING DRAFT SEQUENCE, 66 unordered pieces.//6.5e-83:239:94//AC006057
F-NT2RP2006219//H.sapiens mRNA for DGCR6 protein.//1.4e-116:618:93//X96484
F-NT2RP2006237//CIT-HSP-2300P9.TR CIT-HSP Homo sapiens genomic clone 2300P9, genomic survey sequence.//2.0e-18:118:97//AQ012480
F-NT2RP2006238//Rattus norvegicus CTD-binding SR-like protein rA8 mRNA, complete cds.//7.6e-102:635:86//U49055
F-NT2RP2006258//RPCI11-9N9.TP RPCI-11 Homo sapiens genomic clone RPCI-11-9N9, genomic survey sequence.//8.6e-05:181:63//B71615
F-NT2RP2006261//H.sapiens mRNA for serine/threonine protein kinase EMK.//0.44:111:71//X97630
F-NT2RP2006275//Pseudorabies virus UL[5,6,7,8,5,9,10,11,12,13] genes.//2.0e-05:501:59//X97257
F-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds.//2.7e-138:679:97//AF035262
F-NT2RP2006320//P.falciparum pfmdr1 gene.//0.00013:425:60//X56851
F-NT2RP2006321//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//4.1e-19:545:62//AC003973
F-NT2RP2006323//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 745I14, WORKING DRAFT SEQUENCE.//8.9e-18:131:90//AL033532
F-NT2RP2006333//Homo sapiens PAC clone DJ0808A01 from 7q21.1-q31.1, complete sequence.//6.2e-125:602:98//AC004893
F-NT2RP2006334//Homo sapiens chromosome 19, cosmid R27139, complete sequence.//2.1e-06:241:65//AC005514
F-NT2RP2006365//Fugu rubripes GSS sequence, clone 171K15aC5, genomic survey sequence.//7.8e-06:148:70//AL029590
F-NT2RP2006393//Human DNA sequence from clone 80I19 on chromosome 6p21.31-22.2 Contains genes and pseudogenes for olfactory receptor like proteins. STS: GSS, complete sequence.//6.8e-36:167:76//AC027207
F-NT2RP2006439//Human DNA sequence from clone 12201 on chromosome 12p12.1-12p13.1 Contains gene and pseudogenes for olfactory receptor like proteins. STS: GSS, complete sequence.//1.1e-34:163:84//AL028048
F-NT2RP2006441//Human DNA sequence from clone 12201 on chromosome 12p12.1-12p13.1 Contains gene and pseudogenes for olfactory receptor like proteins. STS: GSS, complete sequence.//1.1e-34:163:84//AL028048
F-NT2RP2006442//Human DNA sequence from clone 12201 on chromosome 12p12.1-12p13.1 Contains gene and pseudogenes for olfactory receptor like proteins. STS: GSS, complete sequence.//1.1e-34:163:84//AL028048
F-NT2RP2006443//Human DNA sequence from clone 12201 on chromosome 12p12.1-12p13.1 Contains gene and pseudogenes for olfactory receptor like proteins. STS: GSS, complete sequence.//1.1e-34:163:84//AL028048
F-NT2RP2006444//Human DNA sequence from clone 12201 on chromosome 12p12.1-12p13.1 Contains gene and pseudogenes for olfactory receptor like proteins. STS: GSS, complete sequence.//1.1e-34:163:84//AL028048
F-NT2RP2006445//Human DNA sequence from clone 12201 on chromosome 12p12.1-12p13.1 Contains gene and pseudogenes for olfactory receptor like proteins. STS: GSS, complete sequence.//1.1e-34:163:84//AL028048
F-NT2RP2006446//Human DNA sequence from clone 12201 on chromosome 12p12.1-12p13.1 Contains gene and pseudogenes for olfactory receptor like proteins. STS: GSS, complete sequence.//1.1e-34:163:84//AL028048
F-NT2RP2006447//Human DNA sequence from clone 12201 on chromosome 12p12.1-12p13.1 Contains gene and pseudogenes for olfactory receptor like proteins. STS: GSS, complete sequence.//1.1e-34:163:84//AL028048
F-NT2RP2006448//Human DNA sequence from clone 12201 on chromosome 12p12.1-12p13.1 Contains gene and pseudogenes for olfactory receptor like proteins. STS: GSS, complete sequence.//1.1e-34:163:84//AL028048
F-NT2RP2006449//Human DNA sequence from clone 12201 on chromosome 12p12.1-12p13.1 Contains gene and pseudogenes for olfactory receptor like proteins. STS: GSS, complete sequence.//1.1e-34:163:84//AL028048
F-NT2RP2006450//Human DNA sequence from clone 12201 on chromosome 12p12.1-12p13.1 Contains gene and pseudogenes for olfactory receptor like proteins. STS: GSS, complete sequence.//1.1e-34:163:84//AL028048
F-NT2RP2006451//Human DNA sequence from clone 12201 on chromosome 12p12.1-12p13.1 Contains gene and pseudogenes for olfactory receptor like proteins. STS: GSS, complete sequence.//1.1e-34:163:84//AL028048
F-NT2RP2006452//Human DNA sequence from clone 12201 on chromosome 12p12.1-12p13.1 Contains gene and pseudogenes for olfactory receptor like proteins. STS: GSS, complete sequence.//1.1e-34:163:84//AL028048
F-NT2RP2006453//Human DNA sequence from clone 12201 on chromosome 12p12.1-12p13.1 Contains gene and pseudogenes for olfactory receptor like proteins. STS: GSS, complete sequence.//1.1e-34:163:84//AL028048
F-NT2RP2006454//Human DNA sequence from clone 12201 on chromosome 12p12.1-12p13.1 Contains gene and pseudogenes for olfactory receptor like proteins. STS: GSS, complete sequence.//1.1e-34:163:84//AL028048
F-NT2RP2006455//Human DNA sequence from clone 12201 on chromosome 12p12.1-12p13.1 Contains gene and pseudogenes for olfactory receptor like proteins. STS: GSS, complete sequence.//1.1e-34:163:84//AL028048
F-NT2RP2006456//Human DNA sequence from clone 12201 on chromosome 12p12.1-12p13.1 Contains gene and pseudogenes for olfactory receptor like proteins. STS: GSS, complete sequence.//1.1e-34:163:84//AL028048
F-NT2RP2006457//Human DNA sequence from clone 12201 on chromosome 12p12.1-12p13.1 Contains gene and pseudogenes for olfactory receptor like proteins. STS: GSS, complete sequence.//1.1e-34:163:84//AL028048
F-NT2RP2006458//Human DNA sequence from clone 12201 on chromosome 12p12.1-12p13.1 Contains gene and pseudogenes for olfactory receptor like proteins. STS: GSS, complete sequence.//1.1e-34:163:84//AL028048
F-NT2RP2006459//Human DNA sequence from clone 12201 on chromosome 12p12.1-12p13.1 Contains gene and pseudogenes for olfactory receptor like proteins. STS: GSS, complete sequence.//1.1e-34:163:84//AL028048
F-NT2RP2006460//Human DNA sequence from clone 12201 on chromosome 12p12.1-12p13.1 Contains gene and pseudogenes for olfactory receptor like proteins. STS: GSS, complete sequence.//1.1e-34:163:84//AL028048
F-NT2RP2006461//Human DNA sequence from clone 12201 on chromosome 12p12.1-12p13.1 Contains gene and

F-NT2RP2006441

F-NT2RP2006454//Sequence 8 from Patent WO9517522 //2.9e-06:180:66//A45338

F-NT2RP2006456

F-NT2RP2006464//Homo sapiens mRNA for AND-1 protein //3.4e-148:545:98//AJ006266

F-NT2RP2006467//Sus scrofa IgM heavy chain gene, switch region and exons encoding ch1-ch4 and secretion domains, partial cds //0.061:201:66//U50149

F-NT2RP2006472

F-NT2RP2006534//Human DNA sequence from clone 272E8 on chromosome Xp22.13-22.31. Contains a pseudogene similar to MDM2-Like P53-binding protein gene. Contains STSs, GSSs and a CA repeat polymorphism, complete sequence //8.8e-10:273:66//Z93929

F-NT2RP2006554//Human DNA mismatch repair protein homolog (hMLH1) gene, exon 6 //0.71:174:59//U40965

F-NT2RP2006565//Homo sapiens secretory carrier-associated membrane protein (SCAMP) mRNA, complete cds //6.6e-114:669:90//AF038966

F-NT2RP2006571//Rabbit cytochrome P-450 isozyme 2 (type B2) mRNA, complete cds, clone B2-1 //6.0e-26:503:63//M20855

F-NT2RP2006573//Molluscum contagiosum virus subtype 1, complete genome //0.44:134:71//U60315

F-NT2RP2006598//Human BRCA2 region, mRNA sequence CG033 //5.0e-16:140:85//U50537

F-NT2RP3000002//***ALU WARNING: Human Alu-Sc subfamily consensus sequence //3.8e-32:214:89//U14571

F-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (JM21) //5.8e-136:637:98//AJ011972

F-NT2RP3000046//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds //5.4e-05:571:60//L14320

F-NT2RP3000047

F-NT2RP3000050//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9 //1.0e-67:626:74//M27877

F-NT2RP3000055//Genomic sequence from Human 9q34, complete sequence //3.5e-10:394:64//AC001227

F-NT2RP3000068

F-NT2RP3000072//Homo sapiens BAC clone RG290G13 from 7q21, complete sequence //1.0:301:61//AC004746

F-NT2RP3000080//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 102D24, WORKING DRAFT SEQUENCE //1.9e-44:297:79//AL021391

F-NT2RP3000085//Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase precursor mRNA, complete cds //4.5e-33:528:65//U12536

F-NT2RP3000092//RPCI11-22M5.TV RPCI-11 Homo sapiens genomic clone RPCI-11-22M5, genomic survey sequence //3.3e-27:157:97//B84237

F-NT2RP3000109//Arabidopsis thaliana 1-amino-1-cyclopropanecarboxylate synthase (ACS5) gene, complete cds //0.92:185:64//L29260

F-NT2RP3000134//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence //1.2e-112:286:89//AC005189

F-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds //9.0e-181:849:98//AB011164

F-NT2RP3000149//Homo sapiens chromosome 17, clone hRPK.264_B_14, complete sequence //4.2e-24:155:94//AC005884

F-NT2RP3000186//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 500L14, WORKING DRAFT SEQUENCE //7.2e-43:269:81//AL023583

F-NT2RP3000197//Homo sapiens interleukin 9 receptor (IL9R) pseudogene, exons 1-9 //0.098:405:57//L39063

F-NT2RP3000207//Drosophila melanogaster DNA sequence (P1 DS00164 (D269)), complete sequence //0.96:608:55//AC004716

F-NT2RP3000220

F-NT2RP3000233//Homo sapiens actin binding protein MAYVEN mRNA, complete cds //2.0e-18:509:58//AF059569

F-NT2RP3000235//Mouse Cosmid ma53a016 from 14D1-D2, complete sequence //3.5e-05:224:65//AC004101

F-NT2RP3000247//Human mRNA for KIAA0218 gene, complete cds //2.1e-109:691:86//D86972

F-NT2RP3000251//Caenorhabditis elegans cosmid ZK930, complete sequence //0.20:119:68//Z70213

F-NT2RP3000252//Homo sapiens cosmid 1F1, complete sequence //9.8e-78:174:88//AF065393

F-NT2RP3000255

F-NT2RP3000267

F-NT2RP3000289//Homo sapiens mRNA for KIAA0218 gene, complete cds //2.1e-109:691:86//D86972

F-NT2RP3000320//RPCI11-36J1.TP RPCI-11 Homo sapiens genomic clone RPCI-11-36J1, genomic survey sequence.//4.4e-06:87:88//AQ047107

F-NT2RP3000324//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds.//5.5e-26:283:79//U78090

5 F-NT2RP3000333//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 973M2, WORKING DRAFT SEQUENCE.//1.0:309:60//AL033533

F-NT2RP3000341//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence.//6.7e-42:465:74//Z97181

F-NT2RP3000348

10 F-NT2RP3000350//Homo sapiens cosmid 1F1, complete sequence.//3.4e-79:174:88//AF065393

F-NT2RP3000359//Bovine mitochondrial GTP:AMP phosphotransferase mRNA, complete cds.//2.2e-127:816:85//M25757

F-NT2RP3000361//Schizosaccharomyces pombe DNA for pre-mRNA splicing factor, complete cds.//0.0075:288:58//D83743

15 F-NT2RP3000366//Mus musculus ras-related protein (rab18) mRNA, complete cds.//7.1e-134:693:94//L04966

F-NT2RP3000393//Rattus norvegicus mRNA for GABA-B R2 receptor.//0.049:308:60//AJ011318

F-NT2RP3000397//S.cerevisiae chromosome VII reading frame ORF YGL120c.//0.00012:441:58//Z72642

F-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds.//5.0e-174:841:97//AF071185

20 F-NT2RP3000418//Homo sapiens chromosome 17, clone hRPK.1053_B_8, complete sequence.//7.9e-53:817:68//AC006083

F-NT2RP3000433//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 862K6, WORKING DRAFT SEQUENCE.//6.1e-31:590:63//AL031681

F-NT2RP3000439//Fugu rubripes GSS sequence, clone 075E22aB10, genomic survey sequence.//4.0e-19:169:81//AL026471

25 F-NT2RP3000441//Human DNA sequence from PAC 93H18 on chromosome 6 contains ESTs heterochromatin protein HP1Hs-gamma pseudogene, STS and CpG island.//2.4e-41:459:65//Z84488

F-NT2RP3000449//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018D12, WORKING DRAFT SEQUENCE.//1.1e-100:365:87//AL031650

30 F-NT2RP3000451//HS_2024_A1_E10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2024 Col=19 Row=I, genomic survey sequence.//0.011:367:57//AQ229420

F-NT2RP3000456//CIT-HSP-2338P5.TR CIT-HSP Homo sapiens genomic clone 2338P5, genomic survey sequence.//1.5e-89:458:96//AQ055548

F-NT2RP3000484//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 90L6, WORKING DRAFT SEQUENCE.//0.043:147:70//Z97353

35 F-NT2RP3000487//H.sapiens CpG island DNA genomic MseI fragment, clone 11b11, forward read cpg11b11.ft1a.//1.7e-11:96:92//Z64440

F-NT2RP3000512//Human HOX2G mRNA from the Hox2 locus.//9.7e-17:109:97//X16667

F-NT2RP3000526//Homo sapiens full-length insert cDNA clone YZ38E04.//4.1e-30:283:76//AF086071

F-NT2RP3000527//Human mRNA for KIAA0211 gene, complete cds.//2.5e-34:706:63//D86966

40 F-NT2RP3000531//Mus musculus immunosuperfamily protein B12 mRNA, complete cds.//1.9e-14:220:70//AF061260

F-NT2RP3000542//Human Chromosome 11p11.2 PAC clone pDJ404m15, complete sequence.//0.00019:361:60//AC002554

45 F-NT2RP3000561//Homo sapiens PAC clone DJ0942I16 from 7q11, complete sequence.//9.0e-171:827:98//AC006012

F-NT2RP3000562

F-NT2RP3000578//F.rubripes GSS sequence, clone 013G07cE7, genomic survey sequence.//1.7e-25:284:74//AL011271

50 F-NT2RP3000582//CIT978SK-A-56H4.TP CIT978SK Homo sapiens genomic clone A-56H4, genomic survey sequence.//5.8e-07:239:66//B73597

F-NT2RP3000584

F-NT2RP3000590//H.sapiens CpG island DNA genomic MseI fragment, clone 170d7, forward read cpg170d7.ft1a.//3.0e-22:128:100//Z59723

55 F-NT2RP3000592//CIT-HSP-2288J7.TR CIT-HSP Homo sapiens genomic clone 2288J7, genomic survey sequence.//2.2e-78:382:98//B98868

F-NT2RP3000598//H.sapiens GSS

sequence.//1.0e-76:43:67//AC109301

F-NT2RP3000599//Caenorhabditis elegans cosmid 1133, complete sequence.//2.0e-30:285:66//Z74704

F-NT2RP3000603//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//0.37:520:57//L14320

F-NT2RP3000605//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//8.8e-155:526:97//AC006128

5 F-NT2RP3000622//HS_3213_A2_D02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=4 Row=G, genomic survey sequence.//4.1e-29:238:85//AQ175104

F-NT2RP3000624//Homo sapiens clone DJ0800G07, complete sequence.//0.47:75:80//AC004890

F-NT2RP3000628//Human DNA sequence from clone 581F12 on chromosome Xq21. Contains Eukaryotic Translation Initiation Factor EIF3 P35 Subunit and 60S Ribosomal protein L22 pseudogenes. Contains ESTs, complete sequence.//0.078:393:58//AL031313

10 F-NT2RP3000632//Human zinc finger protein zfp6 (ZF6) mRNA, partial cds.//1.4e-96:541:79//U71363

F-NT2RP3000644//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//5.2e-46:421:77//AC005089

F-NT2RP3000661

15 F-NT2RP3000665//Human DNA sequence from clone 1191B2 on chromosome 22q13.2-13.3. Contains part of the BIK (NBK, BP4, BIP1) gene for BCL2-interacting killer (apoptosis-inducing), a 40S Ribosomal Protein S25 pseudogene and part of an alternatively spliced novel Acyl Transferase gene similar to *C. elegans* C50D2.7. Contains ESTs, STSs, GSSs, two putative CpG islands and genomic marker D22S1151, complete sequence.//1.7e-11:292:65//AL022237

20 F-NT2RP3000685//H.sapiens mRNA for novel protein.//2.4e-80:460:92//X99961

F-NT2RP3000690//H.sapiens flow-sorted chromosome 6 TaqI fragment, SC6pA10F6.//1.0:141:65//Z77872

F-NT2RP3000736//Human mRNA for KIAA0140 gene, complete cds.//6.1e-20:127:96//D50930

F-NT2RP3000739//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//1.1e-46:622:67//AF015264

25 F-NT2RP3000742//Rattus norvegicus phospholipase C delta-4 mRNA, complete cds.//4.7e-37:429:70//U16655

F-NT2RP3000753

F-NT2RP3000759//Caenorhabditis elegans cosmid Y57G11C, complete sequence.//2.8e-38:519:69//Z99281

F-NT2RP3000815//HS_2237_A2_D12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=24 Row=G, genomic survey sequence.//0.79:151:61//AQ067252

30 F-NT2RP3000825//Campanula ramosa chloroplast NADH dehydrogenase (ndhF) gene, complete cds.//0.36:378:58//L39387

F-NT2RP3000826//Suid herpesvirus 1 Kaplan glycoprotein L (UL1) and uracil-DNA glycosylase (UL2) genes, complete cds, and (UL3) gene, partial cds.//0.0025:291:62//U02513 F-NT2RP3000836//Mouse complement factor H-related protein mRNA, complete cds, clone 9C4.//0.69:563:57//M29009

35 F-NT2RP3000841//Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome 6 HindIII fragment ESTs. polymorphic CA repeat, CpG island, CpG island genomic fragments.//2.1e-46:666:68//Z86062

F-NT2RP3000845//Homo sapiens chromosome 19, cosmid R31237, complete sequence.//3.4e-92:193:93//AC005581

40 F-NT2RP3000847//Human HepG2 3' region cDNA, clone hmd5d02.//3.4e-32:261:81//D16938

F-NT2RP3000850//Homo sapiens clone RG271G13, WORKING DRAFT SEQUENCE, 7 unordered pieces.//5.1e-44:358:81//AC005082

F-NT2RP3000852//Homo sapiens DNA sequence from PAC 117P20 on chromosome 1q24. Contains the LNHR (SELL) gene coding for Lymph Node Homing Receptor (L-Selectin precursor, LAM-1 Leukocyte Adhesion Molecule, Leukocyte surface antigen Leu-8, TQ1, GP90-MEL, LECAM1 Leukocyte-Endothelial Cell Adhesion Molecule 1, CD62L). Contains the SELE gene coding for E-Selectin precursor (CD62E, ELAM-1 Endothelial Leukocyte Adhesion Molecule 1, LECAM-2 Leukocyte-Endothelial Cell Adhesion Molecule 2). Contains an unknown gene with homology to predicted yeast, plant and worm proteins. Contains ESTs and STSs, complete sequence.//4.4e-123:150:98//AL021940

50 F-NT2RP3000859//T19M2TF TAMU Arabidopsis thaliana genomic clone T19M2, genomic survey sequence.//0.016:185:65//B60831

F-NT2RP3000865

F-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.//2.0e-29:766:60//U53445

55 F-NT2RP3000869//H.sapiens gene for plectin.//1.1e-12:700:60//Z54367

F-NT2RP3000875//HS_2237_A2_D12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=24 Row=G, genomic survey sequence.//0.79:151:61//AQ067252

F-NT2RP3000876//Suid herpesvirus 1 glycoprotein L (UL1) and uracil-DNA glycosylase (UL2) genes, complete cds, and (UL3) gene, partial cds.//0.0025:291:62//U02513

F-NT2RP3000877//Suid herpesvirus 1 glycoprotein L (UL1) and uracil-DNA glycosylase (UL2) genes, complete cds, and (UL3) gene, partial cds.//0.0025:291:62//U02513

AF021340

F-NT2RP3000904//Rat Na⁺ channel mRNA, 3' end.//3.6e-106:505:99//M27223

F-NT2RP3000917//Mouse mRNA for Dhml protein, complete cds.//3.1e-132:691:93//D38517

F-NT2RP3000919//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//3.2e-97:585:88//AF015264

F-NT2RP3000968//Human Chromosome 16 BAC clone CIT987SK-A-234F9, complete sequence//5.8e-70:181:89//U91326

F-NT2RP3000980//R.norvegicus CYP3A1 gene, 5' flanking region.//6.1e-26:507:66//X98335

F-NT2RP3000994//HS-1049-B2-F03-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 771 Col=6 Row=L, genomic survey sequence.//1.5e-22:128:100//B39529

F-NT2RP3001004//H.sapiens CpG island DNA genomic MseI fragment, clone 39c1, reverse read cpg39c1.rt1a./15.9e-27:150:99//Z60925

F-NT2RP3001007//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.11:610:57//AC006039

F-NT2RP3001055//Drosophila melanogaster; Chromosome 2R; Region 47F1-47F7; P1 clone DS02304, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.8e-23:352:67//AC005653

F-NT2RP3001057//H.sapiens HZF4 mRNA for zinc finger protein.//1.4e-49:437:77//X78927

F-NT2RP3001081//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.//8.4e-50:534:74//AF060219

F-NT2RP3001084//Homo sapiens mRNA for KIAA0782 protein, partial cds.//1.2e-14:474:60//AB018325

F-NT2RP3001096//CIT-HSP-2305P8.TF CIT-HSP Homo sapiens genomic clone 2305P8, genomic survey sequence.//3.4e-37:222:93//AQ021278

F-NT2RP3001107//Human mRNA for KIAA0215 gene, complete cds.//8.5e-33:712:64//D86969

F-NT2RP3001109//Human Chromosome 15q26.1 PAC clone pDJ457j11 containing DNA polymerase gamma (polg) gene, complete sequence.//2.7e-116:186:99//AC005317

F-NT2RP3001111

F-NT2RP3001113//Human DNA sequence from cosmid U157D4, between markers DXS366 and DXS87 on chromosome X.//2.4e-05:702:58//Z68871

F-NT2RP3001115//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//1.9e-170:821:98//AC005189

F-NT2RP3001116//HS_3075_A1_F01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=1 Row=K, genomic survey sequence.//7.3e-49:290:92//AQ120581

F-NT2RP3001119//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//1.4e-121:598:97//AL031864

F-NT2RP3001120//Human zinc finger protein ZNF136.//7.4e-76:687:75//U09367

F-NT2RP3001126//Bovine herpesvirus type 1 DNA for UL36, UL37, UL38, UL39, UL40 and UL41.//6.8e-05:344:64//Z49078

F-NT2RP3001133//Nephila clavipes minor ampullate silk protein MiSp1 mRNA, partial cds.//0.00021:529:60//AF027735

F-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds.//3.6e-179:851:98//AB018305

F-NT2RP3001147//RPCI11-3M16.TP RPCI-11 Homo sapiens genomic clone RPCI-11-3M16, genomic survey sequence.//2.1e-15:106:96//B48859

F-NT2RP3001150//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE.//2.0e-159:418:95//AL034379

F-NT2RP3001155//Homo sapiens mRNA for AND-1 protein.//5.1e-190:891:98//AJ006266

F-NT2RP3001176//Human DNA sequence from clone 879K22 on chromosome 1q32.1-41 Contains GSS, complete sequence.//1.1e-69:207:97//AL034351

F-NT2RP3001214//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.16:475:58//AC005507

F-NT2RP3001216//Homo sapiens clone DJ0635O05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.3e-05:561:56//AC004845

F-NT2RP3001221

F-NT2RP3001232//Mouse mRNA for serine protease PC6, complete cds.//1.0e-11:120:87//D12619

F-NT2RP3001236

F-NT2RP3001239//Mouse MAP1B mRNA for MAP1B microtubule associated protein 1B.//1.2e-11:120:87//D12619
 F-NT2RP3001240//Human DNA sequence from clone 423B22, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.0e-159:418:95//AL034379

F-NT2RP3001253//CITBI-E1-2505N14. TR CITBI-E1 Homo sapiens genomic clone 2505N14, genomic survey sequence.//0.83:235:60//AQ260430

F-NT2RP3001260//Homo sapiens mRNA for KIAA0726 protein, complete cds.//3.8e-47:761:64//AB018269

F-NT2RP3001268//Homo sapiens zinc finger protein (HZF6) mRNA, 5' UTR and partial cds.//2.3e-64:618:72//AF027513

F-NT2R3001272//Mus musculus mRNA for macrophage actin-associated-tyrosine-phosphorylated protein//
2.6e-99:669:83/Y18101

F-NT2RP3001274//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds//0.99:400:58//U07561

F-NT2RP3001281//Homo sapiens chromosome 17, clone hRPK.318_A_15, complete sequence//5.9e-39:304:70//AC005837

F-NT2RP3001297//Human mRNA for KIAA0281 gene, complete cds.//7.6e-47:544:69//D87457

F-NT2RP3001307//Ambystoma tigrinum RPE65 protein mRNA, complete cds//2.4e-27:547:63//AF047465

F-NT2RP3001318//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.00022:624:60//AC004709

F-NT2RP3001325//Caenorhabditis elegans cosmid F36H12.//0.25:523:59//AF078790

F-NT2RP3001338//Human mRNA for KIAA0211 gene, complete cds.//5.1e-29:345:73/D86966

F-NT2RP3001339//Rattus norvegicus myotonic dystrophy kinase-related Cdc42-binding kinase (MRCK) mRNA, complete cds//1.2e-151:821:91//AF021935

F-NT2RP3001340//Homo sapiens HMG box factor SOX-13 mRNA, complete cds.//5.3e-27:247:81//AF083105

F-NT2RP3001355//Homo sapiens Chromosome 22q11.2 BAC Clone 77h2 In CES Region, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.1e-16:130:76//AC000052

F-NT2RP3001356

F-NT2RP30013/4

F-NT2R3P3001383//Homo sapiens DNA sequence from PAC 140C12 on chromosome 6q26-q27//0.00082:365:61//AL008628

F-NT2RP3001384//Homo sapiens HRIHFB2018 mRNA, partial cds//6.4e-157:743:98//AB015332

F-NT2RP3001392//Human DNA sequence from PAC 302D9 on chromosome 22q11.2-qter. Contains STS, complete sequence.//0.045:359:61//Z82198

F-NT2RNP3001396//Drosophila melanogaster DNA sequence (P1 DS08860 (D181)), complete sequence.//1.3e-16:336:65//AC004296

F-NT2RP3001398//Mus musculus zinc finger protein (Zfp64) mRNA, complete cds//3.1e-100:711:82//U49046

F-NT2RP3001399//Homo sapiens PAC clone DJ1106E03 from 7q31.3-7q3, complete sequence.//5.4e-20:245:73//AC005521

F-NT2RP3001407//RPCI11-41A20.TP RPCI-11 Homo sapiens genomic clone RPCI-11-41A20, genomic survey sequence.//0.051:306:59//AQ029031

F-NT2RP3001420//Human DNA sequence from PAC 12409 on chromosome 6q21. Contains DNAJ2 (HDJ1) like pseudogene, ESTs, STSs and GSSs.//0.90:170:65//AL021327

F-NT2RP3001426//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 126A5, WORKING DRAFT SEQUENCE.//2.9e-89:138:98//AL031447

F-NT2RP3001427//CIT-HSP-2302H24.TF CIT-HSP Homo sapiens genomic clone 2302H24, genomic survey sequence.//8.1e-36:212:94//AQ020997

F-NT2RP3001428//Human nuclear pore complex-associated protein TPR (tpr) mRNA, complete cds//8.5e-73:
431:91//U69668

F-NT2RP3001432//HS_3032_B1_A03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
nomic clone Plate=3032 Col=5 Row=B. genomic survey sequence //0.00024:111:76//AQ096619

F-NT2RP3001447

F-NT2RP3001449//Human DNA sequence from clone 283E3 on chromosome 1p36.21-36.33. Contains the alternatively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract MIFR1, -2, MMP21/22A, -B and -C, a novel gene, the alternatively spliced CDC2L2 gene for Cell Division Cycle 2-Like 2 (PITSLRE, p58/GTA, Galactosyltransferase Associated Protein Kinase) beta 1, beta 2-1, beta 2-2 and alpha 2-4, a 40S Ribosomal Protein S7 pseudogene, part of the KIAA0447 gene, a novel alternatively spliced gene similar to many (archae) bacterial, worm and yeast hypothetical genes, and the GNB1 gene for Guanine Nucleotide Binding Protein (G protein), Beta polypeptide 1 (Transducin Beta chain 1). Contains putative CpG islands, ESTs, STSs and GSSs, complete sequence.//2.1e-105:223:99//AL031282

[illegible]

F-NT2RP3001457

F-NT2RP3001459

F-NT2RP3001472//Homo sapiens Sox-like transcriptional factor mRNA, complete cds.//1.3e-08:168:70//AF072836

F-NT2RP3001490

F-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds.//1.0e-26:191:90//U13395

F-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds.//8.5e-171:804:98//AF064801

F-NT2RP3001527//Human lymphoid-specific SP100 homolog (LYSP100-A) mRNA, complete, cds.//8.9e-140:743:91//U36499

F-NT2RP3001529//Streptomyces griseus DNA for ribosoma protein L21, ribosomal protein L27, Obg, complete cds.//2.1e-14:517:59//D87916

F-NT2RP3001538//Capra hircus hircus clone 12 RAPD PCR sequence, genomic survey sequence.//4.7e-05:217:63//AF078176

F-NT2RP3001554//Rattus norvegicus microtubule-associated protein 1A MAP1A (Mtap-1) mRNA, complete cds.//4.3e-17:332:67//M83196

F-NT2RP3001580//RPC111 Homo sapiens genomic clone R-91E19, genomic survey sequence.//4.2e-15:110:91//AQ281332

F-NT2RP3001587//S.pombe chromosome II cosmid c16H5.//6.6e-28:491:64//AL022104

F-NT2RP3001589//RPC111-68M15.TK RPC111 Homo sapiens genomic clone R-68M15, genomic survey sequence.//8.7e-108:517:98//AQ237629

F-NT2RP3001607//Homo sapiens Xp22 BAC GSHB-600G8 (Genome Systems Human BAC library) complete sequence.//1.0e-09:257:65//AC004674

F-NT2RP3001608//Methylococcus capsulatus methane monooxygenase component A alpha chain, methane monooxygenase A beta chain and methane monooxygenase component C genes, complete cds.//0.59:450:57//M90050

F-NT2RP3001621//Human DNA sequence from clone 24o18 on chromosome 6p21.31-22.2 Contains zinc finger protein pseudogene, VNO-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST, STS, GSS, complete sequence.//1.8e-42:278:79//AL021808

F-NT2RP3001629

F-NT2RP3001634//Homo sapiens mRNA for Ariadne-2 protein.//1.5e-63:276:97//AJ130978

F-NT2RP3001642//Caenorhabditis elegans cosmid F45E6, complete sequence.//0.018:127:66//Z68117

F-NT2RP3001646

F-NT2RP3001671//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//3.4e-171:816:98//AJ012449

F-NT2RP3001672//Drosophila melanogaster transcriptional repressor protein (Scm) mRNA, complete cds.//1.6e-38:542:66//U49793

F-NT2RP3001676//HS_3090_B1_B04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3090 Col=7 Row=D, genomic survey sequence.//3.1e-07:333:64//AQ123250

F-NT2RP3001678//Drosophila melanogaster; Chromosome 3L; Region 63C5-63D3; P1 clone DS01859, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.0:539:57//AC004358

F-NT2RP3001679//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11.//2.8e-130:355:96//AB020860

F-NT2RP3001688//Rattus norvegicus glucocorticoid modulatory element binding protein 2 mRNA, complete cds.//2.1e-37:512:70//AF059273

F-NT2RP3001690//CIT-HSP-2300P9.TR CIT-HSP Homo sapiens genomic clone 2300P9, genomic survey sequence.//2.8e-19:123:95//AQ012480

F-NT2RP3001698//Rat mRNA for RhoGAP, complete cds.//9-4e-11:167:74//D31962

F-NT2RP3001708//H.sapiens CpG island DNA genomic MseI fragment, clone 4g7, reverse read cpg4g7.rt1d.//1.3e-17:113:97//Z61312

F-NT2RP3001712//M.musculus mRNA for HP1-BP74 protein.//2.2e-95:601:88//X99642

F-NT2RP3001716

F-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds.//1.4e-159:565:97//AF054177

F-NT2RP3001727//Rattus norvegicus implantation-associated protein (IAG2)-mRNA, partial cds.//1.7e-132:786:88//AF008554

F-NT2RP3001728//Homo sapiens mRNA for HSP70, complete cds.//1.1e-159:565:97//AF054177
 F-NT2RP3001729//Homo sapiens mRNA for HSP70, complete cds.//1.1e-159:565:97//AF054177
 F-NT2RP3001730//Homo sapiens mRNA for HSP70, complete cds.//1.1e-159:565:97//AF054177

F-NT2RP3001752//Human DNA sequence from clone 105D16 on chromosome Xp11.3-11.4 Contains pseudogene similar to laminin-binding protein, CA repeat, STS, complete sequence.//5.2e-31:311:77//AL031311

F-NT2RP3001753//Sequence 29 from patent US 5658882.//0.11:513:58//I62381

F-NT2RP3001764//Sequence 6 from Patent WO9706245.//6.4e-47:673:66//A59888

F-NT2RP3001777//Caenorhabditis elegans cosmid T10E10.//0.078:290:63//U39644

F-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds.//2.8e-151:710:98//AB007928

F-NT2RP3001792//Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds.//1.2e-26:213:85//U13262

F-NT2RP3001799//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 469D22, WORKING DRAFT SEQUENCE.//8.4e-51:168:95//AL031284

F-NT2RP3001819//S.glaucescens genes strU, strX, strV and strW for 5'-hydroxystreptomycin prduction and transport polypeptides.//0.084:526:58//X89010

F-NT2RP3001844//HS_3110_B1_E10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3110 Col=19 Row=J, genomic survey sequence.//1.5e-40:232:82//AQ140433

F-NT2RP3001854//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.14:452:58//AC005505

F-NT2RP3001855//Mus musculus homeobox protein PKNOX1 (Pknox1) mRNA, complete cds.//2.7e-39:575:67//AF061270

F-NT2RP3001857//M.musculus tex292 mRNA (5'region).//8.7e-07:106:81//X80434

F-NT2RP3001896

F-NT2RP3001898//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 163G9, WORKING DRAFT SEQUENCE.//0.094:456:60//AL008733

F-NT2RP3001915//Caenorhabditis elegans cosmid C12D8, complete sequence.//0.58:482:56//Z73969

F-NT2RP3001926//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE.//0.42:401:58//AL034557

F-NT2RP3001929//Homo sapiens chromosome 16, cosmid clone RT102 (LANL), complete sequence.//3.1e-28:263:77//AC004651

F-NT2RP3001931

F-NT2RP3001938//CIT-HSP-2165E8.TR CIT-HSP Homo sapiens genomic clone 2165E8, genomic survey sequence.//3.6e-24:182:91//B95475

F-NT2RP3001943//Homo sapiens mRNA for KIAA0675 protein, complete cds.//1.8e-165:815:96//AB014575

F-NT2RP3001944

F-NT2RP3001969//Homo sapiens chromosome 12p13.3 clone RPC111-350L7, WORKING DRAFT SEQUENCE, 72 unordered pieces.//4.8e-62:304:89//AC005844

F-NT2RP3001989//Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein (cg2), and CG7 (cg7) genes, complete cds.//8.2e-10:564:60//AF030694

F-NT2RP3002002//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.//2.5e-57:361:80//Z83822

F-NT2RP3002004//Sequence 3 from patent US 5798245.//1.6e-26:104:100//AR025386

F-NT2RP3002007//Human Chromosome 15q11-q13 PAC clone pDJ223c9 from the Prader-Willi/Angelman Syndrome region, complete sequence.//0.0053:633:58//AC004137

F-NT2RP3002014//Drosophila melanogaster DNA sequence (P1s DS07528 (D169) and DS06665 (D220)), complete sequence.//1.3e-32:334:68//AC004640

F-NT2RP3002033//H.sapiens DNA sequence.//0.012:214:63//Z22493

F-NT2RP3002045//Rat mRNA for alpha-c large chain of the protein complex AP-2 associated with clathrin.//8.7e-116:713:86//X53773

F-NT2RP3002054//Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.//1.6e-12:613:60//AL021841

F-NT2RP3002056//Human DNA sequence from PAC 358H7 on chromosome X.//0.17:566:59//Z77249

F-NT2RP3002057//Homo sapiens clone NH0084K19, WORKING DRAFT SEQUENCE, 30 unordered pieces.//3.3e-24:167:82//AC005682

F-NT2RP3002062

F-NT2RP3002063//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4.//0.24:508:58//AJ235272

F-NT2RP3002097

F-NT2RP3002097//Human DNA sequence from PAC 358H7 on chromosome X.//0.17:566:59//Z77249

F-NT2RP3002097//Homo sapiens XP22150 BAC GSHB-309P15 (Genome Systems Human BAC Library) cont

plete sequence.//9.6e-66:562:77//AC006210

F-NT2RP3002102//CIT-HSP-2307B10.TR CIT-HSP Homo sapiens genomic clone 2307B10, genomic survey sequence.//5.9e-16:214:74//AQ018040

F-NT2RP3002108

F-NT2RP3002142//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-319E8, complete sequence.//7.6e-29:414:68//AC004020

F-NT2RP3002146//Pseudomonas fluorescens polyketide synthase type I (pltB) and polyketide synthase type I (pltC) genes, complete cds.//0.96:434:60//AF003370

F-NT2RP3002147//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 329F2, WORKING DRAFT SEQUENCE.//1.3e-63:380:91//AL031710

F-NT2RP3002151//Human chromosome 16p13.1 BAC clone CIT987SK-551G9 complete sequence.//9.9e-60:315:80//U95742

F-NT2RP3002163

F-NT2RP3002165//M.musculus HCNBP mRNA.//1.4e-142:867:87//X68061

F-NT2RP3002166//Homo sapiens chromosome X, clone hCIT.200_L_4, complete sequence.//0.090:394:59//AC006121

F-NT2RP3002173//HS_3062_B1_G05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3062 Col=9 Row=N, genomic survey sequence.//3.3e-101:509:96//AQ193219

F-NT2RP3002181//Human DNA sequence from clone 24o18 on chromosome 6p21.31-22.2 Contains zinc finger protein pseudogene, VNO-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST, STS, GSS, complete sequence.//4.5e-106:432:84//AL021808

F-NT2RP3002244//Homo sapiens chromosome 19, cosmid R27377, complete sequence.//0.63:353:60//AC005321

F-NT2RP3002248//HS_3029_A1_D10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3029 Col=19 Row=G, genomic survey sequence.//3.5e-10:125:79//AQ094880

F-NT2RP3002255//Bovine herpesvirus type 1 immediate-early transcriptional control protein (BICP4) gene, 5' end.//5.6e-09:629:59//L14321

F-NT2RP3002273//cSRL-165E12-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-165E12, genomic survey sequence.//4.9e-35:366:74//B03004

F-NT2RP3002276//B.taurus mRNA for B15 subunit of NADH: ubiquinone oxidoreductase complex.//0.023:326:60//X64898

F-NT2RP3002303//Methanobacterium thermoautotrophicum from bases 172512 to 182957 (section 16 of 148) of the complete genome.//3.8e-12:643:57//AE000810

F-NT2RP3002304//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.6e-09:490:60//AC005504

F-NT2RP3002330//Human DNA sequence from cosmid L58b6, Huntington's Disease Region, chromosome 4p16.3, containing STS matches.//1.9e-93:572:88//Z49862

F-NT2RP3002343//HS_3010_A2_B08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3010 Col=16 Row=C, genomic survey sequence.//9.0e-75:373:97//AQ119068

F-NT2RP3002351//Human mRNA for NAD-dependent methylene tetrahydrofolate dehydrogenase cyclohydrolase (EC 1.5.1.15).//4.9e-64:588:75//X16396

F-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A) gene, alternatively spliced form.//1.3e-164:770:98//Y16355

F-NT2RP3002377//Homo sapiens mRNA for KIAA0788 protein, partial cds.//1.4e-190:911:98//AB018331

F-NT2RP3002399

F-NT2RP3002402//Rattus norvegicus mRNA for dipeptidyl peptidase III, complete cds.//7.2e-25:249:79//D89340

F-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds.//1.2e-138:649:99//AB014578

F-NT2RP3002484//CIT-HSP-367N3.TP.1 CIT-HSP Homo sapiens genomic clone 367N3, genomic survey sequence.//5.0e-18:115:96//B78927

F-NT2RP3002501//Caenorhabditis elegans cosmid K01C8, complete sequence.//0.00020:170:65//Z49068

F-NT2RP3002512//Homo sapiens clone 664 unknown mRNA, partial sequence.//1.6e-59:308:97//AF091088

F-NT2RP3002529//Human vacuolar protein sorting homolog h-vps45 mRNA, complete cds.//1.4e-144:763:93//U35246

F-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds.//1.8e-178:833:98//AB018272

F-NT2RP3002549//Homo sapiens clone DJ0098O22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.7e-123:72//AC004821

F-NT2RP3002556//Streptococcus pneumoniae serotype 4 strain 4/92, complete cds.//1.4e-138:649:99//AB014578

F-NT2RP3002587//Homo sapiens clone 164 M2, complete cds.//1.4e-138:649:99//AB014578

AC004617

F-NT2RP3002590//*Porphyra purpurea* chloroplast, complete genome.//0.88:284:60//U38804

F-NT2RP3002602//CIT978SK-A-441H11-2.TPB CIT978SK Homo sapiens genomic clone A-441H11, genomic survey sequence.//2.0e-22:140:95//B68331

5 F-NT2RP3002603

F-NT2RP3002628//*C.acetobutylicum* dnaJ and orfB genes.//2.0e-05:333:60//X69050

F-NT2RP3002631

F-NT2RP3002650//*Mus musculus* mRNA for cartilage-associated protein (CASP).//1.5e-20:641:62//AJ006469

F-NT2RP3002659//Bovine herpesvirus type 1 UL22-35 genes.//5.2e-05:621:59//Z78205

10 F-NT2RP3002660//Homo sapiens PAC clone DJ1006K12 from 7q31.2-q31, complete sequence.//0.98:453:57//AC004946

F-NT2RP3002663//Homo sapiens chromosome 19, cosmid F6697, complete sequence.//3.3e-22:407:67//AC006129

F-NT2RP3002671//*S.pombe* chromosome III cosmid c553.//1.0e-12:336:66//AL02370415 F-NT2RP3002682//*Caenorhabditis elegans* cosmid F17C11, complete sequence.//1.3e-21:448:64//Z72507

F-NT2RP3002687//CIT978SK-A-789B1.TP CIT978SK Homo sapiens genomic clone A-789B1, genomic survey sequence.//2.5e-25:173:91//B51656

F-NT2RP3002688//Mouse mRNA for kinesin-like protein (Kif1b), complete cds.//1.2e-73:728:74//D17577

20 F-NT2RP3002701//CITBI-E1-2507L14.TF CITBI-E1 Homo sapiens genomic clone 2507L14, genomic survey sequence.//0.0012:55:92//AQ263530

F-NT2RP3002713

F-NT2RP3002763//*Caenorhabditis elegans* cosmid T20F10, complete sequence.//0.98:209:63//Z81594

F-NT2RP3002770

25 F-NT2RP3002785//Homo sapiens laminin beta-4 chain precursor (LAMB4) mRNA, alternatively spliced short variant, partial cds.//0.78:515:57//AF029325

F-NT2RP3002799//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs, complete sequence.//1.9e-21:167:79//AL022718

30 F-NT2RP3002810//Homo sapiens chromosome 17, clone hRPK.215_E_13, complete sequence.//0.32:187:66//AC005549

F-NT2RP3002818//Homo sapiens jerky gene product homolog mRNA, complete cds.//6.9e-54:615:70//AF004715

F-NT2RP3002861//*Caenorhabditis elegans* cosmid M03F4.//4.2e-05:226:65//U64601F-NT2RP3002869//*Mus musculus* semaphorin VIa mRNA, complete cds.//2.0e-93:638:83//AF030430

35 F-NT2RP3002876//Homo sapiens mRNA for B120, complete cds.//8.5e-89:557:88//AB001895

F-NT2RP3002877//Homo sapiens chromosome 12p13.3 clone RPCI11-433J6, WORKING DRAFT SEQUENCE, 100 unordered pieces.//7.9e-12:160:78//AC006087

F-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds.//5.7e-180:853:98//AB018314

40 F-NT2RP3002911//RPCI11-24N15.TPC RPCI-11 Homo sapiens genomic clone RPCI-11-24N15, genomic survey sequence.//2.3e-13:442:61//B88815

F-NT2RP3002948//, complete sequence.//2.2e-110:637:91//AC005500

F-NT2RP3002953//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//1.7e-166:793:98//AC005754

F-NT2RP3002955//Human HepG2 partial cDNA, clone hmd3c02m5.//0.00011:61:95//D17024

45 F-NT2RP3002969//Rat mRNA for brain acyl-CoA synthetase II, complete cds.//1.2e-128:808:85//D30666

F-NT2RP3002972//H.sapiens (xs168) mRNA, 381bp.//1.5e-43:312:85//Z36820

F-NT2RP3002978//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00044:527:57//AC005505

F-NT2RP3002985//Genomic sequence from Human 9q34, complete sequence.//0.92:341:60//AC001644

50 F-NT2RP3002988//HS_3015_A1_B07_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3015 Col=13 Row=C, genomic survey sequence.//4.4e-05:379:58//AQ091708

F-NT2RP3003008//*Mus musculus* major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes.//1.4e-72:197:79//AF10990555 F-NT2RP3003032//*Plasmodium falciparum* DNA *** SEQUENCING IN PROGRESS *** from contig 3-80, complete sequence.//1.6e-08:809:58//AF109905

F-NT2RP3003032//*Plasmodium falciparum* DNA *** SEQUENCING IN PROGRESS *** from contig 3-80, complete sequence.//1.6e-08:809:58//AF109905
 F-NT2RP3003032//*Plasmodium falciparum* DNA *** SEQUENCING IN PROGRESS *** from contig 3-80, complete sequence.//1.6e-08:809:58//AF109905

F-NT2RP3003061//Human mRNA for ankyrin (variant 2.1)//1.4e-12:633:59//X16609
 F-NT2RP3003068//Human BAC clone RG264L19 from 7p15-p21, complete sequence//0.034:282:60//AC002410
 F-NT2RP3003071//H.sapiens CpG island DNA genomic MseI fragment, clone 13d12, reverse read
 cpg13d12.r1c.//6.8e-15:95:100//Z64565
 5 F-NT2RP3003078
 F-NT2RP3003101//Mouse mRNA for tetracycline transporter-like protein, complete cds//8.1e-72:732:71//D88315
 F-NT2RP3003121
 F-NT2RP3003133//Homo sapiens chromosome 19, cosmid R30385, complete sequence//3.5e-12:168:76//
 AC004510
 10 F-NT2RP3003138//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds//4.0e-148:908:87//
 D12646
 F-NT2RP3003139//Rattus norvegicus kappa opioid receptor gene, exon 4 and complete cds//2.0e-31:658:63//
 U17995
 F-NT2RP3003145//Mus musculus carboxypeptidase X2 mRNA, complete cds//3.5e-22:430:63//AF017639
 15 F-NT2RP3003150
 F-NT2RP3003157//HS_3055_B1_G05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3055 Col=9 Row=N, genomic survey sequence//1.9e-92:493:94//AQ155489
 F-NT2RP3003185//Rattus norvegicus brain-enriched guanylate kinase-associated protein 1 mRNA, complete
 cds//8.6e-06:228:65//AF064868
 20 F-NT2RP3003193//H.sapiens HZF10 mRNA for zinc finger protein//7.4e-73:737:71//X78933
 F-NT2RP3003197
 F-NT2RP3003203//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds//
 4.1e-48:640:67//AF015264
 F-NT2RP3003204//Human Mermaid LINE-1 element mRNA sequence//0.0033:69:81//U31059
 25 F-NT2RP3003210//Homo sapiens SYBL1 gene//1.1e-34:430:70//AJ004799
 F-NT2RP3003212//Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds//6.3e-75:
 776:74//U20286
 F-NT2RP3003230//Rattus norvegicus mRNA for coronin-like protein//1.8e-62:575:74//AJ006064
 F-NT2RP3003242//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds//3.7e-128:617:98//AF055460
 30 F-NT2RP3003251//H.sapiens Staf50 mRNA//3.5e-67:651:76//X82200
 F-NT2RP3003264//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING
 DRAFT SEQUENCE, 8 unordered pieces//0.015:473:58//AC004153
 F-NT2RP3003278//H.sapiens CpG island DNA genomic MseI fragment, clone 28b4, forward read cpg28b4.ft1a.//
 4.0e-27:174:93//Z60555
 35 F-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds//1.3e-131:694:93//L36983
 F-NT2RP3003290//Homo sapiens nickel-specific induction protein (Cap43) mRNA, complete cds//1.7e-64:662:
 71//AF004162
 F-NT2RP3003301//Spinacia oleracea mRNA for ATP-dependent protease Lon, complete cds//4.9e-37:682:64//
 D85610
 40 F-NT2RP3003302//Homo sapiens, clone hRPK.15_A_1, complete sequence//4.6e-95:680:82//AC006213
 F-NT2RP3003311//Homo sapiens chromosome 21, Neurofibromatosis 1 (NF1) related locus, complete se-
 quence//1.0:191:62//AC004527
 F-NT2RP3003313//Streptomyces coelicolor cosmid 5A7//0.0084:403:61//AL031107
 F-NT2RP3003327//H.sapiens Staf50 mRNA//2.5e-29:253:67//X82200
 45 F-NT2RP3003330
 F-NT2RP3003344
 F-NT2RP3003346//Homo sapiens chromosome 17, clone hRPK.795_F_17, complete sequence//9.0e-41:296:
 84//AC005284
 F-NT2RP3003353//Human DNA sequence from PAC 970D1 on chromosome 1q24. Contains ESTs, STSs and a
 BAC end-sequence (GSS)//0.047:404:60//AL021069
 50 F-NT2RP3003377//Homo sapiens clone DJ0919J22, WORKING DRAFT SEQUENCE, 34 unordered pieces//
 8.3e-122:632:96//AC005519
 F-NT2RP3003384//Homo sapiens Chromosome 2 BAC Clone 376a1, WORKING DRAFT SEQUENCE, 17 unor-
 dered pieces//0.0036:127:74//AC000360
 55 F-NT2RP3003385//Mus musculus SKD3 mRNA, complete cds//2.0e-110:843:79//U09874
 F-NT2RP3003403//Human Chromosome X, complete sequence//7.5e-21:647:61//AC002410

F-NT2RP3003411//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//4.2e-139:524:90//AF071317

F-NT2RP3003427//HS-1051-A1-D03-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 773 Col=5 Row=G, genomic survey sequence.//8.8e-18:111:97//B40173

5 F-NT2RP3003433//HS_2219_B2_A11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2219 Col=22 Row=B, genomic survey sequence.//1.2e-57:410:83//AQ145866

F-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//5.2e-181:853:98//AF004828

F-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds.//1.6e-173:826:98//AB018268

10 F-NT2RP3003491//CIT-HSP-2344O1.TR CIT-HSP Homo sapiens genomic clone 2344O1, genomic survey sequence.//1.2e-39:213:97//AQ057124

F-NT2RP3003500//HS_3000_B1_C07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3000 Col=13 Row=F, genomic survey sequence.//0.025:253:60//AQ090347

15 F-NT2RP3003543//Homo sapiens chromosome 16, cosmid clone 399H11 (LANL), complete sequence.//0.95:279:60//AC004234

F-NT2RP3003552//Homo sapiens clone UWGC:y54c222 from 6p21, complete sequence.//1.8e-88:166:84//AC006049

F-NT2RP3003555//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 228H13, WORKING DRAFT SEQUENCE.//8.9e-17:245:72//AL031985

20 F-NT2RP3003564//HS_3141_B1_G10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3141 Col=19 Row=N, genomic survey sequence.//2.7e-79:442:93//AQ187798

F-NT2RP3003572

F-NT2RP3003576//Homo sapiens clone RG031N19, WORKING DRAFT SEQUENCE, 1 unordered pieces.//5.8e-55:275:84//AC005632

25 F-NT2RP3003589//Canine rab10 mRNA for ras-related GTP-binding protein.//1.1e-94:488:95//X56387

F-NT2RP3003621//Homo sapiens chromosome 16, cosmid clone 432A1 (LANL), complete sequence.//6.0e-88:463:84//AC004235

F-NT2RP3003625//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 390E6, WORKING DRAFT SEQUENCE.//0.98:307:60//AL031600

30 F-NT2RP3003656

F-NT2RP3003659//F.rubripes GSS sequence, clone 013G07cE7, genomic survey sequence.//1.7e-25:284:74//AL011271

F-NT2RP3003665//Homo sapiens chromosome 9q34, clone 63G10, complete sequence.//0.011:279:65//AC002096

35 F-NT2RP3003672

F-NT2RP3003680//Drosophila melanogaster; Chromosome 2R; Region 39B1-39B3; P1 clone DS05527, WORKING DRAFT SEQUENCE, 9 unordered pieces.//3.4e-16:425:64//AC005811

F-NT2RP3003686//HS_3064_B2_A04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, genomic survey sequence.//3.1e-27:153:98//AQ136993

40 F-NT2RP3003701

F-NT2RP3003716//Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds.//4.6e-107:788:82//U42975

F-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds.//2.3e-148:700:98//AB018300

45 F-NT2RP3003746//CIT-HSP-2306A10.TF CIT-HSP Homo sapiens genomic clone 2306A10, genomic survey sequence.//0.39:212:61//AQ015785

F-NT2RP3003795//Human DNA sequence from clone 333H23 on chromosome 22q12.1-12.3. Contains the (possibly alternatively spliced) RPL3 gene for 60S Ribosomal Protein L3 and the threefold alternatively spliced gene for Synaptogyrin 1A, 1B and 1C (SYNGR1A, SYBGR1B, SYNGR1C), both genes downstream of a putative CpG island. Contains ESTs, an STS, GSSs, genomic marker D22S1155 and a ca repeat polymorphism, complete sequence.//4.2e-21:445:66//AL022326

50 F-NT2RP3003799//Homo sapiens DNA from chromosome 19-cosmids R31158, R31874, and R28125, genomic sequence, complete sequence.//1.0:257:63//AF038458

F-NT2RP3003800//Mouse neuronal proto-oncogene c-src mRNA encoding tyrosine-specific protein kinase, complete cds.//1.2e-63:484:81//M17031

55 F-NT2RP3003805//Homo sapiens chromosome 19, cosmid R27377, complete sequence.//0.96:353:60//AC005321

F-NT2RP3003806//Homo sapiens chromosome 19, cosmid R27377, complete sequence.//0.96:353:60//AC005321
F-NT2RP3003807//Homo sapiens chromosome 19, cosmid R27377, complete sequence.//0.96:353:60//AC005321

F-NT2RP3003825

F-NT2RP3003828//Human rRNA primary transcript internal transcribed spacer 2 (ITS2)//6.2e-16:543:62//X17626

F-NT2RP3003831//RPC111-50N15.TJ RPC111 Homo sapiens genomic clone R-50N15, genomic survey sequence//1.1e-21:174:85//AQ082633

5 F-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence//8.0e-47:242:98//AF070611

F-NT2RP3003842//RPC111-44E5.TJ RPC111 Homo sapiens genomic clone R-44E5, genomic survey sequence//9.7e-25:143:97//AQ195884

F-NT2RP3003846//Homo sapiens mRNA for KIAA0725 protein, partial cds//4.2e-36:335:68//AB018268

F-NT2RP3003870//Homo sapiens mRNA for KIAA0800 protein, complete cds//4.1e-174:805:99//AB018343

10 F-NT2RP3003876//Rattus norvegicus Rabin3 mRNA, complete cds//2.7e-109:709:84//U19181

F-NT2RP3003914//Drosophila melanogaster UDP-glucose:glycoprotein glucosyltransferase mRNA, complete cds//8.9e-11:193:70//U20554

F-NT2RP3003918//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds//2.6e-47:404:77//AF057358

15 F-NT2RP3003932//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces//0.68:597:55//AC005504

F-NT2RP3003989//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 404H4, WORKING DRAFT SEQUENCE//0.37:548:56//AL031661

F-NT2RP3003992//Human cGMP-gated cation channel beta subunit (CNCG2) mRNA, complete cds//0.021:433:58//U58837

20 F-NT2RP3004013//M.musculus Spnr mRNA for RNA binding protein//1.4e-164:838:94//X84692

F-NT2RP3004016//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018K9, WORKING DRAFT SEQUENCE//0.00042:356:62//AL031726

F-NT2RP3004041//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 809F4, WORKING DRAFT SEQUENCE//6.8e-112:627:82//AL022400

25 F-NT2RP3004051//Human mRNA for KIAA0319 gene, complete cds//2.2e-61:774:67//AB002317

F-NT2RP3004070//Homo sapiens DNA sequence from PAC 352A20 on chromosome 6q24.1-25.1. Contains a pseudogene similar to yeast, bacterial, worm and slime mold hypothetical genes, and a gene coding for an aldehyde dehydrogenase family protein. Contains ESTs, STSs and GSSs, complete sequence//7.9e-17:484:62//AL021939

30 F-NT2RP3004078//M.musculus (BALB/c) MRFX2 mRNA//1.9e-102:684:83//X76089

F-NT2RP3004093//F24P17-Sp6 IGF Arabidopsis thaliana genomic clone F24P17, genomic survey sequence//0.021:207:63//B09433

F-NT2RP3004095//Homo sapiens clone NH0486122, WORKING DRAFT SEQUENCE, 5 unordered pieces//3.5e-25:272:77//AC005038

35 F-NT2RP3004110//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence//8.6e-28:223:73//AC003973

F-NT2RP3004125//Homo sapiens TTF-I interacting peptide 20 mRNA, partial cds//2.2e-28:637:63//AF000560

F-NT2RP3004145

F-NT2RP3004148

40 F-NT2RP3004155//Homo sapiens timing protein CLK-1 mRNA, complete cds//6.5e-120:578:98//AF032900

F-NT2RP3004189//M.musculus tex292 mRNA (5'region)//1.1e-06:102:82//X80434

F-NT2RP3004206//D.melanogaster cm mRNA//7.3e-69:715:71//X58374

F-NT2RP3004207//Mouse mRNA for seizure-related gene product 6 type 2 precursor, complete cds//4.8e-42:650:66//D64009

45 F-NT2RP3004209//Human cosmid Q7A10 (D21S246) insert DNA, complete sequence//8.4e-55:184:84//D42052

F-NT2RP3004215//Homo sapiens chromosome 5, Pac clone 9c13 (LBNL H127), complete sequence//0.22:458:60//AC006084

F-NT2RP3004242//Caenorhabditis elegans cosmid ZK632, complete sequence//1.6e-29:409:69//Z22181

F-NT2RP3004246//Homo sapiens chromosome 10 clone CIT987SK-1010K1 map 10q25, complete sequence//3.6e-117:242:100//AC005385

50 F-NT2RP3004253//H.sapiens 28S rRNA V8 region (LAN5-6)//2.6e-12:589:59//X69353

F-NT2RP3004258//Rattus norvegicus Zis mRNA, complete cds//1.2e-88:489:91//AF013967

F-NT2RP3004262//Homo sapiens heat shock protein hsp40-3 mRNA, complete cds//3.1e-153:733:98//AF088982

F-NT2RP3004282//Homo sapiens torsinA (DYT1) mRNA, complete cds//1.3e-24:597:61//AF007871

55 F-NT2RP3004332

F-NT2RP3004334//Human DNA sequence from chromosome 6p22.1, contains a pseudogene, complete sequence//1.4e-98:66//Z93021

F-NT2RP3004348//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//1.4e-103:600:82//X67877
 F-NT2RP3004349//Homo sapiens Xp22 BAC GS-321G17 (Genome Systems Human BAC library) complete sequence.//5.1e-49:480:75//AC004025
 F-NT2RP3004378//Drosophila melanogaster; Chromosome 2R; Region 47F1-47F7; P1 clone DS02304, WORK-
 5 ING DRAFT SEQUENCE, 5 unordered pieces.//1.8e-23:352:67//AC005653
 F-NT2RP3004399//H.sapiens mRNA for leucine-rich primary response protein 1.//7.2e-140:804:90//X97249
 F-NT2RP3004424//Mus musculus mRNA for nuclear protein SA3.//6.8e-53:413:81//AJ005678
 F-NT2RP3004428//Salmo salar DNA for a cryptic repeat.//3.2e-07:270:63//AJ012206
 F-NT2RP3004451//RPCI11-51J15.TK RPCI11 Homo sapiens genomic clone R-51J15, genomic survey se-
 10 quence.//8.8e-19:180:82//AQ052326
 F-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds.//6.2e-123:583:99//AB007917
 F-NT2RP3004466//HS_3038_B2_F08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3038 Col=16 Row=L, genomic survey sequence.//0.41:172:59//AQ102458
 F-NT2RP3004470//H.sapiens CpG island DNA genomic MseI fragment, clone 81a11, reverse read
 15 cpg81a11.r11a.//7.0e-25:148:96//Z56029
 F-NT2RP3004472//RPCI11-42M5.TJ RPCI11 Homo sapiens genomic clone R-42M5, genomic survey sequence.//
 1.6e-20:143:92//AQ052792
 F-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds.//3.0e-150:715:98//AB007925
 F-NT2RP3004480//Mus musculus maternal-embryonic 3 (Mem3) mRNA, complete cds.//1.0e-119:679:90//
 20 U47024
 F-NT2RP3004490//Homo sapiens mRNA for Musashi, complete cds.//7.1e-155:752:97//AB012851
 F-NT2RP3004498//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//
 4.0e-67:265:84//AC006023
 F-NT2RP3004503//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library)
 25 complete sequence.//1.2e-55:415:78//AC004673
 F-NT2RP3004504//M.musculus mRNA for CPEB protein.//2.0e-110:618:91//Y08260
 F-NT2RP3004507//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//9.3e-46:433:76//
 AC005328
 F-NT2RP3004527//Homo sapiens mRNA; transcriptional unit N144, 5' end.//1.1e-100:508:97//AJ002574
 30 F-NT2RP3004534//Mouse oncogene (ect2) mRNA, complete cds.//2.0e-93:442:84//L11316
 F-NT2RP3004539//Homo sapiens mRNA for KIAA0632 protein, partial cds.//8.5e-145:679:98//AB014532
 F-NT2RP3004544//Homo sapiens mRNA for KIAA0554 protein, partial cds.//2.8e-169:793:98//AB011126
 F-NT2RP3004566//Mus musculus kruppel-related zinc finger protein (Emzf1) mRNA, complete cds.//6.9e-18:433:
 64//AF031955
 35 F-NT2RP3004569//CITBI-E1-2522H6.TF CITBI-E1 Homo sapiens genomic clone 2522H6, genomic survey se-
 quence.//5.3e-15:138:84//AQ280780
 F-NT2RP3004572//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete cds.//1.0e-179:860:97//
 AF026445
 F-NT2RP3004578//Homo sapiens mRNA for KIAA0477 protein, complete cds.//4.2e-150:711:98//AB007946
 40 F-NT2RP3004594//Homo sapiens mRNA for AND-1 protein.//1.1e-158:796:95//AJ006266
 F-NT2RP3004617//Homo sapiens clone DJ1152C17, WORKING DRAFT SEQUENCE, 1 unordered pieces.//9.3e-
 14:360:65//AC004977
 F-NT2RP3004618//Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds.//2.9e-52:539:
 73//AF005355
 45 F-NT2RP3004669//Bm-3a=class V POU transcription factor [mice, CD/CD, embryo fibroblast cells, Genomic, 2160
 nt].//0.046:437:57//S69350
 F-NT2RP3004670//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 356B8, WORKING
 DRAFT SEQUENCE.//1.9e-05:625:59//Z98882
 F-NT2RP4000008//Homo sapiens chromosome X, clone hCIT.200_L_4, complete sequence.//1.5e-155:844:92//
 50 AC006121
 F-NT2RP4000023//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24G6, complete sequence.//
 0.012:417:59//AB012242
 F-NT2RP4000035//Homo sapiens BAC clone NH0353P23 from 2, complete sequence.//8.0e-18:242:74//
 AC005035
 55 F-NT2RP4000049//Homo sapiens decoy receptor 2 mRNA, complete cds.//2.1e-81:556:85//AF029761
 F-NT2RP4000051//Mus musculus mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000052//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000053//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000054//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000055//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000056//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000057//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000058//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000059//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000060//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000061//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000062//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000063//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000064//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000065//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000066//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000067//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000068//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000069//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000070//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000071//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000072//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000073//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000074//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000075//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000076//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000077//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000078//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000079//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000080//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000081//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000082//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000083//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000084//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000085//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000086//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000087//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000088//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000089//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000090//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000091//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000092//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000093//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000094//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000095//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000096//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000097//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000098//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000099//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444
 F-NT2RP4000100//Homo sapiens mRNA for cartilage associated protein CASP.//1.6e-19:654:63//AF011444

F-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds.//4.4e-166:774:99//AB011538
 F-NT2RP4000111//B.taurus mRNA for cleavage and polyadenylation specificity factor.//2.6e-137:678:91//X75931
 F-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds.//3.3e-114:548:98//AB007952
 5 F-NT2RP4000147//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//1.2e-104:677:85//U35776
 F-NT2RP4000150//Rat proto-oncogene (Ets-1) mRNA, complete cds.//7.2e-54:327:74//L20681
 F-NT2RP4000151//Homo sapiens clone 664 unknown mRNA, partial sequence.//2.2e-62:360:92//AF091088
 F-NT2RP4000159//RPC111-75N16.TJ RPC111 Homo sapiens genomic clone R-75N16, genomic survey sequence.//2.6e-19:119:98//AQ267551
 10 F-NT2RP4000167//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//3.3e-49:683:67//AC006210
 F-NT2RP4000185//Homo sapiens clone DT1P1E11 mRNA, CAG repeat region.//1.1e-99:543:93//U92989
 F-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds.//4.9e-174:825:98//AB014600
 F-NT2RP4000212//, complete sequence.//4.0e-131:233:94//AC005300
 15 F-NT2RP4000214//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//1.8e-161:751:99//AC005261
 F-NT2RP4000218//RPC111-69B7.TJ RPC111 Homo sapiens genomic clone R-69B7, genomic survey sequence.//1.7e-84:413:98//AQ268504
 F-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP).//2.6e-156:771:97//AJ006470
 20 F-NT2RP4000246//Mus musculus neural variant mena+++ protein (Mena) mRNA, complete cds.//2.1e-120:707:87//U72523
 F-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence.//2.8e-128:604:99//AF091092
 F-NT2RP4000263//CIT-HSP-2336N24.TF CIT-HSP Homo sapiens genomic clone 2336N24, genomic survey sequence.//0.27:124:69//AQ043515
 25 F-NT2RP4000290//S.cerevisiae chromosome XIV reading frame ORF YNL132w.//8.6e-32:619:63//Z71408
 F-NT2RP4000312//Human mRNA for KIAA0147 gene, partial cds.//4.7e-41:685:63//D63481
 F-NT2RP4000321//Mus musculus transcription factor HOXA13 (Hoxa13) gene, complete cds.//6.9e-05:756:59//U59322
 F-NT2RP4000323
 30 F-NT2RP4000355
 F-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds.//2.0e-140:654:99//AB018281
 F-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//2.6e-135:649:97//AF044195
 F-NT2RP4000370//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4.//2.0e-23:524:62//AJ235272
 35 F-NT2RP4000376//Sequence 1 from patent US 5580968.//1.6e-115:716:87//I30536
 F-NT2RP4000381//Mus musculus mRNA for hepatoma-derived growth factor, complete cds, strain:BALB/c.//4.3e-05:450:58//D63850
 F-NT2RP4000398//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//9.2e-37:336:69//AC006116
 40 F-NT2RP4000415//Caenorhabditis elegans cosmid C42D8.//0.30:222:60//U56966
 F-NT2RP4000417//Drosophila melanogaster cosmid clone 86E4.//1.8e-48:580:69//AL021086
 F-NT2RP4000424//Homo sapiens chromosome 17, clone HRPC41C23, complete sequence.//1.6e-42:265:81//AC003101
 45 F-NT2RP4000448//CIT-HSP-2370F8.TF CIT-HSP Homo sapiens genomic clone 2370F8, genomic survey sequence.//2.0e-56:287:98//AQ110194
 F-NT2RP4000449//CIT-HSP-2366N18.TR CIT-HSP Homo sapiens genomic clone 2366N18, genomic survey sequence.//2.4e-42:236:95//AQ076183
 F-NT2RP4000455//Homo sapiens PAC clone 166H1 from 12q, complete sequence.//0.17:158:67//AC003982
 50 F-NT2RP4000457//H.sapiens mRNA for herpesvirus associated ubiquitin-specific protease (HAUSP).//0.00034:532:57//Z72499
 F-NT2RP4000480//Rhodothermus marinus R-21 DNA ligase gene, complete cds.//0.0094:616:58//U10483
 F-NT2RP4000481
 F-NT2RP4000498//S.cerevisiae chromosome IX cosmid 9150.//5.7e-24:633:60//Z38125
 55 F-NT2RP4000500//G.gallus mRNA for LRP/alpha-2-macroglobulin receptor.//2.4e-62:667:73//X74904
 F-NT2RP4000515

- F-NT2RP4000518//Homo sapiens mRNA for ATP-dependent RNA helicase, partial//6.7e-33:203:93//AJ010840
 F-NT2RP4000519//Mus musculus tyrosine kinase growth factor receptor (Etk2/tyro3) gene, alternative 5' coding exon 2C//0.26:162:61//U23720
- 5 F-NT2RP4000524//Rattus norvegicus rsec8 mRNA, partial cds//1.2e-139:809:89//U32498
 F-NT2RP4000528//Caenorhabditis elegans cosmid F59E12//1.0e-06:404:59//AF003386
 F-NT2RP4000541//Drosophila melanogaster DNA sequence (P1 DS02109 (D53)), complete sequence//1.3e-05:498:58//AC002443
- 10 F-NT2RP4000556//Sequence 1 from Patent EP 0285405//1.2e-18:586:61//I05465
 F-NT2RP4000560//Murine genomic DNA; partially digested Sau3A fragment, cloned into cosmid vector pEMBLcos2, complete sequence//2.5e-53:183:82//AF059580
 F-NT2RP4000588//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 414D7, WORKING DRAFT SEQUENCE//0.00062:253:65//AL033543
- 15 F-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds//3.2e-138:666:98//AF067730
 F-NT2RP4000638//HS_3042_B2_D05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3042 Col=10 Row=H, genomic survey sequence//3.0e-06:78:89//AQ099333
 F-NT2RP4000648//Homo sapiens KNSL4 and MAZ genes for kinesin-like DNA binding protein and Myc-associated zinc finger protein, complete cds//1.9e-11:104:85//AB017335
- 20 F-NT2RP4000657//Mus musculus bone morphogenetic factor 11 (Bmp11) gene, exon 1//0.34:350:62//AF100904
 F-NT2RP4000704//Homo sapiens mRNA expressed in 19week fetal lung, clone IMAGE:300856//3.3e-167:785:99//AB004852
 F-NT2RP4000713//Gallus gallus atonal homolog 1 (Cath1) gene, complete cds//3.7e-07:261:65//U61149
 F-NT2RP4000724//Human endogenous retrovirus env mRNA//9.2e-136:474:89//X82272
- 25 F-NT2RP4000728//Homo sapiens mRNA for KIAA0606 protein, partial cds//3.1e-41:350:71//AB011178
 F-NT2RP4000737//Myxococcus xanthus ATP-dependent protease (bsgA) gene, complete cds//1.0:504:58//L19301
 F-NT2RP4000739//CIT-HSP-2010O22.TR CIT-HSP Homo sapiens genomic clone 2010O22, genomic survey sequence//1.1e-24:161:93//B57903
- 30 F-NT2RP4000781//Homo sapiens clone DJ0892G19, complete sequence//0.052:493:58//AC004917
 F-NT2RP4000787//Cricetulus griseus SRD-2 mutant sterol regulatory element binding protein-2 (SREBP-2) mRNA, complete cds//9.6e-18:259:68//U22818
 F-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds//1.5e-174:816:98//AB007939
 F-NT2RP4000833//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence//0.97:52:92//AC005189
- 35 F-NT2RP4000837//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1112F19, WORKING DRAFT SEQUENCE//2.1e-128:644:97//AL034420
 F-NT2RP4000839//RPCI11-6D8.TP RPCI-11 Homo sapiens genomic clone RPCI-11-6D8, genomic survey sequence//1.5e-44:281:91//B48216
 F-NT2RP4000855//Rattus norvegicus mRNA for aminopeptidase-B, complete cds//9.5e-43:722:64//D87515
- 40 F-NT2RP4000865//Human zinc finger protein ZNF136//6.8e-95:415:78//U09367
 F-NT2RP4000878//Mus musculus mRNA for myeloid associated differentiation protein//7.0e-87:646:80//AJ001616
 F-NT2RP4000879//N.tabaccum mRNA for ubiquitin activating enzyme E1//9.0e-17:806:58//Y10804
- 45 F-NT2RP4000907//Mouse NLRR-1 mRNA for leucine-rich-repeat protein, complete cds//6.8e-153:934:86//D45913
 F-NT2RP4000915//Homo sapiens mRNA for ZNF198 protein//9.4e-79:584:78//AJ224901
 F-NT2RP4000918//Drosophila melanogaster DNA sequence (P1 DS04106 (D172)), complete sequence//2.0e-08:609:58//AC004290
- 50 F-NT2RP4000925//Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds//3.5e-64:415:87//U42975
 F-NT2RP4000927//H.sapiens genomic DNA (chromosome 3; clone NRL062R)//0.75:175:62//X87547
 F-NT2RP4000928//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds//3.5e-163:781:97//AF069532
- 55 F-NT2RP4000929//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence WORKING DRAFT SEQUENCE, 4 unordered pieces//0.94:763:56//AC004688
 F-NT2RP4000958//Homo sapiens DNA sequence (P1 DS04106 (D172)), complete sequence//2.0e-08:609:58//AC004290
 F-NT2RP4000959//Caenorhabditis elegans cosmid F59E12//1.0e-06:404:59//AF003386

F-NT2RP4000975//CIT-HSP-230716.TF CIT-HSP Homo sapiens genomic clone 230716, genomic survey sequence.//6.5e-31:317:79//AQ015742

F-NT2RP4000979//Human bullous pemphigoid antigen mRNA, 3' end.//0.88:54:90//M22942

F-NT2RP4000984//Rhodobacter sphaeroides mRNA.//0.76:214:64//M83823

5 F-NT2RP4000989//F.rubripes GSS sequence, clone 011A11aE12, genomic survey sequence.//1.0:149:65//AL010911

F-NT2RP4000996//Penaeus setiferus microsatellite Pse017 repeat region.//3.3e-08:139:74//AF047358

F-NT2RP4000997//Rattus norvegicus RNA polymerase I 127 kDa subunit mRNA, complete cds.//3.6e-126:824:84//AF025424

10 F-NT2RP4001004

F-NT2RP4001006//Mus musculus ROSA 26 transcription AS ROSA26AS mRNA, complete cds.//1.4e-110:861:78//U83176

F-NT2RP4001010//Rattus norvegicus PSD-95/SAP90-associated protein-4 mRNA, complete cds.//2.0e-135:789:89//U67140

15 F-NT2RP4001029//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//3.7e-120:718:88//U20086

F-NT2RP4001041//Schizosaccharomyces pombe mRNA, partial cds, clone: SY 0717.//4.1e-22:452:64//D89170

F-NT2RP4001057

F-NT2RP4001064//Mus musculus mRNA for cartilage-associated protein (CASP).//1.2e-20:639:62//AJ006469

20 F-NT2RP4001078//Streptomyces coelicolor cosmid 1C2.//0.0025:474:59//AL031124

F-NT2RP4001079//Rat alternatively spliced mRNA.//1.4e-141:832:88//M93018

F-NT2RP4001080//H.sapiens PTB-4 gene for polypurimidine tract binding protein.//9.0e-64:628:70//X65372

F-NT2RP4001086//Homo sapiens mRNA for KIAA0592 protein, partial cds.//4.7e-84:604:86//AB011164

F-NT2RP4001095

25 F-NT2RP4001100//CITBI-E1-2503J7.TR CITBI-E1 Homo sapiens genomic clone 2503J7, genomic survey sequence.//9.4e-17:185:79//AQ263402

F-NT2RP4001117//Canis familiaris sec61 homologue mRNA, complete cds.//1.0e-143:760:87//M96629

F-NT2RP4001122

30 F-NT2RP4001126//Homo sapiens shox gene, alternatively spliced products, complete cds.//4.2e-17:636:61//U82668

F-NT2RP4001138//Homo sapiens PAC clone DJ1121E10 from 7q21.1-q2, complete sequence.//2.5e-23:408:60//AC004969

F-NT2RP4001143//Sequence 5 from patent US 5753432.//1.8e-39:276:86//AR008079

35 F-NT2RP4001148//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.7e-116:684:89//AC005095

F-NT2RP4001149//Mouse mRNA for thymic epithelial cell surface antigen, complete cds.//3.0e-48:581:66//D67067

F-NT2RP4001150//Homo sapiens clone DJ1032D07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//9.4e-25:193:67//AC004952

40 F-NT2RP4001159//Human FMR1 gene, 5' end.//0.28:130:66//L19476

F-NT2RP4001174//FMR1 {CGG repeats} [human, Fragile X syndrome patient, Genomic, 429 nt].//0.0014:187:67//S74494

F-NT2RP4001206//Dictyostelium discoideum random slug cDNA19 protein (rscI9) mRNA, partial cds.//0.032:453:58//U82511

45 F-NT2RP4001207//HS_2248_A1_C03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2248 Col=5 Row=E, genomic survey sequence.//0.00018:58:94//AQ192358

F-NT2RP4001210//Homo sapiens chromosome 10 clone CIT987SK-1019O18 map 10p11.2-10p12.1, complete sequence.//0.93:515:58//AC005877

50 F-NT2RP4001213//Human KRAB zinc finger protein (ZNF177) mRNA, splicing variant, complete cds.//3.6e-44:187:74//U37251

F-NT2RP4001219//Caenorhabditis elegans cosmid Y47H9C, complete sequence.//1.3e-15:288:67//AL032657

F-NT2RP4001228//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//2.2e-26:855:60//AF059569

55 F-NT2RP4001235//RPCI11-18E11.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-18E11, genomic survey sequence.//2.7e-15:101:98//B88081

F-NT2RP4001236

F-NT2RP4001237

F-NT2RP4001260//Sequence 2 from Patent WO9601901.//0.0018:246:63//A48324

F-NT2RP4001274//Homo sapiens, complete sequence//2.5e-05:201:67//AC005854
 F-NT2RP4001276//CIT-HSP-2324B15.TF CIT-HSP Homo sapiens genomic clone 2324B15, genomic survey sequence//3.5e-18:138:92//AQ040728
 5 F-NT2RP4001313//Homo sapiens mitochondrial outer membrane protein (TOM40) mRNA, nuclear gene encoding mitochondrial protein, complete cds//7.4e-30:535:65//AF043250
 F-NT2RP4001315//Bos taurus mRNA for Rab5 GDP/GTP exchange factor, Rabex5//3.5e-145:795:91//AJ001119
 F-NT2RP4001336//CIT-HSP-2169F21.TR CIT-HSP Homo sapiens genomic clone 2169F21, genomic survey sequence//8.4e-16:109:94//B89870
 10 F-NT2RP4001339//HS_3205_B1_E08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3205 Col=15 Row=J, genomic survey sequence//7.1e-24:305:73//AQ183725
 F-NT2RP4001343//Homo sapiens PAC clone DJ0894A10 from 7q32-q32, complete sequence//1.9e-17:106:91//AC004918
 F-NT2RP4001345//G.gallus mRNA for lecithin-cholesterol acyltransferase//7.6e-40:631:66//X91011
 15 F-NT2RP4001351//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 184J9, WORKING DRAFT SEQUENCE//2.7e-30:608:64//AL031428
 F-NT2RP4001353//Streptomyces coelicolor cosmid 5A7//0.23:540:57//AL031107
 F-NT2RP4001372//RPCI11-49L11.TJ RPCI11 Homo sapiens genomic clone R-49L11, genomic survey sequence//8.5e-23:129:100//AQ051701
 F-NT2RP4001373//G.gallus genomic DNA repeat region, clone 16E1//0.15:213:61//X78609
 20 F-NT2RP4001375
 F-NT2RP4001379//Homo sapiens chromosome 17, clone hRPK.311_F_12, complete sequence//7.3e-28:153:88//AC005722
 F-NT2RP4001389//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence//7.2e-47:518:73//AC004691
 25 F-NT2RP4001407//P.falciparum glutamic acid-rich protein gnen, complete cds//0.00079:686:57//J03998
 F-NT2RP4001414//Human mRNA for KIAA0202 gene, partial cds//2.0e-76:818:71//D86957
 F-NT2RP4001433//H.sapiens HZF10 mRNA for zinc finger protein//3.5e-87:839:73//X78933
 F-NT2RP4001442
 F-NT2RP4001447//Homo sapiens mRNA for KIAA0783 protein, complete cds//0.21:218:63//AB018326
 30 F-NT2RP4001474//Human NotI linking clone 924A058R, genomic survey sequence//7.6e-14:109:90//U49884
 F-NT2RP4001483//Human mRNA for 2-oxoglutarate dehydrogenase, complete cds//2.5e-59:480:75//D10523
 F-NT2RP4001498//Homo sapiens huntingtin interacting protein HYPH mRNA, partial cds//9.7e-39:392:72//AF049612
 F-NT2RP4001502//H.sapiens (D8S135) DNA segment containing GT repeat//2.7e-24:147:96//X61693
 35 F-NT2RP4001507//Plasmid pSB24.2 (from S.cyanogenus) neomycin resistance protein gene, complete cds//0.87:583:58//M32513
 F-NT2RP4001524//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces//0.93:394:58//AC005308
 F-NT2RP4001529//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds//3.1e-143:820:89//U20086
 40 F-NT2RP4001547//S.cerevisiae chromosome XIV reading frame ORF YNR048w//2.2e-05:319:61//Z71663
 F-NT2RP4001551//S.pombe chromosome II p1 p8B7//0.64:335:60//AL032684
 F-NT2RP4001555//Homo sapiens 12q24.2 BAC RPCI11-360E11 (Roswell Park Cancer Institute Human BAC Library) complete sequence//1.0:309:58//AC004806
 45 F-NT2RP4001567//HS_2166_B1_C07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2166 Col=13 Row=F, genomic survey sequence//0.99:188:59//AQ086290
 F-NT2RP4001568//Human mRNA for KIAA0167 gene, complete cds//7.0e-53:566:72//D79989
 F-NT2RP4001571//RPCI11-21F20.TP RPCI-11 Homo sapiens genomic clone RPCI-11-21F20, genomic survey sequence//2.8e-19:119:97//B85885
 50 F-NT2RP4001574//B.primigenius mRNA for coat protein gamma-cop//5.8e-129:813:85//X92987
 F-NT2RP4001575//Rattus norvegicus mRNA for ARE1 protein//3.4e-131:795:86//AJ223830
 F-NT2RP4001592//S.aureus gene for isoleucyl-tRNA synthetase//1.3e-14:663:59//X74219
 F-NT2RP4001610//Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12, U115B9 (Lawrence Livermore human cosmid library) complete sequence//6.4e-10:135:73//AC002364
 55 F-NT2RP4001614//HS_3042_B2_D05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3042 Col=2 Row=D, genomic survey sequence//1.1e-24:305:73//AQ183725
 F-NT2RP4001634
 F-NT2RP4001638//CHN110-100-100-100 sorted chromosome 11 specific cosmid Homo sapiens genomic

clone cSRL-161F1, genomic survey sequence.//4.9e-12:144:76//B02870

F-NT2RP4001644//M.musculus mRNA for map kinase interacting kinase, Mnk2.//3.8e-69:437:86//Y11092

F-NT2RP4001656//HS_2013_A1_D01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2013 Col=1 Row=G, genomic survey sequence.//2.0e-30:207:89//AQ224793

5 F-NT2RP4001677//Hylobates lar huntingtin gene, partial exon.//0.23:105:71//L49362

F-NT2RP4001679//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 462O23, WORKING DRAFT SEQUENCE.//2.7e-45:351:84//AL031431

F-NT2RP4001696//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence.//1.8e-30:163:88//U96629

10 F-NT2RP4001725//Drosophila melanogaster DNA sequence (P1 DS08860 (D181)), complete sequence.//1.1e-13:402:63//AC004296

F-NT2RP4001730//RPCI11-37M21.TK RPCI-11 Homo sapiens genomic clone RPCI-11-37M21, genomic survey sequence.//0.88:177:67//AQ029840

F-NT2RP4001739

15 F-NT2RP4001753//H.sapiens telomeric DNA sequence, clone 12QTEL023, read 12QTELOO023.seq.//4.9e-36:192:98//Z96232

F-NT2RP4001760//Mouse oncogene (ect2) mRNA, complete cds.//2.3e-140:866:86//L11316

F-NT2RP4001790//Homo sapiens clone NH0569124, complete sequence.//1.4e-29:327:74//AC005678

F-NT2RP4001803

20 F-NT2RP4001822//Homo sapiens tetraspan TM4SF (TSPAN-4) mRNA, complete cds.//1.0e-16:576:60//AF054841

F-NT2RP4001823//Human DNA sequence from clone 181C9 on chromosome 22q13.2-13.33. Contains a PHAPI2 Leucine Rich Acidic Nuclear Protein pseudogene, part of a putative novel gene, ESTs, STSs and GSSs, complete sequence.//2.1e-08:601:59//Z98743

25 F-NT2RP4001828

F-NT2RP4001838//Human mRNA for KIAA0071 gene, partial cds.//2.2e-53:555:73//D31888

F-NT2RP4001841

F-NT2RP4001849//Homo sapiens mRNA for KIAA0672 protein, complete cds.//1.7e-55:813:65//AB014572

F-NT2RP4001861//Human simple repeat polymorphism.//0.0014:145:66//M87691

30 F-NT2RP4001889//HS_2052_B1_H06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2052 Col=11 Row=P, genomic survey sequence.//1.0e-23:187:86//AQ270425

F-NT2RP4001893//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//7.3e-76:178:95//AC005014

F-NT2RP4001896//T3B4TFC TAMU Arabidopsis thaliana genomic clone T3B4, genomic survey sequence.//0.99:354:61//B26193

35 F-NT2RP4001901//Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.//0.031:409:60//AB011413

F-NT2RP4001927//HS_2216_B1_D03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2216 Col=5 Row=H, genomic survey sequence.//4.9e-32:216:89//AQ184677

40 F-NT2RP4001938//Mus musculus zinc finger protein (Zfp64) mRNA, complete cds.//1.2e-83:709:79//U49046

F-NT2RP4001946//HS_3021_B2_H10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3021 Col=20 Row=P, genomic survey sequence.//7.6e-09:120:76//AQ133185

F-NT2RP4001950//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.1e-18:421:65//AL022577

45 F-NT2RP4001953//CIT-HSP-2294D14.TR CIT-HSP Homo sapiens genomic clone 2294D14, genomic survey sequence.//0.030:358:61//AQ005028

F-NT2RP4001966//Mus musculus DOC4 (Doc4) mRNA, complete cds.//2.5e-68:812:68//AF059485

50 F-NT2RP4001975//Homo sapiens chromosome 17, clone hCIT.91_J_4, complete sequence.//1.9e-57:555:75//AC003976

F-NT2RP4002018//cSRL-143G4-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-143G4, genomic survey sequence.//8.9e-21:123:98//B01950 F-NT2RP4002047//Saccharomyces cerevisiae chromosome XII cosmid 8003.//1.6e-29:520:64//U17243

55 F-NT2RP4002052//CIT-HSP-2045A15.TF CIT-HSP Homo sapiens genomic clone 2045A15, genomic survey sequence.//0.8e-25:131:46//B50043

F-NT2RP4002058//Homo sapiens chromosome 17, clone hCIT.91_J_4, complete sequence.//1.9e-57:555:75//AC003976

F-NT2RP4002071//CIT-HSP-2314J9.TF CIT-HSP Homo sapiens genomic clone 2314J9, genomic survey sequence.//0.99:163:63//AQ027223

F-NT2RP4002075//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y57G11, WORKING DRAFT SEQUENCE.//0.15:506:59//Z92841

5 F-NT2RP4002078//RPC111-73M20.TJ RPC111 Homo sapiens genomic clone R-73M20, genomic survey sequence.//4.8e-21:130:96//AQ269030

F-NT2RP4002081//F.rubripes GSS sequence, clone 190O22bB9, genomic survey sequence.//0.0024:350:60//Z92062

F-NT2RP4002083//M.musculus tex27 mRNA.//8.2e-77:456:89//X80437

10 F-NT2RP4002408//Caenorhabditis elegans serine/threonine kinase LET-502 (let-502) mRNA, complete cds.//3.7e-18:541:62//U85515

F-NT2RP4002791

F-NT2RP4002888//Homo sapiens BAC clone RG067E13 from 7q21, complete sequence.//4.7e-39:385:75//AC002383

15 F-NT2RP4002905//Homo sapiens chromosome 17, clone hRPC.842_A_23, complete sequence.//6.5e-91:672:83//AC004662

F-NT2RP5003459//Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA, complete cds.//2.9e-37:193:99//M33197

F-NT2RP5003461//Human DNA sequence from PAC 506G2 contains ESTs.//7.9e-51:300:80//Z82901

20 F-NT2RP5003477//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//6.7e-77:150:100//AC000380

F-NT2RP5003492

F-NT2RP5003500//Human DNA sequence from cosmid 97K10, between markers DXS6791 and DXS8038 on chromosome X contains STSs and CpG island.//1.7e-111:623:93//Z81365

25 F-NT2RP5003506//H.sapiens CpG island DNA genomic Mse1 fragment, clone 71h2, reverse read cpg71h2.rt1a.//1.4e-49:283:93//Z62703

F-NT2RP5003512//HS_3084_A1_D04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3084 Col=7 Row=G, genomic survey sequence.//7.7e-18:117:95//AQ186312

F-NT2RP5003522//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces.//3.8e-101:211:96//AC005236

30 F-NT2RP5003524//Homo sapiens beta-spectrin (HSpTB1) gene, exon 14 and partial cds.//0.00056:650:57//AF013178

F-NT2RP5003534//H.sapiens CpG island DNA genomic Mse1 fragment, clone 14c10, forward read cpg14c10.ft1b.//0.00013:70:91//Z54631

35 F-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds.//1.2e-67:373:94//AB007934

F-OVARC1000004//Homo sapiens chromosome 4 clone B368A9 map 4q25, complete sequence.//5.8e-93:518:81//AC005510

F-OVARC1000006//Gallus gallus histone H2A (H2A-VIII) gene, complete cds.//9.1e-56:392:84//U38933

F-OVARC1000013

40 F-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds.//5.6e-170:815:98//AF058922

F-OVARC1000017//Streptomyces glaucescens tcm operon.//0.37:347:60//M80674

F-OVARC1000035//Homo sapiens GA17 protein mRNA, complete cds.//6.8e-36:238:89//AF064603

F-OVARC1000058

F-OVARC1000060//Homo sapiens ribonuclease 6 precursor, mRNA, complete cds.//2.5e-36:192:98//U85625

45 F-OVARC1000068//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 404K8, WORKING DRAFT SEQUENCE.//0.14:554:57//AL023883

F-OVARC1000071//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 596C15, WORKING DRAFT SEQUENCE.//5.3e-104:197:100//AL031387

F-OVARC1000085//Human DNA sequence from clone 191N21 on chromosome 6q27 Contains genes for PDCD2 (PROGRAMMED CELL DEATH-2/RP8 HOMOLOG), TATA factor (TFIID), proteasome subunit HC5, EST, STS, GSS, complete sequence.//1.6e-116:588:96//AL031259

50 F-OVARC1000087//HS_2004_B2_E11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2004 Col=22 Row=J, genomic survey sequence.//7.1e-11:94:94//AQ221037

F-OVARC1000091//nbxb0020P17r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0020P17r, genomic survey sequence //5 2e-05:238 64//AQ258489

55

omic clone Plate=3212 Col=24 Row=N, genomic survey sequence.//9.9e-05:141:73//AQ175369

F-OVARC1000109

F-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds.//1.6e-133:663:96//AF069250

5 F-OVARC1000114//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1111N9, WORKING DRAFT SEQUENCE.//2.3e-51:547:70//AL022574

F-OVARC1000133//Homo sapiens clone GS512I21, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.62:349:61//AC005027

F-OVARC1000139//Caenorhabditis elegans cosmid F09D1.//2.5e-18:314:64//AF040640

10 F-OVARC1000145//HS_2257_B2_D11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2257 Col=22 Row=H, genomic survey sequence.//5.8e-30:203:90//AQ304854

F-OVARC1000148//CIT-HSP-2345A22.TR CIT-HSP Homo sapiens genomic clone 2345A22, genomic survey sequence.//1.1e-26:146:100//AQ056703

F-OVARC1000151//Sequence 1 from patent US 5665588.//2.6e-61:677:70//I64695

15 F-OVARC1000168//Homo sapiens chromosome 19, cosmid R31343, complete sequence.//4.9e-19:381:63//AC005764

F-OVARC1000191//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE.//1.3e-06:745:57//AL034557

20 F-OVARC1000198//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//6.4e-161:781:97//AC004604

F-OVARC1000209//Oryza sativa submergence induced protein 2A mRNA, complete cds.//9.2e-33:511:65//AF068332

F-OVARC1000212//F.rubripes GSS sequence, clone 185L11aC1, genomic survey sequence.//1.1e-13:139:79//AL019910

25 F-OVARC1000240//Sequence 1 from patent US 5710024.//1.4e-129:623:98//I81226

F-OVARC1000241//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds.//1.1e-112:697:87//AF060194

F-OVARC1000288 2.2e-22:181:83//J00345

30 F-OVARC1000302//A-192A9.TP CIT978SK Homo sapiens genomic clone A-192A9, genomic survey sequence.//4.8e-18:110:99//B18003

F-OVARC1000304//Mouse mRNA from Mov10 locus.//5.5e-100:631:85//X52574

F-OVARC1000309

F-OVARC1000321//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces.//3.1e-122:325:95//AC005236

35 F-OVARC1000326//Rattus norvegicus lamina-associated polypeptide 1C (LAP1C) mRNA, complete cds.//4.0e-46:339:84//U19614

F-OVARC1000335//Caenorhabditis elegans cosmid F15B10.//0.020:545:57//AF036696

F-OVARC1000347//Homo sapiens clone GS051M12, complete sequence.//0.71:252:59//AC005007

F-OVARC1000384//Homo sapiens expanded SCA7 CAG repeat.//2.2e-09:276:64//AF020275

40 F-OVARC1000408//Human Chromosome 11p15.5 PAC clone pDJ915f1 containing KvLQT1 gene, complete sequence.//0.61:343:59//AC003693

F-OVARC1000411//S.cerevisiae chromosome XI reading frame ORF YKL202w.//0.075:242:60//Z28201

F-OVARC1000414//Homo sapiens PAC clone DJ0905M06 from 7q31, complete sequence.//0.00088:285:62//AC005166

45 F-OVARC1000420//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 371H6, WORKING DRAFT SEQUENCE.//0.14:487:60//AL031718

F-OVARC1000427//Homo sapiens clone UWGC:rg041a03 from 7p14-15, complete sequence.//4.9e-30:195:84//AC005826

F-OVARC1000431//Plasmodium falciparum MAL3P2, complete sequence.//1.3e-05:651:59//AL034558

50 F-OVARC1000437//Chicken tensin mRNA, complete cds.//9.6e-54:296:78//M74165

F-OVARC1000440//Human PINCH protein mRNA, complete cds.//2.7e-19:116:99//U09284

F-OVARC1000442//Human DNA sequence from clone 816K17 on chromosome 20p12.2-13 Contains TGM3 (PROTEIN-GLUTAMINE GLUTAMYLTRANSFERASE E3 PRECURSOR (EC 2.3.2.13) (TGASE E3) (TRANS-GLUTAMINASE 3), and another member of the Transglutaminase family, complete sequence.//1.0e-21:202:79//AL031678

55 F-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds.//1.0e-138:566:99//AB014582

CLASSIFICATION

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124:650:93//AF023451

F-OVARC1000466//Homo sapiens DNA from chromosome 19, cosmid R29144, complete sequence//1.0e-15:510:59//AC004221

F-OVARC1000473//Ciona intestinalis genomic fragment, clone 3F4, genomic survey sequence//2.5e-06:272:62//AJ227191

F-OVARC1000479//cDNA encoding novel rat protein TIP120 which is formed of complex with TBP (TATA binding protein)//1.1e-117:652:90//E12829

F-OVARC1000486//Homo sapiens DNA sequence from PAC 262D12 on chromosome 1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neuroneurin, Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30S ribosomal protein S14-LIKE gene preceded by a CpG island. Contains ESTs, genomic marker D1S2691 and STSs//1.7e-13:709:60//Z99297

F-OVARC1000496//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 455J7, WORKING DRAFT SEQUENCE//6.0e-23:316:72//AL031733

F-OVARC1000520//Homo sapiens supervillin mRNA, complete cds//2.1e-113:539:99//AF051850

F-OVARC1000526//Homo sapiens clone GS438P06, WORKING DRAFT SEQUENCE, 17 unordered pieces//8.0e-149:716:98//AC005024

F-OVARC1000533//Homo sapiens chromosome 19, cosmid R30385, complete sequence//5.8e-137:545:97//AC004510

F-OVARC1000543//HS_3055_A2_F10_MF CIT Approved Human Genomic_Sperm Library D Homo sapiens genomic clone Plate=3055 Col=20 Row=K, genomic survey sequence//0.19:104:71//AQ102820

F-OVARC1000556//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS, CpG island, complete sequence//4.4e-136:670:97//AL022069

F-OVARC1000557//Human DNA from chromosome 19-specific cosmid R27090, genomic sequence, complete sequence//1.3e-15:262:69//AC002985

F-OVARC1000564//Mus musculus clone OST7314, genomic survey sequence//1.9e-41:476:70//AF046733

F-OVARC1000573//HS_3241_B1_H03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3241 Col=5 Row=P, genomic survey sequence//2.2e-101:530:95//AQ211942

F-OVARC1000576//Human Chromosome X, WORKING DRAFT SEQUENCE, 2 unordered pieces//9.7e-97:445:90//AC002414

F-OVARC1000578//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence//9.1 e-27:354:72//AC003973

F-OVARC1000588//Human DNA sequence from clone 497J21 on chromosome 6q26-27. Contains a KOC (KH-domain containing transcript overexpressed in cancer) pseudogene, genomic marker D6S193, ESTs, STSs and GSSs, and a ca repeat polymorphism, complete sequence//0.97:276:62//AL023775

F-OVARC1000605

F-OVARC1000622//Homo sapiens (subclone 2_d8 from P1 H42) DNA sequence, complete sequence//7.2e-60:457:82//L81648

F-OVARC1000640//Human BAC clone RG326K09 from 7q21, complete sequence//6.2e-58:499:80//AC002069

F-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA for GRB-7 SH2 domain protein, complete cds//5.1e-77:424:93//D43772

F-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds//4.8e-99:536:94//AB011162

F-OVARC1000678//cSRL-29c7-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-29c7, genomic survey sequence//2.5e-57:336:91//B04244

F-OVARC1000679//Rattus norvegicus mRNA for myosin-RhoGAP protein Myr 7//1.6e-81:291:84//AJ001713

F-OVARC1000681//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 257E24, WORKING DRAFT SEQUENCE//8.2e-158:782:96//AL034424

F-OVARC1000682//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//1.5e-151:549:99//AF027156

F-OVARC1000689//nbxb0003aG01f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0003M01f, genomic survey sequence//0.17:499:60//AQ050003

F-OVARC1000700

F-OVARC1000703//Drosophila melanogaster DNA repair protein (mei-41) gene, complete cds, and TH1 gene, partial cds//3.5e-26:425:65//U34925

F-OVARC1000722//Homo sapiens chromosome 1q21-1q23 beta-1,4-galactosyltransferase mRNA, complete cds//3.7e-109:451:91//AF038661

F-OVARC1000730

F-OVARC1000731

F-OVARC1000764//Homo sapiens DNA from chromosome 19, cosmid R29144, complete sequence//1.0e-15:510:59//AC004221

F-OVARC1000764//Homo sapiens DNA from chromosome 19, cosmid R29144, complete sequence//1.0e-15:510:59//AC004221

F-OVARC1000771//M.musculus mRNA for GTP-binding protein.//2.2e-62:305:78//X95403
 F-OVARC1000781//Sequence 5 from Patent WO9722695.//1.9e-89:705:78//A63552
 F-OVARC1000787//Homo sapiens PAC clone DJ430N08 from 22q12.1-qter, complete sequence.//3.0e-131:631:98//AC004542
 5 F-OVARC1000800//Human Chromosome 11q23 PAC clone pDJ254e13, complete sequence.//1.7e-32:295:80//AC003691
 F-OVARC1000802//Homo sapiens chromosome Xp22-67-68, WORKING DRAFT SEQUENCE, 99 unordered pieces.//3.2e-55:356:88//AC004469
 F-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CALC.//9.5e-27:163:94//Y17711
 10 F-OVARC1000846//Homo sapiens mRNA for KIAA0643 protein, partial cds.//6.0e-150:432:100//AB014543
 F-OVARC1000850//Homo sapiens PB39 mRNA, complete cds.//1.0e-135:632:99//AF045584
 F-OVARC1000862//M.musculus mRNA for FT1.//2.6e-109:769:83//Z67963
 F-OVARC1000876//S.cerevisiae chromosome IX cosmid 9150.//7.4e-21:541:61//Z38125
 F-OVARC1000883//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//2.2e-08:98:88//U20086
 15 F-OVARC1000885//B.subtilis 25 kb genomic DNA segment (from sspE to katA).//0.25:231:61//Z82044
 F-OVARC1000886//CIT-HSP-2171H6.TR CIT-HSP Homo sapiens genomic clone 2171H6, genomic survey sequence.//0.00035:139:69//B89721
 F-OVARC1000890
 F-OVARC1000891
 20 F-OVARC1000897//Human DNA sequence from clone 215F16 on chromosome 22q12.1-12.3. Contains part of a Homeobox domain containing gene and GSSs, complete sequence.//1.4e-18:473:64//AL024494
 F-OVARC1000912//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//8.9e-08:378:63//L14320
 F-OVARC1000915//Homo sapiens mRNA for KIAA0600 protein, partial cds.//7.7e-85:440:95//AB011172
 25 F-OVARC1000924//HS_2022_A1_C01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2022 Col=1 Row=E, genomic survey sequence.//5.7e-21:122:99//AQ269493
 F-OVARC1000936//Human PAC clone DJ0093I03 from Xq23, complete sequence.//1.2e-113:476:91//AC003983
 F-OVARC1000937//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 20208, WORKING DRAFT SEQUENCE.//0.00066:436:61//AL031848
 30 F-OVARC1000945//Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds.//5.0e-89:556:86//AB005549
 F-OVARC1000948//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.98:160:64//X95276
 F-OVARC1000959//CIT-HSP-2348O16.TR CIT-HSP Homo sapiens genomic clone 2348O16, genomic survey sequence.//0.99:270:59//AQ062850
 35 F-OVARC1000960//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1p35. Contains delta opiate receptor, CpG island, CA repeat.//3.9e-41:577:72//AL009181
 F-OVARC1000964//P.falciparum malaria antigen (M26-32-2) gene, partial cds.//0.19:83:73//M63270
 F-OVARC1000971//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y57G11, WORKING DRAFT SEQUENCE.//0.013:670:57//Z92841
 40 F-OVARC1000984//Leishmania major chromosome 1, complete sequence.//0.80:345:58//AE001274
 F-OVARC1000996//MO25 gene [mice, embryos, mRNA, 2322 nt].//2.6e-55:403:82//S51858
 F-OVARC1000999//Synthetic construct galanin receptor type 3 (GALR3) gene, complete cds.//0.33:105:69//AF042785
 F-OVARC1001000//HS_2247_A1_H05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2247 Col=9 Row=O, genomic survey sequence.//3.1e-60:315:96//AQ153910
 45 F-OVARC1001004//Homo sapiens from UWGC:y18c282 from 6p21, complete sequence.//3:1e-124:595:98//AC004190
 F-OVARC1001010//CIT-HSP-2034M3.TF CIT-HSP Homo sapiens genomic clone 2034M3, genomic survey sequence.//1.0:151:60//B74290
 50 F-OVARC1001011//Human DNA sequence from cosmid U85A3, between markers DXS366 and DXS87 on chromosome X contains rad21 and T-cell cyclophorin pseudogenes, STS.//3.0e-08:149:79//Z78021
 F-OVARC1001032//Yeast (S.cerevisiae) mitochondrial Tyr-tRNA gene.//3.2e-13:667:60//M12451
 F-OVARC1001034//Mus musculus Fn54 mRNA, partial cds.//2.5e-119:737:86//AF001533
 F-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds.//2.7e-150:733:97//AF099149
 55 F-OVARC1001040//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces //2.8e-29:277:76//AC005081

F-OVARC1001702//Homo sapiens mRNA for hSOX20 protein, complete cds.//1.8e-47:393:81//AB006867
 F-OVARC1001703//CIT-HSP-2164L6.TF CIT-HSP Homo sapiens genomic clone 2164L6, genomic survey sequence.//0.94:85:69//B92840
 F-OVARC1001711//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 317C6, WORKING DRAFT SEQUENCE.//1.9e-06:489:61//Z97651
 F-OVARC1001713//Rattus norvegicus neuroligin 2 mRNA, complete cds.//1.0:262:59//U41662
 F-OVARC1001726//Human telomere associated repeat sequence, complete sequence.//7.5e-08:283:65//M57752
 F-OVARC1001731//Mus musculus gene for beta-tropomyosin.//2.6e-83:606:81//X12650
 F-OVARC1001745//HS_3007_B2_G09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3007 Col=18 Row=N, genomic survey sequence.//0.00020:269:60//AQ164522
 F-OVARC1001762//S.pombe chromosome III cosmid c338.//3.0e-17:624:61//AL023781
 F-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//4.2e-149:706:98//U97670
 F-OVARC1001767//Homo sapiens mRNA for KIAA0675 protein, complete cds.//3.0e-115:580:96//AB014575
 F-OVARC1001768
 F-OVARC1001791//Homo sapiens BAC clone RG118P15 from 8q21, complete sequence.//5.7e-64:477:78//AC005066
 F-OVARC1001795//Homo sapiens chromosome 4 clone B341C20 map 4q25, complete sequence.//6.5e-11:171:76//AC004704
 F-OVARC1001802//CITBI-E1-2502A17.TR CITBI-E1 Homo sapiens genomic clone 2502A17, genomic survey sequence.//0.98:214:61//AQ264481
 F-OVARC1001805//Human DNA sequence from clone 511E16 on chromosome 6p24.3-25.1. Contains the last coding exon of the gene for P18 component of aminoacyl-tRNA synthetase complex, part of an unknown gene downstream of a putative CpG island, and an STS with a CA repeat polymorphism, complete sequence.//9.5e-151:712:99//AL023694
 F-OVARC1001809//Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds.//2.7e-56:522:75//AF068748
 F-OVARC1001812//Homo sapiens chromosome 17, clone HCIT104N19, complete sequence.//1.7e-63:526:81//AC003662
 F-OVARC1001813//Human DNA sequence from cosmid U144A10, between markers DXS366 and DXS87 on chromosome X contains STS.//0.17:214:65//Z70224
 F-OVARC1001820//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 445N2, WORKING DRAFT SEQUENCE.//3.2e-55:379:82//AL031779
 F-OVARC1001828//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence.//2.8e-17:509:62//AC005609
 F-OVARC1001846//Human DNA sequence from cosmid U73E8, between markers DXS366 and DXS87 on chromosome X.//0.35:403:58//Z73361
 F-OVARC1001861//CIT-HSP-2165M3.TR CIT-HSP Homo sapiens genomic clone 2165M3, genomic survey sequence.//2.4e-25:148:96//B94622
 F-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence.//1.2e-18:122:95//AF070611
 F-OVARC1001879//HS_3026_B1_F09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3026 Col=17 Row=L, genomic survey sequence.//4.9e-29:204:87//AQ207748
 F-OVARC1001880//Human interferon regulatory factor 5 (Humirf5) mRNA, complete cds.//3.5e-05:489:60//U51127
 F-OVARC1001883//Homo sapiens clone GS259H13, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.9e-29:350:74//AC005020
 F-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//8.6e-56:300:96//AF061749
 F-OVARC1001901//Human DNA sequence from clone 103M22 on chromosome 6p24. Contains STSs and GSSs, complete sequence.//2.3e-10:253:66//AL031904
 F-OVARC1001911//HS_2196_B2_H11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2196 Col=22 Row=P, genomic survey sequence.//3.4e-09:123:78//AQ294069
 F-OVARC1001916//HS_3054_B1_C11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=21 Row=F, genomic survey sequence.//1.2e-31:126:97//AQ099979
 F-OVARC1001928
 F-OVARC1001942//H.sapiens CpG island DNA genomic Mse1 fragment, clone 21d7, forward read cpq21d7 ft1a //

- F-OVARC1001949//Human KRAB zinc finger protein (ZNF177) mRNA, complete cds//1.7e-16:294:67//U37263
 F-OVARC1001950//Homo sapiens *** SEQUENCING IN PROGRESS *** WORKING DRAFT SEQUENCE//1.5e-20:261:68//AJ011929
- 5 F-OVARC1001987//D.melanogaster G6PD gene, exons 2-4//0.99:447:57//Z19021
 F-OVARC1001989//Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 20 unordered pieces//2.9e-19:178:83//AC005995
 F-OVARC1002044//Plasmodium falciparum MAL3P7, complete sequence//0.17:232:62//AL034559
 F-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds//2.1e-158:739:98//AB007934
 F-OVARC1002066//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 4/15, WORKING DRAFT SEQUENCE//3.0e-17:781:59//AP000011
- 10 F-OVARC1002082//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces//5.4e-136:683:96//AC006015
 F-OVARC1002107//Homo sapiens BAC clone RG276003 from 7q22-q31.1, complete sequence//1.0:220:61//AC004668
- 15 F-OVARC1002112//Homo sapiens histone macroH2A1.2 mRNA, complete cds//6.1e-115:557:98//AF041483
 F-OVARC1002127//Homo sapiens chromosome 9, clone hRPK.202_H_3, complete sequence//0.013:461:57//AC006241
 F-OVARC1002138//Caenorhabditis elegans cosmid F32D1//1.0e-29:545:64//AF016427
 F-OVARC1002143//CIT-HSP-2343H20.TR CIT-HSP Homo sapiens genomic clone 2343H20, genomic survey sequence//2.3e-11:258:67//AQ055576
- 20 F-OVARC1002156
 F-OVARC1002158//F17O7-T7 IGF Arabidopsis thaliana genomic clone F17O7, genomic survey sequence//1.8e-16:383:66//B11616
 F-OVARC1002165//H.sapiens BDP1 mRNA for protein-tyrosinephosphatase//0.0041:300:64//X79568
- 25 F-OVARC1002182//F.rubripes GSS sequence, clone 123I23aA7, genomic survey sequence//1.4e-10:240:66//AL017241
 F-PLACE1000004//CIT-HSP-2294H13.TF CIT-HSP Homo sapiens genomic clone 2294H13, genomic survey sequence//8.2e-10:158:75//AQ003859
 F-PLACE1000005//Mouse alpha-1 antitrypsin gene, segment 1//4.8e-15:89:93//M12585
- 30 F-PLACE1000007//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//3.8e-51:550:72//AF022789
 F-PLACE1000014
 F-PLACE1000031//Homo sapiens clone DJ0098O22, WORKING DRAFT SEQUENCE, 5 unordered pieces//0.91:333:61//AC004821
- 35 F-PLACE1000040//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island//2.6e-20:279:67//Z93023
 F-PLACE1000048//Homo sapiens chromosome 17, clone HCIT462L7, complete sequence//3.6e-63:488:82//AC005177
 F-PLACE1000050//Mus musculus chromosome 14 marker um-m24 GA dinucleotide DNA sequence//2.3e-10:141:75//U31508
- 40 F-PLACE1000061//Human ribosomal protein L37a mRNA sequence//1.9e-30:190:94//L22154
 F-PLACE1000066//Homo sapiens PAC clone DJ1106E03 from 7q31.3-7q3, complete sequence//6.0e-63:597:74//AC005521
 F-PLACE1000078//Homo sapiens chromosome 11 clone CIT987SK-1012F4, WORKING DRAFT SEQUENCE, 6 unordered pieces//5.2e-09:143:73//AC005848
- 45 F-PLACE1000081//Human DNA from chromosome 19 specific cosmid R28461, genomic sequence, complete sequence//0.52:390:60//AC002389
 F-PLACE1000094
 F-PLACE1000133//Human DNA sequence from clone 372K1 on chromosome 6q24 Contains EST, STS, GSS and CpG Island, complete sequence//4.4e-129:731:92//AL023580
- 50 F-PLACE1000142//H.sapiens AUH mRNA//6.4e-09:328:62//X79888
 F-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds//7.7e-150:737:97//AF058291
 F-PLACE1000185//Sequence 15 from patent US 5691147//5.7e-106:558:94//I76211 F-PLACE1000213
- 55 F-PLACE1000214//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence. WORKING DRAFT SEQUENCE//2.6e-08:11:63//AL032816
 F-PLACE1000236//Human DNA sequence from clone 372K1 on chromosome 6q24 Contains EST, STS, GSS and CpG Island, complete sequence//4.4e-129:731:92//AL023580

F-PLACE1000246//HS_2008_A2_D04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2008 Col=8 Row=G, genomic survey sequence.//0.96:153:61//AQ269813

F-PLACE1000292//Drosophila melanogaster Oregon-R mitochondrial A+T region.//5.1e-12:571:60//U11584

F-PLACE1000308//D.teissieri mitochondrial DNA for tRNA-fmet, tRNA-Ile, tRNA-Gln & amp; tRNA-Val.//0.00013:369:59//X54011

F-PLACE1000332//HS_2016_B2_D08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2016 Col=16 Row=H, genomic survey sequence.//7.5e-83:424:96//AQ232106

F-PLACE1000347//CIT-HSP-2326A16.TV CIT-HSP Homo sapiens genomic clone 2326A16, genomic survey sequence.//0.13:46:100//AQ047350

F-PLACE1000374//Mus musculus putative CCAAT binding factor 1 (mCBF) mRNA, alternatively spliced transcript mCBF1, complete cds.//0.00048:84:83//U19891

F-PLACE1000380//F.rubripes GSS sequence, clone 047P21aA10, genomic survey sequence.//0.43:198:62//Z88163

F-PLACE1000383//Homo sapiens myotubularin related protein 1 (MTMR1) mRNA, partial cds.//8.7e-149:740:96//U58032

F-PLACE1000401//Pinctada fucata mRNA for insoluble protein, complete cds.//0.22:484:56//D86074

F-PLACE1000406//Human nuclear matrix protein 55 (nmt55) mRNA, complete cds.//3.3e-19:372:65//U89867

F-PLACE1000420//Homo sapiens chromosome 17, clone hRPK.227_G_15, complete sequence.//1.6e-85:421:87//AC005899

F-PLACE1000421//Human GT334 protein (GT334) gene, exons 16 and 17.//0.88:145:68//U61515

F-PLACE1000424//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//0.076:196:66//AC005189

F-PLACE1000435//HS_3217_A2_A12_MR CIT Approved Human Genomic-Sperm Library D Homo sapiens genomic clone Plate=3217 Col=24 Row=A, genomic survey sequence.//2.2e-47:438:76//AQ181698

F-PLACE1000444//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence.//6.9e-61:616:71//AC004382

F-PLACE1000453//Murine genomic DNA; partially digested Sau3A fragment, cloned into cosmid vector pEMBLcos2, complete sequence.//5.8e-18:314:69//AF059580

F-PLACE1000481//Homo sapiens Chromosome 22q11.2 Cosmid Clone 94a In DGCR Region, complete sequence.//1.1e-33:349:76//AC002491

F-PLACE1000492//Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds.//1.1e-34:256:83//U35245

F-PLACE1000540//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.099:336:58//X95276

F-PLACE1000547//Arabidopsis thaliana GDP-mannose pyrophosphorylase (GMP1) mRNA, complete cds.//5.4e-11:279:63//AF076484

F-PLACE1000562//, complete sequence.//1.7e-97:559:88//AC005409

F-PLACE1000564

F-PLACE1000583//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//3.3e-46:631:68//M27877

F-PLACE1000588//Human guanylate binding protein isoform I (GBP-2) mRNA, complete cds.//7.3e-84:503:88//M55542

F-PLACE1000596//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//3.8e-164:798:97//AJ012449

F-PLACE1000599//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.018:295:61//X95276

F-PLACE1000610//HS_2056_A1_D10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2056 Col=19 Row=G, genomic survey sequence.//5.3e-24:188:87//AQ235967

F-PLACE1000611//Rattus norvegicus neural membrane protein 35 mRNA, complete cds.//2.4e-47:687:66//AF044201

F-PLACE1000636

F-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//1.5e-152:747:96//AF102265

F-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNLc110F1857Q7 (RZPD Berlin)).//2.3e-156:775:97//AJ005896

F-PLACE1000706//nuclear protein TIF1 [mice, mRNA, 3951 nt]//8.0e-60:675:70//S78219

F-PLACE1000712

F-PLACE1800716//HS-1057-A1-A03-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CIT 779 Col=5 Row=A, genomic survey sequence.//1.1e-100:1000:100//S78219

F-PLACE1800716//HS-1057-A1-A03-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CIT 779 Col=5 Row=A, genomic survey sequence.//1.1e-100:1000:100//S78219

F-PLACE1800716//HS-1057-A1-A03-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CIT 779 Col=5 Row=A, genomic survey sequence.//1.1e-100:1000:100//S78219

F-PLACE1800716//HS-1057-A1-A03-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CIT 779 Col=5 Row=A, genomic survey sequence.//1.1e-100:1000:100//S78219

F-PLACE1000749//*Plasmodium falciparum* MAL3P7, complete sequence.//0.099:664:57//AL034559
 F-PLACE1000755//*H.sapiens* DNA 3' flanking simple sequence region clone wg2c3.//0.00068:206:62//X76589
 F-PLACE1000769//RPCI11-3J18.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-3J18, genomic survey se-
 quence.//6.5e-08:93:89//B63806
 5 F-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds.//3.5e-138:663:98//AB014548
 F-PLACE1000786//*Drosophila melanogaster* cosmid 80H7.//1.4e-43:589:68//AL031027
 F-PLACE1000793//*H.sapiens* CpG island DNA genomic MseI fragment, clone 13d12, reverse read
 cpg13d12.rt1c.//4.6e-09:71:100//Z64565
 F-PLACE1000798//Human Chromosome 16 BAC clone CIT987SK-A-635H12, complete sequence.//5.0e-14:235:
 10 72//AC002310
 F-PLACE1000841//Homo sapiens clone NH0441G08, WORKING DRAFT SEQUENCE, 12 unordered pieces.//
 0.013:404:60//AC006158
 F-PLACE1000849//*H.sapiens* CpG island DNA genomic MseI fragment, clone 72a10, reverse read
 cpg72a10.rt1a.//3.3e-09:82:92//Z62712
 15 F-PLACE1000856//*Hydra vulgaris* HT4 mRNA for collagen-like protein, partial cds.//1.0:317:59//AB008935
 F-PLACE1000863//*H.sapiens* CpG island DNA genomic MseI fragment, clone 53d2, forward read cpg53d2.ft1b.//
 7.3e-37:199:98//Z55621
 F-PLACE1000909//*H.sapiens* CpG island DNA genomic MseI fragment, clone 173f8, reverse read
 cpg173f8.rt1a.//1.5e-17:128:92//Z57391
 20 F-PLACE1000931//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1p35. Contains delta opiate
 receptor, CpG island, CA repeat.//8.1e-55:647:72//AL009181
 F-PLACE1000948
 F-PLACE1000972//RPCI11-61B1.TJ RPCI11 Homo sapiens genomic clone R-61B1, genomic survey sequence.//
 1.0e-26:148:99//AQ194348
 25 F-PLACE1000977//Homo sapiens mRNA for KIAA0672 protein, complete cds.//6.1e-08:413:61//AB014572
 F-PLACE1000979//*H.sapiens* CpG island DNA genomic MseI fragment, clone 76e8, reverse read cpg76e8.rt1a.//
 2.7e-10:84:94//Z55963
 F-PLACE1000987//Homo sapiens mRNA for KIAA0724 protein, complete cds.//8.0e-140:694:96//AB018267
 F-PLACE1001000//*Herpetomonas muscarum muscarum* kinetoplast 12S rRNA gene.//0.0056:443:58//U01011
 30 F-PLACE1001007//CIT-HSP-2013L15.TF CIT-HSP Homo sapiens genomic clone 2013L15, genomic survey se-
 quence.//0.99:277:58//B58681
 F-PLACE1001010//Human cosmid g1572c101, complete sequence.//3.6e-55:294:88//AC000357
 F-PLACE1001015//Homo sapiens PAC clone DJ0754J18 from 7p21, complete sequence.//7.2e-33:333:73//
 AC004741
 35 F-PLACE1001024
 F-PLACE1001036//CIT-HSP-2373I10.TF CIT-HSP Homo sapiens genomic clone 2373I10, genomic survey se-
 quence.//1.1e-80:393:98//AQ108662
 F-PLACE1001054//*Arabidopsis thaliana* genomic DNA, chromosome 5, TAC clone: K9I9, complete sequence.//
 8.8e-40:483:66//AB013390
 40 F-PLACE1001062//*Mus musculus* mRNA encoding lysine-ketoglutarate reductase/saccharopine dehydroge-
 nase.//1.2e-23:224:80//AJ224761
 F-PLACE1001076//HS_2195_B1_D05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=2195 Col=9 Row=H, genomic survey sequence.//0.0014:168:66//AQ066659
 F-PLACE1001088
 45 F-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds.//3.1e-95:489:96//AF065485
 F-PLACE1001104//Caprine arthritis-encephalitis virus envelope glycoprotein (env) gene, partial cds.//0.0073:253:
 62//U81400
 F-PLACE1001118//Homo sapiens KRAB domain zinc finger protein (ZFP37) mRNA, complete cds.//2.5e-64:676:
 71//AF022158
 50 F-PLACE1001136//Human amphiregulin (AR) gene, exon 5, clones lambda-ARH(6,12).//3.8e-26:174:93//M30702
 F-PLACE1001168
 F-PLACE1001171//Homo sapiens subtelomeric cosmid 11b-1, complete sequence.//7.6e-23:245:68//AC005603
 F-PLACE1001185//Human DNA sequence from clone 889N15 on chromosome Xq22.1-22.3. Contains part of the
 gene for a novel protein similar to *X. laevis* Cortical Thymocyte Marker-CTX, the possibly alternatively spliced gene
 55 for 26S Proteasome subunit p28 (Ankyrin repeat protein), a novel gene and exons 36 through 45 of the COL4A6
 gene. Collagen Alpha 4 (X) Chain (COL4A6) cDNA, partial cds.//1.0e-10:100:100//U01011
 F-PLACE1001238//*Mod1* mRNA (mRNA polymerase-associated factor (PAF53), complete cds.//9.3e-82:684:

77//D14336

F-PLACE1001241

F-PLACE1001257//Caenorhabditis elegans cosmid R12E2.//1.1e-16:480:60//AF067219

F-PLACE1001272//H.sapiens subunit of coatomer complex.//0.31:50:96//X70476

5 F-PLACE1001279//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.054:352:60//AC005507

F-PLACE1001280//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//1.0e-10:620:61//L14320

F-PLACE1001294//M.musculus GEG-154 mRNA.//5.0e-107:826:80//X71642

10 F-PLACE1001304//Mouse Zfp-35 mRNA for zinc finger protein ZFP-35.//1.2e-67:510:77//X17617

F-PLACE1001311//Homo sapiens clone DJ0826E18, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.6e-47:491:73//AC005282

F-PLACE1001323//HS-1007-A2-B10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 328 Col=20 Row=C, genomic survey sequence.//9.6e-26:142:100//B31181

15 F-PLACE1001351

F-PLACE1001366//Homo sapiens mRNA for KIAA0799 protein, partial cds.//8.6e-25:155:95//AB018342

F-PLACE1001377//H.sapiens MADM gene (exon 1).//1.6e-43:393:79//Z48614

F-PLACE1001383//Human DNA sequence from clone 246H3 on chromosome 22q11.21-12.2 Contains LRP5 (Lipoprotein Receptor Related Protein) pseudogene, EST, CA repeats (D22S414, D22S925, D22S926), STS, GSS and CpG island, complete sequence.//1.5e-119:705:91//AL022324

20 F-PLACE1001384//Homo sapiens mRNA for multi PDZ domain protein.//5.7e-08:117:84//AJ001319

F-PLACE1001387//Sequence 3 from patent US 5610018.//1.7e-06:395:58//I57340

F-PLACE1001395//Plasmodium falciparum circular DNA rpoB and rpoC genes for beta and beta-prime subunits of RNA polymerase (EC 2.7.7.6).//7.2e-11:620:60//X52177

25 F-PLACE1001399//Homo sapiens chromosome 17, clone hRPK.22_N_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//3.0e-145:700:98//AC005412

F-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence.//2.0e-69:365:96//AF091087

F-PLACE1001414//Homo sapiens chromosome 9, clone hRPK.202_H_3, complete sequence.//8.2e-121:608:97//AC006241

30 F-PLACE1001440//Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.3e-06:437:61//AC000384

F-PLACE1001456//Homo sapiens Xp22 GS-52411 (Genome Systems Human BAC library), complete sequence.//0.98:348:60//AC003106

F-PLACE1001468//Homo sapiens DNA sequence from PAC 435A7 on chromosome Xq22.1-q22.3. Contains STS.//4.4e-05:358:62//AL022148

35 F-PLACE1001484//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 387E22, WORKING DRAFT SEQUENCE.//5.7e-31:195:93//AL031660

F-PLACE1001502//Human fibroblast growth factor receptor 3 (FGFR3) gene, exon L//0.00015:333:59//L78720

F-PLACE1001503//Drosophila melanogaster DNA sequence (P1 DS05273 (D80)), complete sequence.//0.00016:161:66//AC004373

40 F-PLACE1001517//Human DNA sequence from PAC 696H22 on chromosome Xq21.1-21.2. Contains a mouse E25 like gene, a Kinesin like pseudogene and ESTs.//3.7e-22:260:76//AL021786

F-PLACE1001534//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 620E11, WORKING DRAFT SEQUENCE.//1.1e-143:713:97//AL031667

45 F-PLACE1001545//Homo sapiens chromosome 3, clone hRPK.165_L_16, complete sequence.//2.7e-139:482:96//AC005669

F-PLACE1001551//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//6.9e-116:681:89//AC005261

F-PLACE1001570//HS_3105_A1_F06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3105 Col=11 Row=K, genomic survey sequence.//1.2e-10:137:79//AQ139817

F-PLACE1001602//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11.//1.8e-102:217:99//AB020860

F-PLACE1001603//Homo sapiens nitrilase homolog 1 (NIT1) gene, alternatively spliced product, complete cds.//3.7e-104:501:98//AF069984

55 F-PLACE1001608//HS_2189_A1_G07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2189 Col=7 Row=G, genomic survey sequence.//1.2e-10:137:79//AQ139817

F-PLACE1001609//Homo sapiens chromosome 1, clone 469M11, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.7e-052:384:AC003500

F-PLACE1001611//Human DNA sequence from clone 1039K5 on chromosome 22q12.3-13.2 Contains gene similar to PICK1 perinuclear binding protein, gene similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS and a CpG island, complete sequence.//0.93:131:71//AL031587

F-PLACE1001632//Homo sapiens mRNA for KIAA0798 protein, complete cds.//1.1e-74:702:75//AB018341

5 F-PLACE1001634//Human p190-B (p190-B) mRNA, complete cds.//1.2e-18:114:100//U17032

F-PLACE1001640//Homo sapiens chromosome 17, clone hRPK.651_L_9, complete sequence.//7.7e-159:788:97//AC005971

10 F-PLACE1001672//Human DNA sequence from clone 71L16 on chromosome Xp11. Contains a probable Zinc Finger protein (pseudo)gene, an unknown putative gene, a pseudogene with high similarity to part of antigen KI-67, a putative Chondroitin 6-Sulfotransferase LIKE gene and a KIAA0267 LIKE putative Na(+)/H(+) exchanger protein gene. Contains a predicted CpG island, ESTs, STSs and GSSs and genomic markers DXS1003 and DXS1055, complete sequence.//7.8e-36:365:73//AL022165

F-PLACE1001691//Homo sapiens chromosome 17, clone hRPK.294_J_22, complete sequence.//9.1e-149:760:96//AC005921

15 F-PLACE1001692//Rat medium-chain S-acyl fatty acid synthetase thio ester hydrolase (MCH), complete cds.//2.9e-57:643:71//M16200

F-PLACE1001705//Homo sapiens chromosome 17, clone hRPK.958_E_11, WORKING DRAFT SEQUENCE, 2 ordered pieces.//3.9e-18:284:71//AC005883

F-PLACE1001716//Human mRNA for KIAA0191 gene, partial cds.//6.6e-68:369:73//D83776

20 F-PLACE1001720//Homo sapiens Chromosome 22q11.2 Cosmid Clone 31f3 In IGLC Region, complete sequence.//1.0:274:59//AC000051

F-PLACE1001729//Streptomyces coelicolor cosmid 1C2.//0.22:433:57//AL031124

F-PLACE1001739//Caenorhabditis elegans cosmid C18H7.//0.049:341:61//AF067607

25 F-PLACE1001740//Homo sapiens chromosome 5, P1 clone 1108H7 (LBNL H81), complete sequence.//4.8e-26:372:68//AC005221

F-PLACE1001745

F-PLACE1001746//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P1, WORKING DRAFT SEQUENCE.//0.018:472:57//AL031744

F-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//8.8e-159:773:97//AF061243

30 F-PLACE1001756//Homo sapiens chromosome 12p13.3 clone RPCI11-303E5, WORKING DRAFT SEQUENCE, 65 unordered pieces.//1.9e-54:274:81//AC005842

F-PLACE1001761//HS_3027_A1_D02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3027 Col=3 Row=G, genomic survey sequence.//0.095:49:93//AQ130972

35 F-PLACE1001771//Homo sapiens transient receptor potential protein 6 mRNA, complete cds.//1.0e-146:709:97//AF080394

F-PLACE1001781 1.3e-08:238:65//AC005637

F-PLACE1001799//HS_3075_B1_H03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=5 Row=P, genomic survey sequence.//1.7e-09:166:69//AQ138474

40 F-PLACE1001810//Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MRC8, complete sequence.//0.00035:196:66//AB020749

F-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//1.1e-108:546:96//AF058953

F-PLACE1001821//RPCI11-35D17.TK RPCI-11 Homo sapiens genomic clone RPCI-11-35D17, genomic survey sequence.//2.1e-55:300:97//AQ045286

45 F-PLACE1001844//Homo sapiens chromosome 17, clone HCIT462L7, complete sequence.//2.8e-67:443:86//AC005177

F-PLACE1001845//Arabidopsis thaliana chromosome I BAC T25B24 genomic sequence, complete sequence.//0.34:219:64//AC005850

50 F-PLACE1001869//Klebsiella pneumoniae ribitol kinase (rbtK) and ribitol transporter (rbtT) genes, complete cds.//7.1e-11:505:57//AF045244

F-PLACE1001897//RPCI11-46D15.TJ RPCI11 Homo sapiens genomic clone R-46D15, genomic survey sequence.//9.3e-08:383:63//AQ194408

F-PLACE1001912

55 F-PLACE1001920//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.//7.3e-156:753:98//AF099935

F-PLACE1001928//HS_2220_B2_G04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2220 Col=2 Row=G, genomic survey sequence.//0.00035:196:66//AB020749

F-PLACE1001983//Human DNA sequence *** SEQUENCING IN PROGRESS *** from MAL1P1, WORKING DRAFT SEQUENCE.//1.6e-07:396:62//AL031586

F-PLACE1001989//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 968D22, WORKING DRAFT SEQUENCE.//1.0e-109:602:93//AL023755

F-PLACE1002004//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 317E23, WORKING DRAFT SEQUENCE.//1.0e-69:475:87//AL020996

5 F-PLACE1002046//Mus musculus ligatin (Lgtn) mRNA, partial cds.//7.2e-97:623:85//U58337

F-PLACE1002052//HS_2178_B2_D05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2178 Col=10 Row=H, genomic survey sequence.//4.8e-22:140:95//AQ307908

F-PLACE1002066//Apis mellifera NADH dehydrogenase subunit 2 (ND2) gene, mitochondrial gene encoding mitochondrial protein, partial cds.//0.0063:371:60//U72284

10 F-PLACE1002072//Homo sapiens tight junction protein ZO (ZO-2) gene, alternative splice products, promoter and exon A.//0.97:248:60//AF043195

F-PLACE1002073//Homo sapiens mRNA for KIAA0606 protein, partial cds.//1.3e-37:635:64//AB011178

F-PLACE1002090//Homo sapiens full-length insert cDNA clone ZA85C09.//7.0e-122:583:98//AF086131

F-PLACE1002115//nbxb0038A20r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0038A20r, genomic survey sequence.//0.039:210:69//AQ291086

15 F-PLACE1002119//Mus musculus IER5 (Ier5) mRNA, complete cds.//7.1e-61:540:77//AF079527

F-PLACE1002140//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and GSSs, complete sequence.//2.1e-125:491:98//AL022162

20 F-PLACE1002150//Plasmodium falciparum MAL3P5, complete sequence.//0.12:408:61//AL034556

F-PLACE1002157//Homo sapiens BAC clone NH0335J18 from 2, complete sequence.//1.1e-44:515:71//AC005539

F-PLACE1002163//Homo sapiens T-cell receptor alpha delta locus from bases 1000498 to 1071650 (section 5 of 5) of the Complete Nucleotide Sequence.//0.98:210:65//AE000662

25 F-PLACE1002170//Homo sapiens Xp22 bins 16-17 BAC GSHB-531117 (Genome Systems Human BAC Library) complete sequence.//1.2e-06:283:60//AC004805

F-PLACE1002171//Mus musculus interferon alpha/beta receptor (IFNAR) gene, exon 11 and partial cds.//1.0e-24:313:71//U06244

F-PLACE1002205//Drosophila melanogaster; Chromosome 3L; Region 79F1-80A2; BAC clone BACR48E05, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.6e-05:428:60//AC005720

30 F-PLACE1002213//HS_3238_B1_G03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=5 Row=N, genomic survey sequence.//2.2e-74:371:98//AQ206965

F-PLACE1002227//HS-1056-B1-C01-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 778 Col=1 Row=F, genomic survey sequence.//2.1e-07:174:71//B42800

35 F-PLACE1002256//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-72, complete sequence.//0.022:458:59//AL010142

F-PLACE1002259//Human DNA sequence from clone 246H3 on chromosome 22q11.21-12.2 Contains LRP5 (Lipoprotein Receptor Related Protein) pseudogene, EST, CA repeats (D22S414, D22S925, D22S926), STS, GSS and CpG island, complete sequence.//3.5e-91:637:84//AL022324

40 F-PLACE1002319

F-PLACE1002342//Caenorhabditis elegans cosmid M03A1.//0.47:403:58//U49956

F-PLACE1002395//Homo sapiens chromosome 19, cosmid R28991, complete sequence.//1.9e-127:487:93//AC004623

F-PLACE1002399//Homo sapiens chromosome 17, clone hRPK.235_I_10, complete sequence.//5.6e-05:474:59//AC005922

45 F-PLACE1002433//Drosophila melanogaster fidipidine gene, exons 1-7.//1.7e-11:613:58//AJ011928

F-PLACE1002437//M.musculus abc1 mRNA.//5.5e-62:452:85//X75926

F-PLACE1002438//Dictyostelium discoideum developmental protein DG1098 (DG1098) gene, partial cds.//0.013:372:59//AF081801

50 F-PLACE1002450//HS_3233_A1_G01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3233 Col=1 Row=M, genomic survey sequence.//3.1e-07:449:59//AQ204769

F-PLACE1002465

F-PLACE1002474//Mus musculus matrilin-2 precursor mRNA, complete cds.//1.5e-110:720:85//U69262

F-PLACE1002477//Homo sapiens Xp22-171-173 BAC GSHB-31214 (Genome Systems Human BAC Library) complete sequence.//3.9e-05:195:71//AC005926

F-PLACE1002493//Homo sapiens 3p22.8 BAC clone

complete sequence.//1.1e-109:602:93//AL023755

55 F-PLACE1002494

F-PLACE1002500//Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds.//2.1e-58:465:80//U50927
 F-PLACE1002514//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 292E10, WORKING
 DRAFT SEQUENCE.//3.7e-08:139:76//Z93930
 F-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds.//9.0e-143:583:95//AB018256
 5 F-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1, complete sequence.//0.00019:193:
 65//AC004774
 F-PLACE1002537//Human DNA sequence from clone 127F18 on chromosome Xp11.4-21.3. Contains part of a
 novel gene with some similarity to parts of chicken Myosin Light Chain and various species' Interleukin-1 Receptor
 Type 1 (IL1-R-1). Contains GSSs, complete sequence.//4.7e-25:198:84//AL031575
 10 F-PLACE1002571//Drosophila melanogaster actin-related protein mRNA, complete cds.//2.0e-13:400:60//L25314
 F-PLACE1002578//Homo sapiens Xq28 BACs 360 F12, GSHB-555C13, complete sequence.//3.5e-11:167:72//
 AC002523
 F-PLACE1002583//Mus musculus glutamate receptor subunit (GluR6) gene, partial cds.//4.2e-09:370:61//U31443
 F-PLACE1002591//H.sapiens mRNA for coronin.//7.2e-26:279:74//X89109
 15 F-PLACE1002598//Homo sapiens clone GS308H05, WORKING DRAFT SEQUENCE, 6 unordered pieces.//
 0.0013:375:64//AC005537
 F-PLACE1002604//Hansenula wingei mitochondrial DNA, complete sequence.//4.7e-05:556:59//D31785
 F-PLACE1002625
 F-PLACE1002655//Homo sapiens PAC clone DJ0722F20 from 7q31.1-q31.3, complete sequence.//1.6e-128:229:
 20 92//AC005281
 F-PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//3.6e-107:706:84//
 AF079765
 F-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds.//3.4e-
 186:804:97//AF068180
 25 F-PLACE1002714//Mus musculus cathepsin S (CatS) gene, promoter region and exons 1 and 2.//2.3e-16:474:
 64//AF051726
 F-PLACE1002722//Sequence 1 from patent US 5686597.//1.7e-107:552:95//I73723
 F-PLACE1002768//Human DNA sequence from clone 726F20 on chromosome 1p36.11-36.23. Contains ESTs
 and a GSS, complete sequence.//0.0076:161:70//AL031273
 30 F-PLACE1002772//HS_3058_A1_D02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3058 Col=3 Row=G, genomic survey sequence.//0.0046:192:64//AQ134567
 F-PLACE1002775//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//7.6e-14:459:62//
 AF084259
 F-PLACE1002782//Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds.//3.6e-43:385:77//U50927
 35 F-PLACE1002794//CIT-HSP-2368A17.TR CIT-HSP Homo sapiens genomic clone 2368A17, genomic survey se-
 quence.//1.3e-71:368:96//AQ075879
 F-PLACE1002811//Human mRNA for KIAA0172 gene, partial cds.//1.8e-44:567:70//D79994
 F-PLACE1002815//Sequence 25 from patent US 5747660.//2.6e-07:150:73//AR005295
 F-PLACE1002816//Homo sapiens antigen NY-CO-9 (NY-CO-9) mRNA, partial cds.//1.3e-68:687:73//AF039691
 40 F-PLACE1002834//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and 9.//9.3e-41:240:93//
 M27877
 F-PLACE1002839//Human BAC clone RG205G13 from 7q31, complete sequence.//0.00087:213:63//AC003045
 F-PLACE1002851//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING
 DRAFT SEQUENCE, 14 unordered pieces.//0.0032:269:66//AC005140
 45 F-PLACE1002853//Leishmania tarentolae kinetoplast pre-edited mitochondrial maxicircle DNA complete tran-
 scribed region and flanks.//0.032:275:62//M10126
 F-PLACE1002881//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 111B22, WORKING
 DRAFT SEQUENCE.//4.7e-38:355:76//Z98200
 F-PLACE1002908//Gallus gallus beta-1,4-galactosyltransferase (CKII) mRNA, complete cds.//0.00012:200:64//
 50 U19889
 F-PLACE1002941//Human BAC clone RG161K23 from 7q21, complete sequence.//1.1e-14:241:70//AC000120
 F-PLACE1002962
 F-PLACE1002968//Plasmodium falciparum MAL3P2, complete sequence.//0.21:410:59//AL034558
 F-PLACE1002991//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 968D22, WORKING
 55 DRAFT SEQUENCE.//6.8e-121:605:93//AL023755
 F-PLACE1002996//Mouse Cb RNA gene.//2.0e-11:100:100//X89109

F-PLACE1003025//Plasmodium falciparum MAL3P6, complete sequence.//0.84:374:58//Z98551
F-PLACE1003027//Homo sapiens mRNA for KIAA0516 protein, partial cds.//6.1e-130:632:97//AB011088
F-PLACE1003044//cDNA encoding novel rat protein TIP120 which is formed of complex with TBP (TATA binding protein).//1.6e-123:687:91//E12829
F-PLACE1003045//H.sapiens CpG island DNA genomic MseI fragment, clone 47g6, forward read cpg47g6.ft1a.//0.0064:52:96//Z61200
F-PLACE1003092//CIT-HSP-387P22.TRB CIT-HSP Homo sapiens genomic clone 387P22, genomic survey sequence.//0.0031:249:63//B60158
F-PLACE1003100//Human Hep27 protein mRNA, complete cds.//8.9e-65:650:73//U31875
F-PLACE1003108
F-PLACE1003136//Homo sapiens chromosome 5, P1 clone 1130f1 (LBNL H40), complete sequence.//6.3e-46:606:68//AC004219
F-PLACE1003145
F-PLACE1003153//RPCI11-13P16.TP RPCI-11 Homo sapiens genomic clone RPCI-11-13P16, genomic survey sequence.//2.7e-63:478:82//B76206
F-PLACE1003174//Human DNA sequence from clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495
F-PLACE1003176//HS_2255_A2_B01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2255 Col=2 Row=C, genomic survey sequence.//6.3e-09:137:76//AQ131934
F-PLACE1003190//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.4e-138:791:901//AC005095
F-PLACE1003200//P.falciparum complete gene map of plastid-like DNA (IR-B).//8.7e-06:728:57//X95276
F-PLACE1003205//Human BAC clone RG354L07 from 7q31, complete sequence.//7.5e-05:249:63//AC002466
F-PLACE1003238//HS_3239_A2_G02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3239 Col=4 Row=M, genomic survey sequence.//0.36:64:87//AQ209954
F-PLACE1003249
F-PLACE1003256
F-PLACE1003258//HS_3223_A1_G10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3223 Col=19 Row=M, genomic survey sequence.//1.4e-07:227:65//AQ190317
F-PLACE1003296//CIT-HSP-2337F11.TF CIT-HSP Homo sapiens genomic clone 2337F11, genomic survey sequence.//1.1e-13:97:95//AQ057429
F-PLACE1003302//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and 9.//2.3e-92:485:95//M27877
F-PLACE1003334
F-PLACE1003342
F-PLACE1003343//Homo sapiens clone DJ1022I14, WORKING DRAFT SEQUENCE, 14 unordered pieces.//1.0e-20:179:84//AC004951
F-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds.//8.0e-143:773:92//U92715
F-PLACE1003361//Human Cosmid g1248a143 from 7q31.3, complete sequence.//1.9e-30:402:70//AC004095
F-PLACE1003366
F-PLACE1003369//Plasmodium falciparum MAL3P2, complete sequence.//7.6e-07:378:60//AL034558
F-PLACE1003373//Homo sapiens PAC clone DJ0740L10 from 7p13-p14, complete sequence.//6.0e-18:471:61//AC005247
F-PLACE1003375
F-PLACE1003383//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 10/10.//2.3e-157:779:96//AB020878
F-PLACE1003394//Sprague-Dawley (clone LRB13) RAB14 mRNA, complete cds.//1.2e-104:596:91//M83680
F-PLACE1003401//RPCI11-71J5.TJ RPCI11 Homo sapiens genomic clone R-71J5, genomic survey sequence.//0.85:140:65//AQ268588
F-PLACE1003420//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y1E3, WORKING DRAFT SEQUENCE.//0.0015:286:60//AL021388
F-PLACE1003454//Plasmodium falciparum microsatellite pe63 sequence.//0.0084:219:61//AF015470
F-PLACE1003478//Homo sapiens calcium-dependent chloride channel-1 (hCLCA1) gene, complete cds.//1.3e-11:746:60//AF039401
F-PLACE1003515//Homo sapiens clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495
F-PLACE1003516//Homo sapiens clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495
F-PLACE1003517//Homo sapiens clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495
F-PLACE1003518//Homo sapiens clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495
F-PLACE1003519//Homo sapiens clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495
F-PLACE1003520//Homo sapiens clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495
F-PLACE1003521//Homo sapiens clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495
F-PLACE1003522//Homo sapiens clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495
F-PLACE1003523//Homo sapiens clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495
F-PLACE1003524//Homo sapiens clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495
F-PLACE1003525//Homo sapiens clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495
F-PLACE1003526//Homo sapiens clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495
F-PLACE1003527//Homo sapiens clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495
F-PLACE1003528//Homo sapiens clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495
F-PLACE1003529//Homo sapiens clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495
F-PLACE1003530//Homo sapiens clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495
F-PLACE1003531//Homo sapiens clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495
F-PLACE1003532//Homo sapiens clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495
F-PLACE1003533//Homo sapiens clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495
F-PLACE1003534//Homo sapiens clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495
F-PLACE1003535//Homo sapiens clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495
F-PLACE1003536//Homo sapiens clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495
F-PLACE1003537//Homo sapiens clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495
F-PLACE1003538//Homo sapiens clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495
F-PLACE1003539//Homo sapiens clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495
F-PLACE1003540//Homo sapiens clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495
F-PLACE1003541//Homo sapiens clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495
F-PLACE1003542//Homo sapiens clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495
F-PLACE1003543//Homo sapiens clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495
F-PLACE1003544//Homo sapiens clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495
F-PLACE1003545//Homo sapiens clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495
F-PLACE1003546//Homo sapiens clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495
F-PLACE1003547//Homo sapiens clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495
F-PLACE1003548//Homo sapiens clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495
F-PLACE1003549//Homo sapiens clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495
F-PLACE1003550//Homo sapiens clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495
F-PLACE1003551//Homo sapiens clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495
F-PLACE1003552//Homo sapiens clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61

F-PLACE1003519//Homo sapiens chromosome 21q22.3 PAC 141B3, complete sequence, containing ribosomal protein homologue pseudogene L23a.//6.2e-21:247:76//AF064859

F-PLACE1003521//Human DNA sequence from PAC 257A7 on chromosome 6p24. Contains two unknown genes and ESTs, STSs and a GSS.//4.4e-68:502:79//AL008729

5 F-PLACE1003528//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//1.0:323:58//AL022336

F-PLACE1003537//Homo sapiens multispinning membrane protein mRNA, complete cds.//0.0054:322:59//U94831

10 F-PLACE1003553//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 97P20, WORKING DRAFT SEQUENCE.//2.9e-78:267:88//AL031297

F-PLACE1003566//Plasmodium falciparum MAL3P3, complete sequence.//0.00026:514:58//Z98547

F-PLACE1003575//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.079:755:54//AC004688

15 F-PLACE1003583//Human DNA sequence from clone 246H3 on chromosome 22q11.21-12.2 Contains LRP5 (Lipoprotein Receptor Related Protein) pseudogene, EST, CA repeats (D22S414, D22S925, D22S926), STS, GSS and CpG island, complete sequence.//1.1e-41:212:74//AL022324

F-PLACE1003584//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-56, complete sequence.//0.0038:465:57//AL010230

20 F-PLACE1003592//Homo sapiens chromosome 17, clone 296K1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//0.72:111:71//AC002557

F-PLACE1003593//Human PAC clone DJ318C15 from Xq23, complete sequence.//0.096:162:66//AC002476

F-PLACE1003596//Mus musculus integral membrane protein 1 (Itm1) mRNA, complete cds.//1.4e-54:685:68//L34260

25 F-PLACE1003602//Homo sapiens mRNA expressed in placenta.//1.1e-138:679:97//D83200

F-PLACE1003605//Homo sapiens chromosome 16, cosmid clone RT81 (LANL), complete sequence.//0.0074:265:63//AC005356

F-PLACE1003611//HS_2198_B1_D02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2198 Col=3 Row=H, genomic survey sequence.//2.1e-23:137:97//AQ184475

30 F-PLACE1003618//Homo sapiens chromosome 4 clone C0011C13 map 4p16, complete sequence.//3.0e-122:725:89//AC006226

F-PLACE1003625//HS_2238_B2_D11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2238 Col=22 Row=H, genomic survey sequence.//4.8e-12:92:94//AQ065662

F-PLACE1003638//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKD10, complete sequence.//0.043:264:63//AB011478

35 F-PLACE1003669

F-PLACE1003704//RPCI11-23H21.TKBF RPCI-11 Homo sapiens genomic clone RPCI-11-23H21, genomic survey sequence.//7.1e-31:199:91//AQ013830

F-PLACE1003709//Homo sapiens mitotic checkpoint kinase Bub1 (BUB1) mRNA, complete cds.//4.3e-132:669:95//AF053305

40 F-PLACE1003711//Homo sapiens DNA sequence from PAC 163M9 on chromosome 1p35.1-p36.21. Contains protein synthesis factor (eIF-4C), D1F15S1A pseudogene, ESTs, STS, GSS, complete sequence.//1.5e-31:166:99//AL021920

F-PLACE1003723//HS_2231_A2_C07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2231 Col=14 Row=E, genomic survey sequence.//1.2e-12:114:90//AQ235672

F-PLACE1003738//Human zinc finger protein 42 (MZF-1) mRNA, complete cds.//5.9e-33:592:67//M58297

F-PLACE1003760//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds.//3.6e-11:92:93//AF054840

F-PLACE1003762

50 F-PLACE1003768//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 7/15, WORKING DRAFT SEQUENCE.//4.8e-77:737:76//AP000014

F-PLACE1003771//Homo sapiens BAC clone GS164B05 from 7p21-p22, complete sequence.//2.1e-164:793:98//AC004160

F-PLACE1003783//HS_2190_A2_C02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2190 Col=4 Row=E, genomic survey sequence.//1.1e-26:147:100//AQ218757

55 F-PLACE1003784//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//4.5e-51:706:68//AC008601

F-PLACE1003785//Homo sapiens Xq28 genomic DNA, chromosome 22q13.31-22q13.32, AMR locus containing the genes for alpha-2-macroglobulin (A2M), arginine vasopressin receptor (AVPR2), and 11p15.5 Antisense (AS)

transferase related protein (TE2), renin-binding protein (RbP), host cell factor 1 (HCF1), and interleukin-1 receptor-associated kinase (IRAK) genes, complete cds, and Xq281u2 gene.//0.015:296:60//J52112

F-PLACE1003833//Homo sapiens DNA sequence from cosmid N75B3 on chromosome 22 Contains EST, exon trap, complete sequence.//0.52:212:64//AL022339

5 F-PLACE1003850//P.falciparum histidine-rich protein genes.//0.39:330:60//M17028

F-PLACE1003858//Human DNA sequence from PAC 332O11 on chromosome 1q24-1q25. Contains ESTs and STSs.//4.8e-07:461:59//Z98043

F-PLACE1003864//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.026:538:56//AC005139

10 F-PLACE1003870//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 54B20, WORKING DRAFT SEQUENCE.//6.5e-06:175:69//Z98304

F-PLACE1003885//Mus musculus poly(A) polymerase VI mRNA, complete cds.//9.4e-75:754:72//J58134

F-PLACE1003886//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//6.7e-20:432:64//AC006030

15 F-PLACE1003888//Human mRNA for phospholipase C, complete cds.//2.6e-53:702:67//D42108

F-PLACE1003892//RPC111-24P17.TV RPC1-11 Homo sapiens genomic clone RPC1-11-24P17, genomic survey sequence.//3.3e-20:245:65//B86759

F-PLACE1003900//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 328E19, WORKING DRAFT SEQUENCE.//2.5e-17:260:71//AL022240

20 F-PLACE1003903//Mus musculus CTP synthetase homolog (CTPsh) mRNA, complete cds.//2.7e-86:533:87//U49385

F-PLACE1003915//Mus musculus clone OST1963, genomic survey sequence.//6.4e-29:251:80//AF046591

F-PLACE1003923//Homo sapiens full-length insert cDNA clone ZD40A05.//2.8e-25:316:70//AF086251

F-PLACE1003932//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.6e-05:652:58//AC005505

25 F-PLACE1003936//CIT-HSP-2387C11.TR.1 CIT-HSP Homo sapiens genomic clone 2387C11, genomic survey sequence.//1.0:223:62//AQ239494

F-PLACE1003968//Rattus norvegicus 5'-AMP-activated protein kinase, gamma-1 subunit mRNA, complete cds.//5.2e-47:505:72//U42413

30 F-PLACE1004103//Homo sapiens chromosome 19, cosmid R28784, complete sequence.//6.7e-29:241:84//AC005954

F-PLACE1004104//Rattus norvegicus rsec5 mRNA, complete cds.//3.0e-115:719:86//AF032666

F-PLACE1004114//Homo sapiens Chromosome 22q11.2 BAC Clone 77h2 In CES Region, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.5e-22:213:80//AC000052

35 F-PLACE1004118//Pseudorabies virus with upstream and downstream sequences.//0.87:209:64//M34651

F-PLACE1004128//M.musculus G protein beta-subunit mRNA, complete cds.//2.5e-62:437:84//M63658

F-PLACE1004149//Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds.//1.4e-16:342:65//AF005355

F-PLACE1004156//Homo sapiens DNA sequence from PAC 57E3 on chromosome 6p12.1-21.1. Contains GSSs and an STS with a TATC repeat polymorphism, complete sequence.//1.2e-26:299:74//AL022099

40 F-PLACE1004161

F-PLACE1004183//Homo sapiens for TOM1-like protein.//1.2e-146:731:96//AJ010071

F-PLACE1004197

F-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds.//4.0e-144:695:98//AF069493

45 F-PLACE1004242//Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence.//2.3e-151:772:95//AL021326

F-PLACE1004256//HS_2010_B2_G04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2010 Col=8 Row=N, genomic survey sequence.//1.5e-44:372:79//AQ252434

50 F-PLACE1004257//Homo sapiens BAC clone NH0342K06 from 2, complete sequence.//0.00011:349:63//AC005034

F-PLACE1004258//Homo sapiens DNA sequence from PAC 779B17 on chromosome 22q13.1. Contains exon trap, complete sequence.//0.77:475:59//AL021806

55 F-PLACE1004270//Human IgA C alpha 1 switch region (Sa1).//1.7e-08:622:61//L19121

F-PLACE1004274//Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence.//2.3e-151:772:95//AL021326

F-PLACE1004277//Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete cds.//2.3e-151:772:95//AL021326

97//AF084830

F-PLACE1004284//*Arabidopsis thaliana* genomic DNA, chromosome 5, P1 clone: MPI7, complete sequence.//0.0060:635:57//AB011480

F-PLACE1004289//HS_3023_B1_E04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3023 Col=7 Row=J, genomic survey sequence.//2.4e-12:86:98//AQ094451

F-PLACE1004302//*Streptomyces coelicolor* cosmid 7H1.//0.26:297:64//AL021411

F-PLACE1004316//H.sapiens mRNA for apoptosis specific protein.//2.9e-150:797:94//Y11588

F-PLACE1004336//*Drosophila melanogaster* DNA sequence (P1 DS07968 (D117)), complete sequence.//0.87:206:59//AC004267

F-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds.//5.9e-139:688:97//AF100153

F-PLACE1004376//*Mus musculus* clone OST20307, genomic survey sequence.//4.1e-81:498:89//AF046631

F-PLACE1004384//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1121J18, WORKING DRAFT SEQUENCE.//3.6e-41:482:73//AL031653

F-PLACE1004388//*Caenorhabditis elegans* cosmid K08F11.//8.6e-26:615:62//U70855

F-PLACE1004405//Homo sapiens clone GS512I21, WORKING DRAFT SEQUENCE, 9 unordered pieces.//9.2e-150:749:96//AC005027

F-PLACE1004425//Homo sapiens PAC clone DJ0733B09 from 7p14-p13, complete sequence.//2.4e-08:129:76//AC005532

F-PLACE1004428//*R. norvegicus* mRNA for Pristanoyl-CoA Oxidase.//7.0e-17:549:61//X95188

F-PLACE1004437//Human NAD⁺-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds.//3.1e-129:536:99//U49283

F-PLACE1004451//Human DNA sequence from PAC 214K23, BRCA2 gene region chromosome 13q12-13 contains BRCA2 exons 1-24, Interferon Induced 56Kd pseudogene and ESTs.//4.8e-23:231:71//Z74739

F-PLACE1004460//Homo sapiens PAC clone DJ1064B22 from 7q21, complete sequence.//0.96:454:56//AC004954

F-PLACE1004467//HS_2058_B1_C09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=17 Row=F, genomic survey sequence.//2.4e-87:433:98//AQ242700

F-PLACE1004471//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//1.4e-74:665:70//M27877

F-PLACE1004473//CIT-HSP-2045A15.TF CIT-HSP Homo sapiens genomic clone 2045A15; genomic survey sequence.//3.3e-20:140:92//B80243

F-PLACE1004491//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//9.9e-05:794:57//AC004709

F-PLACE1004506//Human Gx-alpha gene.//1.0e-05:231:63//D90150

F-PLACE1004510//Homo sapiens TATA binding protein associated factor (TAFII150) mRNA, complete cds.//3.2e-146:699:98//AF040701

F-PLACE1004516//Human DNA sequence from cosmid SRL9A13, chromosome region 11p13. Contains EST.//1.4e-33:367:71//Z86001

F-PLACE1004518

F-PLACE1004548//*Dictyostelium discoideum* MigA (migA) gene, complete cds.//2.6e-05:318:62//U86962

F-PLACE1004550//Human FMR1 gene, 5' end.//0.0018:142:66//L19476

F-PLACE1004564//*B. taurus* mRNA for cleavage and polyadenylation specificity factor.//1.7e-114:513:85//X75931

F-PLACE1004629//*Anolis carolinensis* Brain-1 gene, complete cds.//0.00013:188:67//AB001868

F-PLACE1004645//*Mycobacterium tuberculosis* H37Rv complete genome; segment 138/162.//0.66:337:60//Z95120

F-PLACE1004646//*Rattus norvegicus* retinal pigment epithelium-specific protein (Rpe65) mRNA, complete cds.//1.1e-19:326:63//AF035673

F-PLACE1004658//H.sapiens CpG island DNA genomic MseI fragment, clone 55h1, forward read cpg55h1.ft1a.//12.4e-34:188:98//Z61632

F-PLACE1004664//*Caenorhabditis elegans* cosmid W10G6, complete sequence.//1.0:148:65//Z81140

F-PLACE1004672//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds.//1.9e-101:182:95//U07561

F-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds.//4.3e-109:625:91//AF035606

F-PLACE1004675//Homo sapiens DNA sequence from PAC clone 1121J18, WORKING DRAFT SEQUENCE

F-PLACE1004676//Homo sapiens DNA sequence from PAC clone 1121J18, WORKING DRAFT SEQUENCE

F-PLACE1004677//Homo sapiens DNA sequence from PAC clone 1121J18, WORKING DRAFT SEQUENCE

SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.//1.2e-34:320:71//Z95152

F-PLACE1004691//HS_3044_A1_G01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3044 Col=1 Row=M, genomic survey sequence.//0.018:191:63//AQ098323

F-PLACE1004693//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.28:573:57//AL022577

F-PLACE1004716//Plasmodium falciparum MAL3P6, complete sequence.//0.00081:428:59//Z98551

F-PLACE1004722//HS_3052_B1_C10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3052 Col=19 Row=F, genomic survey sequence.//2.3e-05:104:75//AQ134959

F-PLACE1004736//CIT-HSP-2365J21.TF CIT-HSP Homo sapiens genomic clone 2365J21, genomic survey sequence.//1.3e-24:180:88//AQ080498

F-PLACE1004740//RPC111-58A7.TJ RPC111 Homo sapiens genomic clone R-58A7, genomic survey sequence.//8.6e-26:522:65//AQ195766

F-PLACE1004743//Mus musculus ubiquitin-protein ligase E3-alpha (Ubr1) mRNA, complete cds.//1.1e-112:711:86//AF061555

F-PLACE1004751

F-PLACE1004773//Homo sapiens inversin protein mRNA, complete cds.//5.4e-171:828:97//AF084367

F-PLACE1004777//Rattus norvegicus mRNA for myosin-RhoGAP protein Myr 7.//4.2e-134:763:90//AJ001713

F-PLACE1004793//Human DNA sequence from clone 323P24 on chromosome Xp11.21-11.23 Contains SPIN (spindlin homolog (PROTEIN DXF34), hypothetical protein EST, STS, GSS, complete sequence.//9.3e-132:759:90//AL022157

F-PLACE1004804

F-PLACE1004813//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//6.5e-06:403:58//AC004710

F-PLACE1004814//Homo sapiens chromosome 17, clone hRPK.294_J_22, complete sequence.//9.8e-39:207:99//AC005921

F-PLACE1004815//Homo sapiens PAC clone DJ0651K02 from 7p21-p22, complete sequence.//8.1e-15:203:73//AC004613

F-PLACE1004824//G.gallus PB1 gene.//1.1e-103:759:80//X90849

F-PLACE1004827//HS_2230_A2_A05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2230 Col=10 Row=A, genomic survey sequence.//4.1e-38:330:81//AQ299313

F-PLACE1004836//H.sapiens nidogen gene (exon 8).//0.97:116:68//X84825

F-PLACE1004838//HS_3241_A2_A04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3241 Col=8 Row=A, genomic survey sequence.//1.8e-87:425:98//AQ206740

F-PLACE1004840//Sequence 2 from patent US 5728819.//6.7e-47:285:91//I92819

F-PLACE1004868

F-PLACE1004885//Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 9.//0.14:465:59//Z97344

F-PLACE1004900

F-PLACE1004902//CITBI-E1-2510J4.TR CITBI-E1 Homo sapiens genomic clone 2510J4, genomic survey sequence.//3.6e-06:56:100//AQ261184

F-PLACE1004913//Homo sapiens BAC clone RG054D04 from 7q31, complete sequence.//2.6e-151:770:91//AC005058

F-PLACE1004918//Mus musculus signaling molecule (ATTP) mRNA, complete cds.//2.6e-68:459:84//U97571

F-PLACE1004930//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds.//4.4e-106:545:95//AF070671

F-PLACE1004934//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudo-gene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//3.5e-45:226:84//AL020989

F-PLACE1004937

F-PLACE1004969

F-PLACE1004972//Homo sapiens PAC clone DJ0612F12 from 7p12-p14, complete sequence.//0.012:316:61//AC004843

F-PLACE1004979//Human DNA sequence from clone 142F18 on chromosome Xq26.3-27.2 Contains part of a gene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//3.5e-45:226:84//AL020989

446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 845, 846, 847, 848, 849, 850, 851, 852, 853, 854, 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872, 873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 885, 886, 887, 888, 889, 890, 891, 892, 893, 894, 895, 896, 897, 898, 899, 900, 901, 902, 903, 904, 905, 906, 907, 908, 909, 910, 911, 912, 913, 914, 915, 916, 917, 918, 919, 920, 921, 922, 923, 924, 925, 926, 927, 928, 929, 930, 931, 932, 933, 934, 935, 936, 937, 938, 939, 940, 941, 942, 943, 944, 945, 946, 947, 948, 949, 950, 951, 952, 953, 954, 955, 956, 957, 958, 959, 960, 961, 962, 963, 964, 965, 966, 967, 968, 969, 970, 971, 972, 973, 974, 975, 976, 977, 978, 979, 980, 981, 982, 983, 984, 985, 986, 987, 988, 989, 990, 991, 992, 993, 994, 995, 996, 997, 998, 999, 1000

- F-PLACE1004985//Plasmodium falciparum chromosome 2, section 10 of 73 of the complete sequence.//8.8e-14:590:61//AE001373
- F-PLACE1005026
- F-PLACE1005027
- 5 F-PLACE1005046
- F-PLACE1005052//Homo sapiens chromosome Xp22-135-136 clone GSHB-56711, WORKING DRAFT SEQUENCE, 35 unordered pieces.//2.1e-135:675:97//AC005867
- F-PLACE1005055//Homo sapiens mRNA for KIAA0576 protein, partial cds.//1.9e-159:761:98//AB011148
- 10 F-PLACE1005066//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//9.2e-10:757:56//AF059569
- F-PLACE1005077
- F-PLACE1005085//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//6.9e-29:253:77//AC004673
- F-PLACE1005086//Homo sapiens chromosome 17, clone HCIT11023, complete sequence.//6.5e-52:446:78//AC002316
- 15 F-PLACE1005101//Homo sapiens clone DJ0414A15, WORKING DRAFT SEQUENCE, 9 unordered pieces.//2.0e-146:734:96//AC005225
- F-PLACE1005102//Homo sapiens chromosome 19, cosmid R29388, complete sequence.//9.8e-83:254:95//AC004476
- 20 F-PLACE1005108//Human BAC clone RG009H02 from 7q31, complete sequence.//0.46:179:64//AC003081
- F-PLACE1005111
- F-PLACE1005128//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//0.00051:287:63//L14320
- F-PLACE1005146//HS_3071_A1_E03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=5 Row=I, genomic survey sequence.//7.4e-38:299:82//AQ103361
- 25 F-PLACE1005162//Human BAC clone GS306C12 from 7q21-q22, complete sequence.//2.6e-44:346:82//AC002451
- F-PLACE1005176
- F-PLACE1005181//CIT-HSP-2340O5.TR CIT-HSP Homo sapiens genomic clone 2340O5, genomic survey sequence.//0.99:211:63//AQ054651
- 30 F-PLACE1005187//CIT-HSP-2358N6.TR CIT-HSP Homo sapiens genomic clone 2358N6, genomic survey sequence.//2.7e-07:80:90//AQ074445
- F-PLACE1005206//Human BAC clone 133K23 from 7q31.2, complete sequence.//0.98:216:61//AC000061
- F-PLACE1005232//Homo sapiens clone DJ1106H14, WORKING DRAFT SEQUENCE, 42 unordered pieces.//0.70:245:63//AC004965
- 35 F-PLACE1005243
- F-PLACE1005261//Caenorhabditis elegans cosmid T05H10, complete sequence.//0.00041:254:61//Z47812
- F-PLACE1005266//H.sapiens mRNA (fetal brain cDNA a4_2g).//9.6e-33:177:98//Z70695
- F-PLACE1005277//Homo sapiens mRNA for KIAA0610 protein, partial cds.//1.6e-148:706:98//AB011182
- 40 F-PLACE1005287//Plasmodium falciparum (MESA) mRNA exons 1-2, complete cds.//2.8e-15:737:60//M69183
- F-PLACE1005305//Bovine mitochondrial GTP:AMP phosphotransferase mRNA, complete cds.//3.8e-111:728:84//M25757
- F-PLACE1005308//Clethrionomys glareolus endogenous retroviral sequence ERV-L pol gene, clone ERV-L Vole Cg14.//1.0:128:67//AJ233621
- 45 F-PLACE1005313//Caenorhabditis elegans cosmid D2092.//8.8e-11:342:62//U88167
- F-PLACE1005327//HS_3080_B2_A12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3080 Col=24 Row=B, genomic survey sequence.//4.1e-25:147:96//AQ139116
- F-PLACE1005331//Homo sapiens chromosome 19, cosmid F20569, complete sequence.//1.4e-132:399:94//AC004794
- 50 F-PLACE1005335//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//5.5e-114:237:92//AC000380
- F-PLACE1005373
- F-PLACE1005374//Homo sapiens chromosome 7 common fragile site, complete sequence.//0.20:305:58//AF017104
- 55 F-PLACE1005409//Human BAC clone RG167B05 from 7q21 complete sequence.//2.5e-148:760:95//AC003991
- F-PLACE1005410//Homo sapiens chromosome 10, cosmid F20569, complete sequence.//1.0e-132:399:94//AC004794
- WORKING DRAFT SEQUENCE.//1.0e-132:399:94//AC004794
- F-PLACE1005467//Rat mRNA.//0.0014:131:70//M59858

F-PLACE1005471//Human DNA sequence from clone 45I4 on chromosome 6q24.1-24.3. Contains two putative unknown genes, ESTs, STSs and GSSs, complete sequence.//3.0e-23:530:67//AL023581

F-PLACE1005477//Human DNA sequence from clone J181N11, WORKING DRAFT SEQUENCE.//3.3e-131:814:88//Z82191

5 F-PLACE1005480//Homo sapiens DNA sequence from PAC 257I20 on chromosome 22q13.1-13.2. Contains cytochrome P450 pseudogenes CYP2D7P, CYP2D8P, CYP2D6(D), TCF20, NADH ubiquinone oxidoreductase B14 subunit, ESTs, CA repeat, STS, GSS.//7.0e-34:246:73//AL021878

F-PLACE1005481//RPCI11-74L17.TJ RPCI11 Homo sapiens genomic clone R-74L17, genomic survey sequence.//0.37:403:57//AQ266885

10 F-PLACE1005494//Homo sapiens transient receptor potential protein 6 mRNA, complete cds.//2.1e-67:325:99//AF080394

F-PLACE1005502//Homo sapiens BAC clone NH0161H12 from 7p14-p15, complete sequence.//0.015:403:61//AC005589

15 F-PLACE1005526//H.sapiens CpG island DNA genomic MseI fragment, clone 9f1, reverse read cpg9f1.rt1a.//3.6e-27:159:96//Z66485

F-PLACE1005528//Homo sapiens genomic DNA, chromosome 21q11.1, segment 9/28, WORKING DRAFT SEQUENCE.//2.6e-28:449:67//AP000038

F-PLACE1005530//Homo sapiens clone DJ0691L07, complete sequence.//6.5e-18:234:72//AC004860

20 F-PLACE1005550//Fugu rubripes GSS sequence, clone 048A08bH3, genomic survey sequence.//1.2e-14:123:75//AL025925

F-PLACE1005554//Leishmania tarentolae mitochondrial 12S ribosomal RNA gene.//0.43:209:66//X02354

F-PLACE1005557//Homo sapiens chromosome 17, clone hRPC.117_B_12, complete sequence.//9.3e-113:536:97//AC004707

25 F-PLACE1005574//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.1e-10:514:59//AC005504

F-PLACE1005584//Homo sapiens mRNA for KIAA0617 protein, complete cds.//0.00056:289:63//AB014517

F-PLACE1005595//Human Chromosome 11q12.2 PAC clone pDJ606g6, complete sequence.//1.2e-111:262:89//AC004126

F-PLACE1005603

30 F-PLACE1005611//F16O5TFC IGF Arabidopsis thaliana genomic clone F16O5, genomic survey sequence.//2.0e-10:209:66//B98589

F-PLACE1005623

F-PLACE1005630//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//1.2e-93:230:98//AC005840

35 F-PLACE1005639//HS_3095_B1_A03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3095 Col=5 Row=B, genomic survey sequence.//1.2e-05:220:63//AQ123022

F-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds.//6.4e-150:721:98//AF083255

40 F-PLACE1005656//H.sapiens RR2 mRNA for small subunit ribonucleotide reductase.//1.3e-51:480:74//X59618

F-PLACE1005666//RPCI11-78O15.TV RPCI11 Homo sapiens genomic clone R-78O15, genomic survey sequence.//8.7e-05:243:62//AQ284667

F-PLACE1005698//Human membrane-associated lectin type-C mRNA.//1.9e-63:374:85//M98457

F-PLACE1005727//Plasmodium falciparum chromosome 2, section 59 of 73 of the complete sequence.//0.69:633:57//AE001422

45 F-PLACE1005730//HS_2026_B1_H11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026 Col=21 Row=P, genomic survey sequence.//2.0e-24:286:74//AQ231147

F-PLACE1005739//Mus musculus IFN-gamma induced (Mg11) mRNA, complete cds.//2.8e-55:621:71//U15635

F-PLACE1005755//HS_2213_A2_H11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2213 Col=22 Row=O, genomic survey sequence.//1.4e-25:290:75//AQ136844

50 F-PLACE1005763//Rat medium-chain S-acyl fatty acid synthetase thio ester hydrolase (MCH), complete cds.//4.5e-40:297:70//M16200

F-PLACE1005799//R.norvegicus mRNA for mitochondrial isoform of cytochrome b5.//0.91:287:63//Y12517

F-PLACE10058021//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.//5.0e-109:530:98//AC004827

55 F-PLACE1005803//HS_3092_B1_A10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3092 Col=10 Row=M, genomic survey sequence.//1.2e-05:220:63//AQ123022

F-PLACE1005804//Homo sapiens alpha-L-mannosidase B1 mRNA, complete cds.//4.4e-53:636:96//AF065482

F-PLACE1005813//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//2.6e-54:739:98//AF065482

F-PLACE1005828//Homo sapiens chromosome 17, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//2.2e-37:355:77//AC004150

F-PLACE1005834//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-105, complete sequence.//0.00080:663:58//AL010283

5 F-PLACE1005845//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00015:340:58//AC004153

F-PLACE1005850//Human DNA sequence from clone 465N24 on chromosome 1p35.1-36.13. Contains two novel genes, ESTs, GSSs and CpG islands, complete sequence.//1.8e-46:278:85//AL031432

F-PLACE1005851

10 F-PLACE1005876//B.taurus mRNA for cleavage and polyadenylation specificity factor.//5.0e-120:701:89//X75931

F-PLACE1005884//CIT-HSP-2333O12.TR CIT-HSP Homo sapiens genomic clone 2333O12, genomic survey sequence.//4.6e-78:385:98//AQ039226

F-PLACE1005890//Schizosaccharomyces pombe bem1/bud5 suppressor (Bem46+) mRNA, partial cds.//9.3e-16:638:57//U29892

15 F-PLACE1005898//Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds.//1.0:178:65//U67136

F-PLACE1005921//M.musculus mRNA for immunity associated protein 38.//6.6e-17:614:59//Y08026

F-PLACE1005923//RPC111-33G19.TJ RPC1-11 Homo sapiens genomic clone RPC1-11-33G19, genomic survey sequence.//4.0e-10:535:57//AQ046151

20 F-PLACE1005925//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 537K23, WORKING DRAFT SEQUENCE.//0.17:159:65//AL034405

F-PLACE1005932

F-PLACE1005934//H.sapiens CpG island DNA genomic MseI fragment, clone 165g2, forward read cpg165g2.ft1a.//8.3e-43:247:93//Z57153

25 F-PLACE1005936//F.rubripes GSS sequence, clone 069K22aG2, genomic survey sequence.//0.91:116:68//AL014719

F-PLACE1005951//Rhodobacter sphaeroides DMSO/TMAO-sensor kinase (dorS), DMSO/TMAO-response regulator (dorR), DMSO/TMAO-cytochrome c-containing subunit (dorC), DMSO-membrane protein (dorB), and DMSO/TMAO-reductase (dorA) genes, complete cds.//0.0022:495:59//AF016236

30 F-PLACE1005953//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence.//2.9e-05:442:61//AC004081

F-PLACE1005955//Caenorhabditis elegans cosmid F01F1.//4.3e-20:409:64//U13070

F-PLACE1005966//P.falciparum aarp3 gene, exon.//0.0083:270:64//Y08925

F-PLACE1005968

35 F-PLACE1005990//Homo sapiens chromosome 12p13.3 clone RPC111-407G6, WORKING DRAFT SEQUENCE, 51 ordered pieces.//1.0e-100:513:96//AC005866

F-PLACE1006002//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 229A8, WORKING DRAFT SEQUENCE.//2.5e-54:444:77//Z86090

F-PLACE1006003//HS-1059-A2-G01-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 781 Col=2 Row=M, genomic survey sequence.//3.4e-05:214:64//B44442

40 F-PLACE1006011//Mus musculus poly-(ADPribose)-transferase homolog PARP mRNA, complete cds.//4.3e-71:580:79//AF072521

F-PLACE1006017//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-113A6 -complete genomic sequence, complete sequence.//8.6e-32:177:83//AC002299

45 F-PLACE1006037//Mus musculus B6D2F1 clone 2C11B mRNA.//1.8e-34:269:83//U01139

F-PLACE1006040//Homo sapiens mRNA for alpha endosulfine.//3.4e-147:719:97//X99906

F-PLACE1006076//Homo sapiens DNA sequence from PAC 79C4 on chromosome 1q24. Contains the PMX1 gene, coding for two alternative forms of the Paired Mesoderm Homeobox protein 1 (PMX-1, PHOX-1). Contains ESTs, STSs and BAC end sequences (GSSs), complete sequence.//0.37:332:62//Z97200

50 F-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds.//1.3e-145:679:99//AF039023

F-PLACE1006129

F-PLACE1006139//Saccharomyces cerevisiae chromosome VI cosmid 9965.//4.8e-27:693:60//D44597

F-PLACE1006143//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 169I5, WORKING DRAFT SEQUENCE.//4.7e-46:435:77//Z93015

55 F-PLACE1006157//Saguinus oedipus mRNA for membrane cofactor protein CD46 complete cds. clone:B2 //

F-PLACE1006159//Homo sapiens chromosome 12p13.3 clone RPC111-407G6, WORKING DRAFT SEQUENCE, 51 ordered pieces.//1.0e-100:513:96//AC005866

F-PLACE1006164//HS_3003_A1_F08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3003 Col=15 Row=K, genomic survey sequence//1.4e-70:388:93//AQ118200
 F-PLACE1006167//Homo sapiens chromosome 19, cosmid F23149, complete sequence//4.3e-78:385:86//AC005239

5 F-PLACE1006170//Mouse mRNA for alpha-adaptin (C)//3.5e-91:630:84//X14972
 F-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds//3.9e-149:694:99//AF091433
 F-PLACE1006195//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Human BAC library) complete sequence//2.5e-16:283:70//AC003658
 F-PLACE1006196//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete

10 cds//2.2e-94:648:84//L25125
 F-PLACE1006205//Human Xp22 cosmid U250A9, complete sequence//0.15:533:58//U75931
 F-PLACE1006223//F24L20-T7 IGF Arabidopsis thaliana genomic clone F24L20, genomic survey sequence//0.0068:175:64//B19803
 F-PLACE1006225//CIT-HSP-2335I23.TF CIT-HSP Homo sapiens genomic clone 2335I23, genomic survey sequence//2.1e-19:149:90//AQ039880

15 F-PLACE1006236//Human chromosome 12p15 BAC clone CIT987SK-99D8 complete sequence//0.51:290:58//U91327
 F-PLACE1006239//Homo sapiens BAC clone RG118D07 from 7q31, complete sequence//7.4e-158:452:96//AC004142

20 F-PLACE1006246//RPCI11-36I23.TK RPCI-11 Homo sapiens genomic clone RPCI-11-36I23, genomic survey sequence//2.6e-31:176:97//AQ045400
 F-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds//2.3e-166:791:98//AB014548
 F-PLACE1006262//342E3.TVD CIT978SKA1 Homo sapiens genomic clone A-342E03, genomic survey sequence//1.0:228:63//B16447

25 F-PLACE1006288//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 20N2, WORKING DRAFT SEQUENCE//6.6e-172:809:99//AL031320
 F-PLACE1006318
 F-PLACE1006325//Homo sapiens PAC clone DJ0988L12 from 7q11.23-q21.1, complete sequence//0.079:396:59//AC004454

30 F-PLACE1006335//Mouse Ig third hypervariable region (HCDR3), nonproductively rearranged alpha-chain gene VHSB32-D-JH2 region//1.0:90:67//M55721
 F-PLACE1006357//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces//0.16:445:56//AC005504
 F-PLACE1006360//Plasmodium falciparum MAL3P7, complete sequence//6.1e-05:625:57//AL034559

35 F-PLACE1006368//X.laevis mRNA for KLP2 protein//3.0e-25:376:68//X94082
 F-PLACE1006371//Homo sapiens chromosome 16, cosmid clone 360H6 (LANL), complete sequence//2.0e-146:711:97//AC004232
 F-PLACE1006382
 F-PLACE1006385//Homo sapiens epsin 2a mRNA, complete cds//5.1e-110:539:97//AF062085

40 F-PLACE1006412//Homo sapiens BAC clone GS588G18 from 7p12-p14, complete sequence//1.3e-23:463:68//AC005029
 F-PLACE1006414//Homo sapiens PCAF associated factor 65 alpha mRNA, complete cds//1.3e-109:525:98//AF069735
 F-PLACE1006438//Homo sapiens mRNA for KIAA0557 protein, partial cds//6.9e-23:531:65//AB011129

45 F-PLACE1006445//HS_3071_A1_C11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=21 Row=E, genomic survey sequence//4.7e-74:392:95//AQ 103347
 F-PLACE1006469//Rhodobacter capsulatus strain SB1003, partial genome//1.1e-40:686:65//AF010496
 F-PLACE1006470//T.brucei kinetoplast maxicircle variable region DNA//0.99:250:59//Z15118
 F-PLACE1006482//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 447C4, WORKING

50 DRAFT SEQUENCE//4.3e-120:328:98//AL021977
 F-PLACE1006488//Canine mRNA for 68kDA subunit of signal recognition particle (SRP68)//6.5e-86:478:91//X53744
 F-PLACE1006492
 F-PLACE1006506

55 F-PLACE1006521//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence//0.0010:547:58//

005080

AC010000 AC010001 AC010002 AC010003 AC010004 AC010005 AC010006 AC010007 AC010008 AC010009
 AC010010 AC010011 AC010012 AC010013 AC010014 AC010015 AC010016 AC010017 AC010018 AC010019

F-PLACE1006534//Caenorhabditis elegans cosmid Y40H7A, complete sequence.//0.00031:671:58//AL033510
 F-PLACE1006540
 F-PLACE1006552//P.falciparum glutamic acid-rich protein gnen, complete cds.//6.0e-10:636:59//J03998
 F-PLACE1006598//Homo sapiens BAC clone NH0539B24 from 7p15.1-p14, complete sequence.//9.8e-25:170:
 5 77//AC006044
 F-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//
 6.7e-167:781:99//U97670
 F-PLACE1006617//Homo sapiens Xp22 BAC GSHB-433024 (Genome Systems Human BAC library) complete
 sequence.//0.98:514:59//AC004470
 10 F-PLACE1006626//H.sapiens DNA 3' flanking simple sequence region clone wg2c3.//0.00079:206:62//X76589
 F-PLACE1006629//Human BAC clone RG333F24 from 7q11.2-q21, complete sequence.//0.0012:576:57//
 AC004015
 F-PLACE1006640//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.0018:588:59//X95276
 F-PLACE1006673//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING
 15 DRAFT SEQUENCE, 4 unordered pieces.//0.0028:469:58//AC004688
 F-PLACE1006678//Mus musculus UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase-I (b3GT1) gene, complete
 cds.//0.00011:184:64//AF029790
 F-PLACE1006704//Mus musculus dentin sialophosphoprotein precursor (DSPP) mRNA, complete cds.//0.0013:
 380:62//U67916
 20 F-PLACE1006731//Human DNA sequence from PAC 408N23 on chromosome 22q13. Contains HIP, HSC70-IN-
 TERACTING PROTEIN (PROGESTERONE RECEPTOR-ASSOCIATED P48 PROTEIN), ESTs and STS.//1.5e-
 78:520:86//Z98048
 F-PLACE1006754//Homo sapiens chromosome 19, cosmid R29124, complete sequencer.//1.9e-135:378:99//
 AC005626
 25 F-PLACE1006760//CIT-HSP-2336O13.TR CIT-HSP Homo sapiens genomic clone 2336O13, genomic survey se-
 quence.//0.018:147:66//AQ039246
 F-PLACE1006779//Plasmodium falciparum chromosome 2, section 63 of 73 of the complete sequence.//2.6e-08:
 823:58//AE001426
 F-PLACE1006782//Homo sapiens clone NH0005N18, WORKING DRAFT SEQUENCE, 2 unordered pieces.//
 30 0.043:252:65//AC005487
 F-PLACE1006792//HS_3165_B1_H01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3165 Col=1 Row=P, genomic survey sequence.//1.4e-11:249:67//AQ149559
 F-PLACE1006795//Mouse eph-related receptor tyrosine kinase (Mek4) mRNA, complete cds.//1.3e-12:155:80//
 M68513
 35 F-PLACE1006800//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-92, complete
 sequence.//6.7e-05:391:62//AL010272
 F-PLACE1006805//paramecium species 1,168 mt dna dimer: replication init. region.//9.1e-09:369:62//K00915
 F-PLACE1006815//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 321D2, WORKING
 DRAFT SEQUENCE.//0.89:465:58//AL031033
 40 F-PLACE1006819//Homo sapiens clone DJ1163L11, complete sequence.//1.5e-121:618:91//AC005230
 F-PLACE1006829//Brn-3a=class V POU transcription factor [mice, CD/CD, embryo fibroblast cells, Genomic, 2160
 nt].//0.011:145:68//S69350
 F-PLACE1006860//Plasmodium falciparum MAL3P7, complete sequence.//2.2e-07:691:58//AL034559
 F-PLACE1006867//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 323M4, WORKING
 45 DRAFT SEQUENCE.//1.5e-132:643:98//AL033378
 F-PLACE1006878
 F-PLACE1006883//Mycobacterium tuberculosis H37Rv complete genome; segment 138/162.//1.0:236:62//
 Z95120
 F-PLACE1006901//Mus musculus t complex testis-specific protein (Tctex2) gene, t haplotype, promoter se-
 50 quence.//2.7e-19:171:81//U21672
 F-PLACE1006904
 F-PLACE1006917//H.sapiens CpG island DNA genomic MseI fragment, clone 79g10, forward read
 cpg79g10.ft1a.//1.3e-21:131:98//Z63175
 F-PLACE1006932//Mus musculus FKBP65 binding protein mRNA, complete cds.//0.99:248:61//L07063
 55 F-PLACE1006935//Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen
 (trypsinogen 10.85 kb) (AF099902)

Seq. 6958 FVL (accession number 6958) (M00644)

Seq. 6958 M00644 (accession number 6958) (M00644) mRNA complete cds.//2.0e-04:463:60

U23921

F-PLACE1006961//*Saccharomyces cerevisiae* mitochondrial tRNA-Tyr, tRNA-Asn, & amp; tRNA-Met genes.//1.6e-06:651:58//AJ223323

F-PLACE1006962//*H.sapiens* ir1B mRNA.//7.1e-15:202:71//X63417

5 F-PLACE1006966//*Caenorhabditis elegans* DNA *** SEQUENCING IN PROGRESS *** from clone Y105E8, WORKING DRAFT SEQUENCE.//1.7e-26:451:61//AL022594

F-PLACE1006989//cSRL-172A4-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-172A4, genomic survey sequence.//1.0:97:67//B03188

10 F-PLACE1007014//*Rattus norvegicus* equilibrative nitrobenzylthioinosine-insensitive nucleoside transporter mRNA, complete cds.//4.2e-07:592:58//AF015305

F-PLACE1007021//Homo sapiens chromosome 19, cosmid F16403; complete sequence.//5.1e-17:285:70//AC005777

F-PLACE1007045//Human DNA sequence from PAC 181N1 on chromosome X contains ESTs, STS polymorphic CA repeat* //6.2e-131:775 :89//Z82899

15 F-PLACE1007053//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.7e-143:675:99//AC004895

F-PLACE1007068//Homo sapiens chromosome 17, clone hRPK.214_O_1, complete sequence.//1.3e-131:652:97//AC005224

20 F-PLACE1007097//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//8.3e-158:768:97//AL021368

F-PLACE1007105//*Mus musculus* muskulin mRNA, complete cds.//4.1e-124:687:91//U72194

25 F-PLACE1007111//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.7e-05:586:56//AC005139

F-PLACE1007112//HS_2234_B2_G10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2234 Col=20 Row=N, genomic survey sequence.//0.26:200:62//AQ087801

30 F-PLACE1007132//CIT978SK-A-211C6.TVB CIT978SK Homo sapiens genomic clone A-211C6, genomic survey sequence.//1.3e-40:255:92//B72112

F-PLACE1007140//QN1 orf [Coturnix coturnix, japonica, K2 neuroretinal cells, mRNA Partial, 3884 nt]//4.9e-15:386:62//S68151

F-PLACE1007178//*Plasmodium falciparum* 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.011:329:61//AC005140

35 F-PLACE1007226//Human lipocortin (LIP) 2 gene, upstream region.//0.0036:180:63//M62899

F-PLACE1007238//FMR1 {CGG repeats} [human, Fragile X syndrome patient, Genomic, 429 nt]//2.8e-08:269:63//S74494

F-PLACE1007239//Homo sapiens mRNA for transcription elongation factor S-II, hS-II-T1, complete cds.//6.3e-57:405:87//D50495

40 F-PLACE1007242//HS_3006_A1_B11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3006 Col=21 Row=C, genomic survey sequence.//0.088:191:59//AQ089443

F-PLACE1007243//Human transporter protein (g17) mRNA, complete cds.//7.9e-12:245:66//U49082

F-PLACE1007257//Homo sapiens mRNA for dia-12c protein.//5.2e-144:677:98//Y15908

45 F-PLACE1007274//HS_3003_A1_D08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3003 Col=15 Row=G, genomic survey sequence.//7.4e-49:345:85//AQ294154

F-PLACE1007276//Fugu rubripes GSS sequence, clone 014O10aG11, genomic survey sequence.//0.0052:228:62//AL024982

F-PLACE1007282//F.rubripes GSS sequence, clone 019O07aB3, genomic survey sequence.//0.024:289:58//AL011743

50 F-PLACE1007286//Human Chromosome 16 BAC clone CIT987SK-A-256A9, complete sequence.//0.0048:185:69//AC002492

F-PLACE1007301//*Dictyostelium discoideum* gene for TRFA, complete cds.//0.069:761:57//AB009080

F-PLACE1007317

F-PLACE1007342

55 F-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds.//5.4e-120:167:38//AF066876

F-PLACE1007375//Caenorhabditis elegans cosmid D2092.//1.8e-12:193:70//U88167

F-PLACE1007386

F-PLACE1007402//HS_2170_A2_D12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2170 Col=24 Row=G, genomic survey sequence.//5.6e-06:162:67//AQ125590

5 F-PLACE1007409//Homo sapiens mitoxantrone resistance protein 2 mRNA, complete sequence.//1.6e-25:165:93//AF093772

F-PLACE1007416

F-PLACE1007450//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//4.9e-34:764:62//AC003973

10 F-PLACE1007452//Mus musculus bet3 (Bet3) mRNA, complete cds.//4.1e-17:374:64//AF041433

F-PLACE1007454//Homo sapiens (clone s153) mRNA fragment.//8.1e-52:317:93//L40391

F-PLACE1007460//Human DNA sequence from clone 914P14 on chromosome Xq23 Contains calpain-like protease gene, DCX (doublecortin) ESTs, CA repeat, GSS, complete sequence.//0.0019:280:64//AL031117

15 F-PLACE1007478//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-345G4 -complete genomic sequence, complete sequence.//2.5e-24:362:71//AC002302

F-PLACE1007484

F-PLACE1007488//Danio rerio faciogenital dysplasia protein (fgd) mRNA, complete cds.//3.8e-14:293:63//AF017370

20 F-PLACE1007507//Human DNA sequence from clone 105D16 on chromosome Xp11.3-11.4 Contains pseudogene similar to laminin-binding protein, CA repeat, STS, complete sequence.//4.6e-10:152:75//AL031311

F-PLACE1007511//Homo sapiens chromosome 17, clone hRPC.1110_E_20, complete sequence.//3.6e-139:477:98//AC004231

F-PLACE1007524//Plasmodium falciparum microsatellite 14C sequence.//0.0055:395:59//AF015461

25 F-PLACE1007525//Trypanoplasma borelli mitochondrion cytochrome oxidase subunit 1 (cox1), cytochrome oxidase subunit 2 (cox2), and apocytochrome b (cytb) genes, complete cds, and complete 9S rRNA gene and partial 12S rRNA gene.//0.0013:550:58//U11682 F-PLACE1007537//H.sapiens CpG island DNA genomic Mse1 fragment, clone 198g6, reverse read cpg198g6.rt1a.//0.98:121:67//Z60280

F-PLACE1007544//Mus musculus chromosome 14 marker um-m24 GA dinucleotide DNA sequence.//2.3e-10:141:75//U31508

30 F-PLACE1007547//Homo sapiens mRNA for KIAA0661 protein, complete cds.//3.1e-69:733:71//AB014561

F-PLACE1007557//Drosophila yakuba mitochondrial DNA molecule.//0.022:393:61//X03240

F-PLACE1007583//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 545L17, WORKING DRAFT SEQUENCE.//3.6e-114:565:97//AL031665

35 F-PLACE1007598//CIT-HSP-2371G14.TF CIT-HSP Homo sapiens genomic clone 2371G14, genomic survey sequence.//2.0e-22:304:70//AQ111183

F-PLACE1007618//Homo sapiens chromosome 17, clone hRPK.642_C_21, complete sequence.//1.0:386:59//AC005245

F-PLACE1007621

40 F-PLACE1007632//Homo sapiens 12p13.3 PAC RPCI5-940J5 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.0e-88:276:96//AC006064

F-PLACE1007645//Bovine elastin mRNA, partial cds.//2.1e-07:110:79//M26132

F-PLACE1007649

F-PLACE1007677//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 968D22, WORKING DRAFT SEQUENCE.//1.2e-21:567:64//AL023755

45 F-PLACE1007688//Pseudorabies virus immediate-early gene.//2.2e-05:287:66//X15120

F-PLACE1007690//Caenorhabditis elegans cosmid R07G3.//0.40:122:70//U23452

F-PLACE1007697//Mus musculus LIM/homeobox (Lhx3) gene fragment.//0.85:117:71//L40483

F-PLACE1007705//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 460J8, WORKING DRAFT SEQUENCE.//0.0035:75:88//AL031662

50 F-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//1.3e-147:709:97//AF061243

F-PLACE1007725//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBB18, complete sequence.//1.0:510:58//AB005231

F-PLACE1007729//Human endogenous retrovirus HML6 proviral clone HML6p, putative leader region, gag, pro and pol pseudogenes.//4.8e-136:516:89//U86698

55 F-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds.//7.9e-155:728:98//AB014585

F-PLACE1007737//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//4.9e-34:764:62//AC003973

F-PLACE1007743//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//4.9e-34:764:62//AC003973

F-PLACE1007744//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//4.9e-34:764:62//AC003973

DRAFT SEQUENCE, 3 unordered pieces.//1.1e-06:510:56//AC005504

F-PLACE1007746//HS_2268_B1_G10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2268 Col=19 Row=N, genomic survey sequence.//0.10:171:63//AQ124780

F-PLACE1007791//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P6, WORKING

5 DRAFT SEQUENCE.//0.63:241:58//AL031749

F-PLACE1007807//Homo sapiens chromosome 17, clone hRPK.879_D_6, complete sequence.//1.0e-120:743:87//AC005273

F-PLACE1007810//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Human BAC library) complete sequence.//1.0e-113:739:86//AC003658

10 F-PLACE1007829//CIT-HSP-2383J22.TR CIT-HSP Homo sapiens genomic clone 2383J22, genomic survey sequence.//1.0e-47:254:97//AQ196438

F-PLACE1007843//F.rubripes GSS sequence, clone 162K02bC12, genomic survey sequence.//1.6e-10:148:72//AL006903

15 F-PLACE1007846//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 3/15, WORKING DRAFT SEQUENCE.//3.4e-177:844:98//AP000010

F-PLACE1007852//Mouse perlecan mRNA, complete cds.//8.5e-39:243:90//M77174

F-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds.//3.9e-189:894:98//AB018309

F-PLACE1007866//CIT-HSP-2353D11.TF.1 CIT-HSP Homo sapiens genomic clone 2353D11, genomic survey sequence.//0.015:279:61//AQ263271

20 F-PLACE1007877

F-PLACE1007897

F-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487.//2.3e-154:755:97//AB007956

25 F-PLACE1007946//Human chromosome Y cosmid 56B5 genomic sequence, WORKING DRAFT SEQUENCE.//1.1e-59:310:81//AC003097

F-PLACE1007954//Homo sapiens BAC clone NH0414C23 from Y, complete sequence.//2.1e-61:522:79//AC006157

F-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds.//2.7e-171:813:98//AF084530

30 F-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//2.5e-153:730:98//AF079529

F-PLACE1007969//Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds.//3.4e-32:383:74//U13262

F-PLACE1007990//H.sapiens genomic DNA fragment (clone J31A212R).//6.6e-35:198:96//Z94758

35 F-PLACE1008000//Mus musculus veli 3 mRNA, complete cds.//1.5e-118:706:88//AF087695

F-PLACE1008002//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces.//6.4e-163:786:98//AC005628

F-PLACE1008044//Rattus norvegicus nuclear pore complex protein NUP107 mRNA, complete cds.//1.2e-95:625:84//L31840

40 F-PLACE1008045//Caenorhabditis elegans cosmid F17C8, complete sequence.//0.016:165:65//Z35719

F-PLACE1008080//Human DNA sequence from cosmid L118G10, Huntington's Disease Region, chromosome 4p16.3.//4.0e-07:251:64//Z68883

F-PLACE1008095//RPCI11-21F19.TP RPCI-11 Homo sapiens genomic clone RPCI-11-21F19, genomic survey sequence.//1.5e-30:166:99//B85883

45 F-PLACE1008111//Aphidius picipes NADH dehydrogenase 1 gene, mitochondrial gene encoding mitochondrial protein, partial cds.//7.5e-06:414:60//AF069163

F-PLACE1008122//S.cerevisiae chromosome XV reading frame ORF YOL125w.//0.046:477:59//Z74867

F-PLACE1008129//Human Chromosome 15q26.1 PAC clone pDJ290i21 containing fur, fes, and alpha mannosidase Iix genes, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0068:446:57//AC004586

50 F-PLACE1008132//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 316D5, WORKING DRAFT SEQUENCE.//3.6e-20:111:93//Z82199

F-PLACE1008177//Mouse mRNA for meiosis-specific nuclear structural protein 1 (MNS1), complete cds.//2.5e-88:866:73//D14849

55 F-PLACE1008181//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 159A1, WORKING DRAFT SEQUENCE.//0.0033:727:56//AL034397

F-PLACE1008198//HS_3073_A1_G06_MB CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3073 Col=6 Row=N, genomic survey sequence.//0.10:171:63//AQ124780

F-PLACE1008201//Homo sapiens chromosome 40B11 hRPK-N11 DRAFT SEQUENCE, 3 unordered pieces.//1.1e-06:510:56//AC005504

F-PLACE1008201//Homo sapiens chromosome 40B11 hRPK-N11 DRAFT SEQUENCE, 3 unordered pieces.//1.1e-06:510:56//AC005504

162:791:97//AC005069

F-PLACE1008209

F-PLACE1008231//Mouse testis-specific protein mRNA, complete cds.//0.65:174:66//M26332

F-PLACE1008244//CIT-HSP-2337B4.TR CIT-HSP Homo sapiens genomic clone 2337B4, genomic survey sequence.//6.7e-28:165:95//AQ039317

F-PLACE1008273//B.primigenius mRNA for coat protein gamma-cop.//2.8e-71:709:71//X92987

F-PLACE1008275//D.discoideum actin A-13 gene, 5' flank.//0.12:131:64//M29123

F-PLACE1008280//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library) complete sequence.//0.011:96:73//AC005913

F-PLACE1008309//Rattus norvegicus putative four repeat ion channel mRNA, complete cds.//8.2e-86:672:77//AF078779

F-PLACE1008329//HS_2027_A1_C06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2027 Col=11 Row=E, genomic survey sequence.//8.7e-09:116:81//AQ244432

F-PLACE1008330//Homo sapiens chromosome 19, cosmid F21431, complete sequence.//2.2e-141:670:98//AC005176

F-PLACE1008331//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.1e-27:157:78//AC005000

F-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds.//1.1e-137:659:98//AB014579

F-PLACE1008368//CIT-HSP-2311C9.TR CIT-HSP Homo sapiens genomic clone 2311C9, genomic survey sequence.//7.1e-08:398:60//AQ016352

F-PLACE1008369//HS_2251_B1_A02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2251 Col=3 Row=B, genomic survey sequence.//2.1e-35:217:93//AQ066512

F-PLACE1008392//Homo sapiens chromosome 17, clone hRPK.136_H_19, complete sequence.//1.4e-11:403:64//AC005656

F-PLACE1008398//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 215D11, WORKING DRAFT SEQUENCE.//3.7e-144:681:99//AL034417

F-PLACE1008401//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//2.8e-45:257:96//AC004604

F-PLACE1008402//Homo sapiens mRNA for p115, complete cds.//4.3e-148:711:98//D86326

F-PLACE1008405//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.089:672:56//AC004688

F-PLACE1008424

F-PLACE1008426//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 7/11.//1.0e-88:331:84//AB020864

F-PLACE1008429//Chromosome 22q13 BAC Clone CIT987SK-384D8 complete sequence.//0.55:530:58//U62317

F-PLACE1008437//CIT-HSP-2376H4.TR CIT-HSP Homo sapiens genomic clone 2376H4, genomic survey sequence.//3.3e-78:349:94//AQ112479

F-PLACE1008455//HS_2064_B1_E09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2064 Col=17 Row=J, genomic survey sequence.//4.7e-59:471:81//AQ246589

F-PLACE1008457//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence.//8.9e-43:307:73//AC004526

F-PLACE1008465//CIT-HSP-2163F24.TR CIT-HSP Homo sapiens genomic clone 2163F24, genomic survey sequence.//8.9e-41:210:99//B90014

F-PLACE1008488//Mus musculus mRNA for testis-specific protein kinase 1, complete cds.//0.00013:516:58//AB003494

F-PLACE1008524//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 34B21, WORKING DRAFT SEQUENCE.//1.3e-161:778:98//AL031778

F-PLACE1008531//Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete cds.//1.1e-78:191:100//AF045555

F-PLACE1008532//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 92N15, WORKING DRAFT SEQUENCE.//3.8e-24:257:70//Z93097

F-PLACE1008533//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter, complete sequence.//1.0e-13:215:71//AC004997

F-PLACE1008568//Human DNA sequence from PAC 388N15 on chromosome Xq21.1.//0.66:263:64//Z99571

F-PLACE1008584//Homo sapiens chromosome 17, cosmid F21431, complete sequence.//2.2e-141:670:98//AC005176

F-PLACE1008584//Homo sapiens chromosome 17, cosmid F21431, complete sequence.//2.2e-141:670:98//AC005176

F-PLACE1008621//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces//3.9e-09:198:71//AC005077

F-PLACE1008625//Homo sapiens chromosome 5, PAC clone 45L14 (LBNL H91), complete sequence//0.68:568:59//AC005373

5 F-PLACE1008626//HS_3221_A2_F03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3221 Col=6 Row=K, genomic survey sequence//1.7e-13:147:82//AQ180967

F-PLACE1008627//Cricetulus griseus mRNA for Zn finger factor//9.7e-98:586:88/Y12836

F-PLACE1008629//CIT-HSP-2012I4.TR CIT-HSP Homo sapiens genomic clone 2012I4, genomic survey sequence//0.00085:203:66//B53732

10 F-PLACE1008630//Sequence 26 from Patent WO9517522//9.7e-05:97:80//A45356

F-PLACE1008643//Human mRNA for inter-alpha-trypsin inhibitor family heavy chain-related protein (IHRP), complete cds//1.4e-23:299:64//D38595

F-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds//1.1e-133:622:99//AF044333

15 F-PLACE1008693//CIT-HSP-2346F2.TF CIT-HSP Homo sapiens genomic clone 2346F2, genomic survey sequence//0.24:89:76//AQ060732

F-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein 8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitochondrial protein, complete cds//1.4e-94:420:97//AF038406

F-PLACE1008715//CIT-HSP-2294K20.TR CIT-HSP Homo sapiens genomic clone 2294K20, genomic survey sequence//2.1e-70:349:98//AQ007199

20 F-PLACE1008748//Arabidopsis thaliana chromosome I BAC T14N5 genomic sequence, complete sequence//0.14:347:59//AC004260

F-PLACE1008757//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence//7.9e-25:244:71//AC003037

25 F-PLACE1008790//Homo sapiens importin alpha 7 subunit mRNA, complete cds//4.5e-120:503:97//AF060543

F-PLACE1008798//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence//0.00026:370:61//AF001549

F-PLACE1008807//CIT-HSP-2334B19.TF CIT-HSP Homo sapiens genomic clone 2334B19, genomic survey sequence//3.3e-08:220:65//AQ036643

30 F-PLACE1008808//Homo sapiens exonuclease homolog RAD1 (RAD1) mRNA, complete cds//1.7e-120:470:97//AF030933

F-PLACE1008813//Rattus norvegicus rsec15 mRNA, complete cds//2.8e-87:504:89//AF032668

F-PLACE1008851//Homo sapiens DNA sequence from PAC 163M9 on chromosome 1p35.1-p36.21. Contains protein synthesis factor (eIF-4C), D1F15S1A pseudogene, ESTs, STS, GSS, complete sequence//4.0e-21:212:74//AL021920

35 F-PLACE1008854

F-PLACE1008867//Human DNA sequence from clone J428A131, WORKING DRAFT SEQUENCE//4.7e-77:477:84//Z82209

F-PLACE1008887//Homo sapiens BAC clone NH0335J18 from 2, complete sequence//3.4e-53:699:70//AC005539

40 F-PLACE1008902//Mouse G-alpha-13 protein mRNA, complete cds//2.1e-06:164:68//M63660

F-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds//6.4e-158:753:98//AB018308

F-PLACE1008925//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-A-180G2, WORKING DRAFT SEQUENCE, 5 unordered pieces//0.00013:400:63//AC002042

45 F-PLACE1008934//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1104E15, WORKING DRAFT SEQUENCE//7.4e-05:145:71//AL022312

F-PLACE1008941//Human zinc finger protein (ZNF141) mRNA, complete cds//4.3e-41:282:87//L15309

F-PLACE1008947//Pseudorabies virus with upstream and downstream sequences//5.9e-15:710:60//M34651

F-PLACE1009020//HS_3051_B1_H01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3051 Col=1 Row=P, genomic survey sequence//1.9e-21:167:86//AQ253727

50 F-PLACE1009027//Human DNA sequence from clone 914P14 on chromosome Xq23 Contains calpain-like protease gene, DCX (doublecortin) ESTs, CA repeat, GSS, complete sequence//4.1e-152:763:97//AL031117

F-PLACE1009039//HS_2034_A2_F08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2034 Col=16 Row=K, genomic survey sequence//0.17:252:59//AQ230137

55 F-PLACE1009045//HS_3185_B2_B03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3185 Col=6 Row=D, genomic survey sequence//1.9e-34:260:86//AQ172861

F-PLACE1009050//Homo sapiens 12q13.1 PAC RPC13-197B17 (Roswell Park Cancer Institute Human PAC library) complete sequence//0.63:280:61//AC004241

F-PLACE1009060//Mus musculus mRNA for Alix (ALG-2-interacting protein X), complete CDS.//5.9e-113:725:85//A-J005073

5 F-PLACE1009090//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1045J21, WORKING
DRAFT SEQUENCE.//9.1e-27:222:84//AL021919

F-PLACE1009091//Homo sapiens clone DJ0968I16. complete sequence.//0.027:630:58//AC006016

F-PLACE1009094

F-PLACE1009099//Mouse zinc finger protein (mkr4) mRNA, partial cds.//2.1e-85;726:76//M36515

10 F-PLACE1009110

F-PLACE1009111//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 138B7, WORKING DRAFT SEQUENCE.//6.0e-12:362:64/Z98752

F-PLACE1009113//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds.//
3.4e-138.671:97//AF035586

15 F-PLACE1009130//Human mRNA for KIAA0032 gene, complete cds.//3.6e-23:718:59//D25215

F-PLACE1009150/Homo sapiens *** SEQUENCING IN PROGRESS ***, WORKING DRAFT SEQUENCE //6.1e-142:684:98/A-J011929

F-PLACE1009155//Homo sapiens genomic DNA, chromosome 21q11.1, segment 2/28, WORKING DRAFT SE-
QUENCE//4.3e-36;227.77//AP000031

20 F-PLACE1009158//H.sapiens genomic sequence for ERCC2 gene 3'region involved in DNA excision repair//1.0:
173:60//X52222

F-PLACE1009166

F-PLACE1009172//Human BAC clone 7E17 from 12q, complete sequence.//4.0e-35:257:85//AC002070

F-PLACE1009174//Homo sapiens Xp22 bins 16-17 BAC GSHB-531i17 (Genome Systems Human BAC Library)
complete sequence//2.9e-19:288:72//AC004805

F-PLACE1009183//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHJ24, complete sequence.
0.053:388:60//AB008266

F-PLACE1009186//Rattus norvegicus fracture callus 1 (FxC1) mRNA, complete cds//1.8e-50:317:89//AF061242

F-PLACE1009190//RPC11-81N5.TJ RPC11 Homo sapiens genomic clone R-81N5, genomic survey sequence.
0.91:114:67//AQ281881

F-PLACE1009200//CITBI-E1-2509J16.TF CITBI-E1 Homo sapiens genomic clone 2509J16, genomic survey sequence.//2.8e-44;175:83//AQ262198

F-PLACE1009230//H.sapiens gene for pregnancy specific beta-1 glycoprotein.//1.1e-106:495:88//X63203

F-PLACE1009246//HS_3058_B1_A06_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3058 Col=11 Row=B. genomic survey sequence//0.10:175:68//AQ185945

F-PLACE1009298//Mus musculus maternal-embryonic 3 (Mem3) mRNA, complete cds//1.8e-94:575:89/UJ47024
F-PLACE1009308//Human clone mcag32 chromosome 7 CTG repeat region//0.0017:350:62/U23862

F-PLACE1009319//Homo sapiens post-synaptic density protein 95 (PSD95) mRNA, complete cds //3.0e-06:411:59//U83192

40 F-PLACE1009328//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 191P20, WORKING
DRAFT SEQUENCE.//5.7e-138:830:86//AL034399

F-PLACE1009335//Human (lambda) DNA for immunoglobulin light chain.//0.071:253:62//D87015

F-PLACE1009338//RPC111-74N24 TV RPC111 Homo sapiens genomic clone R-74N24, genomic survey sequence//2 4e-34:180:100//AQ268811

45 F-PLACE1009368

F-PLACF1009375

F-PLACE1009388//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1014D13, WORKING
DRAFT SEQUENCE //2.0e-37:288:84//AL022311

F-PLACE1009398//Human DNA binding protein (HPF2) mRNA, complete cds.//4.3e-78:730:74//M27878

50 F-PLACE1009404//SmD homolog [mice, liver, mRNA Partial, 199 nt]//0.16:95:71//S71494

F-PLACE1009410//Homo sapiens chromosome 17, clone hRPK.142_H_19, complete sequence.//1.6e-150:701:99//AC005919

F-PLACE1009434//Mus musculus clone OST431, genomic survey sequence.//2.9e-73:442:88//AF046700

F-PLACE1009443//Mycobacterium tuberculosis H37Rv complete genome; segment 148/162.//0.012:582:56//AL022022

5 PL ACE1009444 1/4 inch x 1/4 inch x 1/4 inch 1/4 inch x 1/4 inch x 1/4 inch

F-PLACE1009468//Sequence 1 from patent US 5580968//1.9e-83:567:84//I30536
 F-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1, complete sequence//1.9e-142:704:97//AC004531
 F-PLACE1009477//Human 11p14.3 PAC clone pDJ939m16, complete sequence//2.2e-09:235:68//AC004601
 5 F-PLACE1009493//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence//2.9e-83:171:92//U91321
 F-PLACE1009524//Homo sapiens DNA sequence from PAC 63G5 on chromosome 22q12.3-13.1. Contains part of a gene for a human SEC7 homolog B2-1 (cytohesin-2, Armo, ARF exchange factor) LIKE protein, an unknown gene and a gene coding for a Leucine rich protein. Contains ESTs, STSs and GSSs, complete sequence//3.8e-69:175:92//Z94160
 10 F-PLACE1009539//Mus musculus synaptojanin 2 isoform alpha mRNA, complete cds.//7.0e-26:237:78//AF041862
 F-PLACE1009542//Human DNA sequence from clone 1039K5 on chromosome 22q12.3-13.2 Contains gene similar to PICK1 perinuclear binding protein, gene similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS and a CpG island, complete sequence.//3.1e-10:126:79//AL031587
 15 F-PLACE1009571//RPC11-60K12.TK RPC11 Homo sapiens genomic clone R-60K12, genomic survey sequence.//1.4e-05:68:91//AQ195869
 F-PLACE1009581
 F-PLACE1009595//Homo sapiens chromosome 5, P1 clone 1029A7 (LBNL H15), complete sequence//6.6e-19:309:70//AC003959
 20 F-PLACE1009596//Rattus norvegicus platelet-activating factor acetylhydrolase beta subunit (PAF-AH beta) gene, complete cds.//9.0e-09:485:59//AF016049
 F-PLACE1009607//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 409J21, WORKING DRAFT SEQUENCE.//4.9e-43:714:66//Z83824
 25 F-PLACE1009613//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.017:655:57//AC004157
 F-PLACE1009621
 F-PLACE1009622//HS-1016-B2-E08-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 791 Col=16 Row=J, genomic survey sequence.//2.7e-15:100:98//B33248
 30 F-PLACE1009637//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.63:130:67//AC005308
 F-PLACE1009639//S.pombe chromosome II cosmid c24E9.//0.86:509:58//AL021816
 F-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds.//1.4e-171:816:98//AB011159
 F-PLACE1009665//Homo sapiens chromosome 17, clone HCIT462L7, complete sequence.//3.4e-67:437:87//AC005177
 35 F-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.//2.5e-147:701:98//AF062534
 F-PLACE1009708//Homo sapiens clone DJ0935K16, complete sequence.//1.5e-98:228:100//AC006011
 F-PLACE1009721//Human Cosmid g0771a222 from 7q31.3, complete sequence.//2.2e-130:736:91//AC000109
 F-PLACE1009731//M.musculus mRNA for immunity associated protein 38.//1.1e-13:311:64//Y08026
 40 F-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds.//4.2e-125:602:98//AF046024
 F-PLACE1009794
 F-PLACE1009798//Hnman DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs, an STS and GSSs, complete sequence.//1.3e-73:271:84//AL030996
 45 F-PLACE1009845
 F-PLACE1009861//B.tauris cathepsin B mRNA, 3' end.//0.00023:147:65//M64620
 F-PLACE1009879//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 159A1, WORKING DRAFT SEQUENCE.//4.9e-27:725:63//AL034397
 50 F-PLACE1009886//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 167A19, WORKING DRAFT SEQUENCE.//8.2e-12:135:82//AL031427
 F-PLACE1009888//F14G3-T7 IGF Arabidopsis thaliana genomic clone F14G3, genomic survey sequence.//0.0044:232:60//AQ251431
 55 F-PLACE1009908//S.pombe chromosome I cosmid c3F10.//1.5e-19:559:59//Z69369

3300

F-PLACE1009924//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-201104 WORKING DRAFT SE

QUENCE, 4 unordered pieces//2.4e-51:481:78//AC004529

F-PLACE1009925//nbxb0027C22r CUGI Rice BAC Library *Oryza sativa* genomic clone nbxb0027C22r, genomic survey sequence//0.98:220:67//AQ272066

F-PLACE1009935//Sequence 16 from patent US 5552281//0.030:152:67//I25655

5 F-PLACE1009947//Homo sapiens clone GS096J14, WORKING DRAFT SEQUENCE, 3 unordered pieces//2.6e-12:322:67//AC006026

F-PLACE1009971

F-PLACE1009992//HS_3178_B1_F04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3178 Col=7 Row=L, genomic survey sequence//4.9e-23:142:95//AQ150311

10 F-PLACE1009995//Caenorhabditis elegans cosmid C01A2, complete sequence//0.00019:231:64//Z81029

F-PLACE1009997//Rattus norvegicus A-kinase anchoring protein AKAP 220 mRNA, complete cds//7.9e-87:552:80//U48288

F-PLACE1010023

15 F-PLACE1010031//Human DNA sequence from clone 30M3 on chromosome 6p22.1-22.3. Contains three novel genes, one similar to *C. elegans* Y63D3A.4 and one similar to (predicted) plant, worm, yeast and archaea bacterial genes, and the first exon of the KIAA0319 gene. Contains ESTs, GSSs and putative CpG islands, complete sequence//6.9e-101:181:98//AL031775

F-PLACE1010053//M.musculus Spnr mRNA for RNA binding protein//2.3e-136:689:95//X84692

20 F-PLACE1010069//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 212A2, WORKING DRAFT SEQUENCE//0.0090:383:60//Z95114

F-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//1.8e-166:792:98//AF065482

F-PLACE1010076//Mouse mRNA for TGF-beta type I receptor, complete cds//7.5e-13:203:77//D25540

F-PLACE1010083//Homo sapiens mRNA for KIAA0456 protein, partial cds//3.0e-152:727:98//AB007925

25 F-PLACE1010089//HS_3111_A1_E08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3111 Col=15 Row=I, genomic survey sequence//4.8e-07:124:78//AQ101268

F-PLACE1010096//R.norvegicus mRNA for 100 kDa protein//1.2e-108:700:85//X64411

F-PLACE1010102//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces//2.1e-07:476:60//AC005506

30 F-PLACE1010105//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//3.8e-25:728:60//AF059569

F-PLACE1010106//Human DNA sequence from PAC 127B14 on chromosome Xq22//6.5e-25:488:63//Z93928

F-PLACE1010134//S.pombe chromosome I cosmid c29B12//1.9e-13:238:67//Z99164

F-PLACE1010148//Homo sapiens partial human cDNA (660 bp)//4.8e-83:409:98//AJ222636

35 F-PLACE1010152//CIT-HSP-2381F24.TF CIT-HSP Homo sapiens genomic clone 2381F24, genomic survey sequence//1.5e-28:163:98//AQ196757

F-PLACE1010181//Homo sapiens PAC clone DJ1139I01 from Xq23, complete sequence//2.4e-15:197:72//AC004973

F-PLACE1010194//Ictalurus punctatus tumor suppressor p53 mRNA, complete cds//3.0e-14:181:74//AF074967

F-PLACE1010202//Homo sapiens mRNA for MBNL protein//1.2e-27:509:66//Y13829

40 F-PLACE1010231//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 287G14, WORKING DRAFT SEQUENCE//2.3e-101:194:95//AL033377

F-PLACE1010261//Homo sapiens mRNA for KIAA0448 protein, complete cds//5.8e-145:693:97//AB007917

F-PLACE1010270//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence; WORKING DRAFT SEQUENCE, 2 unordered pieces//2.1e-05:347:60//AC004710

45 F-PLACE1010274//Caenorhabditis elegans cosmid C01A2, complete sequence//0.00040:231:64//Z81029

F-PLACE1010293//Homo sapiens chromosome 2 PAC RPC13-417E16 (Roswell Park Cancer Institute Human PAC library) complete sequence//6.5e-25:344:70//AC004464

F-PLACE1010310//Homo sapiens DNA sequence from PAC 329E20 on chromosome 1p34.4-36.13. Contains endothelin-converting-enzyme 1 (ECE-1), EST, STS, CA repeat, complete sequence//3.5e-10:185:67//AL031005

50 F-PLACE1010321//Human DNA sequence from clone 299D3 on chromosome 22q13.3, complete sequence//0.010:524:58//Z84468

F-PLACE1010324//CIT-HSP-2335J21.TR CIT-HSP Homo sapiens genomic clone 2335J21, genomic survey sequence//9.1e-90:448:97//AQ041837

F-PLACE1010329//Apis mellifera ligustica complete mitochondrial genome//2.8e-08:384:64//L06178

55 F-PLACE1010341//HS-1047-A2-C04-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=1047 Col=8 Row=L, genomic survey sequence//4.1e-21:141:92//B38251

Accession numbers: M5626, M5627, M5628, M5629, M5630, M5631, M5632, M5633, M5634, M5635, M5636, M5637, M5638, M5639, M5640, M5641, M5642, M5643, M5644, M5645, M5646, M5647, M5648, M5649, M5650, M5651, M5652, M5653, M5654, M5655, M5656, M5657, M5658, M5659, M5660, M5661, M5662, M5663, M5664, M5665, M5666, M5667, M5668, M5669, M5670, M5671, M5672, M5673, M5674, M5675, M5676, M5677, M5678, M5679, M5680, M5681, M5682, M5683, M5684, M5685, M5686, M5687, M5688, M5689, M5690, M5691, M5692, M5693, M5694, M5695, M5696, M5697, M5698, M5699, M5700, M5701, M5702, M5703, M5704, M5705, M5706, M5707, M5708, M5709, M5710, M5711, M5712, M5713, M5714, M5715, M5716, M5717, M5718, M5719, M5720, M5721, M5722, M5723, M5724, M5725, M5726, M5727, M5728, M5729, M5730, M5731, M5732, M5733, M5734, M5735, M5736, M5737, M5738, M5739, M5740, M5741, M5742, M5743, M5744, M5745, M5746, M5747, M5748, M5749, M5750, M5751, M5752, M5753, M5754, M5755, M5756, M5757, M5758, M5759, M5760, M5761, M5762, M5763, M5764, M5765, 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F-PLACE1010364//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y102G3, WORKING DRAFT SEQUENCE.//0.11:404:56//AL020985

F-PLACE1010383//Homo sapiens chromosome 17, clone hCIT.186_H_2, complete sequence.//0.066:88:76//AC004675

5 F-PLACE1010401//CIT-HSP-2367K17.TR CIT-HSP Homo sapiens genomic clone 2367K17, genomic survey sequence.//2.4e-71:454:88//AQ076825

F-PLACE1010481//Bos taurus C5-glucuronyl epimerase mRNA, partial cds.//7.5e-134:722:93//AF003927

F-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds.//2.2e-150:702:99//AF039081
F-PLACE1010492

10 F-PLACE1010522//Homo sapiens cosmid LM1937 from Xq28.//0.022:405:60//U82695

F-PLACE1010529//Sequence 1 from patent US 5776717.//2.9e-145:684:98//AR016417

F-PLACE1010547//Human DNA sequence from clone 790B6 on chromosome 20p11.22-12.2. Contains STSs and GSSs, complete sequence.//1.0:283:61//AL031677

F-PLACE1010562//RPC111-65116.TK RPC111 Homo sapiens genomic clone R-65116, genomic survey sequence.//0.017:216:67//AQ200831

15 F-PLACE1010579//Homo sapiens full-length insert cDNA YI23D12.//3.9e-19:147:89//AF075014

F-PLACE1010580//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete cds.//6.4e-96:559:89//L25125

F-PLACE1010599//Homo sapiens peroxisomal membrane anchor protein HsPex14p (PEX14) mRNA, complete cds.//3.1e-146:707:97//AF045186

20 F-PLACE1010616//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.045:454:59//AC005308

F-PLACE1010622//Plasmodium falciparum MAL3P2, complete sequence.//9.1e-07:378:60//AL034558

F-PLACE1010624//Streptomyces coelicolor cosmid 5A7.//1.4e-05:516:61//AL031107

25 F-PLACE1010628//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//5.0e-137:675:97//AC004846

F-PLACE1010629//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-259H10, complete sequence.//2.5e-17:187:80//AC004682

F-PLACE1010630//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21P3, complete sequence.//0.21:159:64//AB016872

30 F-PLACE1010631//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//1.2e-144:720:97//AC005069

F-PLACE1010661

F-PLACE1010662//Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7 (ESSA project).//0.90:257:61//AL021960

35 F-PLACE1010702//Human repressor transcriptional factor (ZNF85) mRNA, complete cds.//3.3e-73:697:74//U35376

F-PLACE1010714//Human Chromosome 15q11-q13 PAC clone pDJ778a2, complete sequence.//0.010:447:59//AC004583

40 F-PLACE1010720//Mouse TPA-induced TIS11 mRNA.//2.0e-86:535:88//X14678

F-PLACE1010739//HS_2013_B2_B10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2013 Col=20 Row=D, genomic survey sequence.//5.7e-87:435:97//AQ235864

F-PLACE1010743//R.norvegicus mRNA for myr5.//1.7e-87:582:85//X77609

F-PLACE1010761//Homo sapiens chromosome 17, clone hRPK.294_J_22, complete sequence.//4.7e-45:235:99//AC005921

45 F-PLACE1010771//M.musculus HCNGP mRNA.//1.6e-135:801:88//X68061

F-PLACE1010786//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-15, complete sequence.//0.35:334:60//AL010221

F-PLACE1010800//RPC111-79H17.TV RPC111 Homo sapiens genomic clone R-79H17, genomic survey sequence.//5.8e-18:168:82//AQ284252

50 F-PLACE1010802//Human Chromosome X clone bWXD531, complete sequence.//1.6e-30:693:63//AC004384

F-PLACE1010811//RPC111-51N5.TK RPC111 Homo sapiens genomic clone R-51N5, genomic survey sequence.//8.3e-11:142:78//AQ052380

F-PLACE1010833//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 467K16, WORKING DRAFT SEQUENCE.//7.3e-40:147:88//AL031283

55 F-PLACE1010856//M.musculus mRNA for tyrophin.//7.3e-17:150:86//X12200

Sequence data from this submission have been deposited in the EMBL/GenBank/DDBJ databases under accession numbers: F000000000, F000000001, F000000002, F000000003, F000000004, F000000005, F000000006, F000000007, F000000008, F000000009, F000000010, F000000011, F000000012, F000000013, F000000014, F000000015, F000000016, F000000017, F000000018, F000000019, F000000020, F000000021, F000000022, F000000023, F000000024, F000000025, F000000026, F000000027, F000000028, F000000029, F000000030, F000000031, F000000032, F000000033, F000000034, F000000035, F000000036, F000000037, F000000038, F000000039, F000000040, F000000041, F000000042, F000000043, F000000044, F000000045, F000000046, F000000047, F000000048, F000000049, F000000050, F000000051, F000000052, F000000053, F000000054, F000000055, F000000056, F000000057, F000000058, F000000059, F000000060, F000000061, F000000062, F000000063, F000000064, F000000065, F000000066, F000000067, F000000068, F000000069, F000000070, F000000071, F000000072, 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F-PLACE1010870//M.musculus mRNA for ZT3 zinc finger factor.//1.3e-93:530:90//Z67747
 F-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds.//1.1e-147:694:98//AB011182
 F-PLACE1010891
 F-PLACE1010896//Mouse BAC mbac20 from 14D1-D2 (T-Cell Receptor Alpha Locus), complete sequence.//3.9e-
 26:394:68//AC003997
 F-PLACE1010900
 F-PLACE1010916//HS_2242_A1_C04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=2242 Col=7 Row=E, genomic survey sequence.//1.0e-78:391:97//AQ146687
 F-PLACE1010917
 F-PLACE1010925//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING
 DRAFT SEQUENCE, 4 unordered pieces.//0.11:629:56//AC004688
 F-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds.//9.5e-138:653:98//AB011126
 F-PLACE1010942//Homo sapiens intersectin short form mRNA, complete cds.//5.6e-90:437:98//AF064243
 F-PLACE1010944//Homo sapiens full-length insert cDNA clone ZD38E12.//1.4e-09:208:68//AF086247
 F-PLACE1010947
 F-PLACE1010954//CIT-HSP-2283D9.TR CIT-HSP Homo sapiens genomic clone 2283D9, genomic survey se-
 quence.//2.1e-29:190:91//B98965
 F-PLACE1010960//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-52, complete
 sequence.//0.00074:421:60//AL010226
 F-PLACE1010965//CIT-HSP-2386K24.TF.1 CIT-HSP Homo sapiens genomic clone 2386K24, genomic survey se-
 quence.//1.8e-84:412:99//AQ240696
 F-PLACE1011026//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-20, complete
 sequence.//0.00037:257:64//AL008972
 F-PLACE1011032//Homo sapiens chromosome 5, BAC clone 118L13 (LBNL H1/6), complete sequence.//3.8e-
 06:315:65//AC005348
 F-PLACE1011041//Human Fas-ligand associated factor 3 mRNA, partial cds.//1.5e-56:286:98//U70669
 F-PLACE1011046//Rat phospholipase C-1 mRNA, complete cds.//1.3e-24:278:76//M20636
 F-PLACE1011054//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 981L23, WORKING
 DRAFT SEQUENCE.//3.8e-27:196:84//AL031686
 F-PLACE1011056//Ovis aries bactinecin 11 (Bac11) gene, exon 4, and complete cds.//5.4e-06:182:67//U77049
 F-PLACE1011057//protein kinase PRK2 [human, DX3 B-cell myeloma cell line, mRNA, 3255 nt].//3.2e-31:169:
 100//S75548
 F-PLACE1011090//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 998H6, WORKING
 DRAFT SEQUENCE.//5.1e-80:479:89//AL031687
 F-PLACE1011109//Rattus norvegicus nuclear-encoded mitochondrial elongation factor G mRNA, complete cds.//
 2.3e-24:192:84//L14684
 F-PLACE1011114//S.cerevisiae chromosome XI reading frame ORF YKR024c.//1.4e-14:346:60//Z28249
 F-PLACE1011133//T7E9-T7.1 TAMU Arabidopsis thaliana genomic clone T7E9, genomic survey sequence.//
 0.010:345:60//B19698
 F-PLACE1011143//CIT-HSP-2375J10.TR CIT-HSP Homo sapiens genomic clone 2375J10, genomic survey se-
 quence.//0.00013:95:76//AQ109305
 F-PLACE1011160//Homo sapiens PAC clone DJ0808A01 from 7q21.1-q31.1, complete sequence.//3.7e-111:692:
 87//AC004893
 F-PLACE1011165//H.sapiens galactokinase (GK2) mRNA, complete cds.//8.4e-31:194:92//M84443
 F-PLACE1011185//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-249B10, complete sequence.//3.1e-
 43:447:72//AC002288
 F-PLACE1011203//Homo sapiens chromosome 18q11 beta-1,4-galactosyltransferase mRNA, complete cds.//
 3.3e-124:584:99//AF038664
 F-PLACE1011214//HS_2046_A2_B01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=2046 Col=2 Row=C, genomic survey sequence.//2.0e-39:346:81//AQ305965
 F-PLACE1011219
 F-PLACE1011221//CITBI-E1-2513F18.TR CITBI-E1 Homo sapiens genomic clone 2513F18, genomic survey se-
 quence.//2.4e-20:119:100//AQ279801
 F-PLACE1011229//Homo sapiens mRNA for KIAA0529 protein, partial cds.//4.4e-146:675:99//AB011101
 F-PLACE1011263//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//1.7e-42:212:84//
 AC005014

F-PLACE1011291//RPCI11-16P9.TP RPCI-11 Homo sapiens genomic clone RPCI-11-16P9, genomic survey sequence.//8.0e-08:66:98//B81770

F-PLACE1011296//Homo sapiens chromosome 16, cosmid clone 443G8 (LANL), complete sequence.//0.027:135:67//AC004647

F-PLACE1011310//H.sapiens CpG island DNA genomic MseI fragment, clone 53c10, reverse read cpg53c10.rt1b.//1.4e-05:57:100//Z61496

F-PLACE1011325//Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial cds.//0.077:193:60//L02290

F-PLACE1011332//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//3.1e-150:699:99//AF102265

F-PLACE1011340//Homo sapiens chromosome 17, clone hRPK.388_F_14, complete sequence.//2.4e-38:186:83//AC005375

F-PLACE1011371//Mus musculus PK-120 precursor (itih-4) mRNA, complete cds.//6.0e-35:689:63//AF023919

F-PLACE1011375//Mus musculus Kv3.4 gene, exon 4.//6.0e-88:584:86//AJ010310

F-PLACE1011399//paramecium species 7,325 mt dna dimer: replication init. region.//0.00011:255:63//K00919

F-PLACE1011419//Homo sapiens chromosome 21 PAC LLNLP704G1150Q13.//0.067:337:62//AJ006996

F-PLACE1011433//Homo sapiens mRNA for KIAA0530 protein, partial cds.//4.6e-157:743:98//AB011102

F-PLACE1011452//Homo sapiens *** SEQUENCING IN PROGRESS ***, WORKING DRAFT SEQUENCE.//1.1e-53:557:73//AJ011929

F-PLACE1011465//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//3.5e-71:498:80//AC004605

F-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds.//4.8e-151:703:99//AB018255

F-PLACE1011477//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//5.2e-145:675:99//AF065482

F-PLACE1011492//Ray (T.californica) acetylcholine receptor beta-subunit mRNA.//1.0:448:59//J00964

F-PLACE1011503

F-PLACE1011520//Homo sapiens clone DJ1119N05, complete sequence.//3.8e-147:692:99//AC004968

F-PLACE1011563//R.norvegicus mRNA for leucocyte common antigen-related protein (3941 bp).//0.00036:296:61//X83546

F-PLACE1011567//Homo sapiens PAC clone DJ1164K10 from 7p21-p22, complete sequence.//1.1e-38:315:82//AC004984

F-PLACE1011576//Homo sapiens hematopoietic cell derived zinc finger protein mRNA, complete cds.//1.3e-65:268:86//AF054180

F-PLACE1011586//Homo sapiens chromosome 17, clone HRPC890E16, complete sequence.//2.0e-82:188:96//AC004477

F-PLACE1011635//Homo sapiens chromosome 17, clone hRPK.214_O_1, complete sequence.//1.8e-153:752:97//AC005224

F-PLACE1011641//Homo sapiens T-cell receptor alpha delta locus from bases 501613 to 752736 (section 3 of 5) of the Complete Nucleotide Sequence.//4.8e-05:190:67//AE000660

F-PLACE1011643//Alcaligenes eutrophus phaP gene.//0.16:466:59//X85729

F-PLACE1011646//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1013A10, WORKING DRAFT SEQUENCE.//9.1e-19:156:76//AL033383

F-PLACE1011649

F-PLACE1011650//Homo sapiens retinol dehydrogenase gene, complete cds.//6.4e-09:172:74//AF037062

F-PLACE1011664//D.melanogaster crn mRNA.//1.1e-52:650:68//X58374

F-PLACE1011675//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.11:443:58//AC005507

F-PLACE1011682//Human DNA sequence from clone 342B11 on chromosome 22q12.1-12.3. Contains ESTs and a GSS, complete sequence.//0.31:127:71//AL008719

F-PLACE1011719//Human BAC clone RG369K23 from 7q31, complete sequence.//4.6e-52:461:77//AC002487

F-PLACE1011725

F-PLACE1011729//Human Chromosome 15q11-q13 clone pDJ276c12 from the Prader-Willi/Angelman syndrome region, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.011:320:62//AC004737

F-PLACE1011749//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.00031:544:59//AC004157

F-PLACE1011762//Homo sapiens BAC clone RG437L15 from 8q21, complete sequence.//2.4e-115:682:90//AC004066

AC004066 Homo sapiens BAC clone RG437L15 from 8q21, complete sequence.//2.4e-115:682:90//AC004066

F-PLACE1011783//CIT-HSP-2317N1.TF CIT-HSP Homo sapiens genomic clone 2317N1, genomic survey sequence.//2.3e-17:120:94//AQ042330

F-PLACE1011858//Gallus domesticus filamin mRNA, complete cds.//4.1e-24:565:64//U00147

F-PLACE1011874//Homo Sapiens Chromosome X clone bWXd312, complete sequence.//2.5e-141:678:98//AC004478

5 F-PLACE1011875//Homo sapiens mRNA for KIAA0580 protein, partial cds.//1.6e-108:526:98//AB011152

F-PLACE1011891//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 439F8, WORKING DRAFT SEQUENCE.//0.0014:330:62//AL021392

F-PLACE1011896//Mus musculus Wnt10a mRNA, complete cds.//1.4e-89:678:82//U61969

10 F-PLACE1011922//Caprine arthritis-encephalitis virus envelope glycoprotein (env) gene, partial cds.//0.069:246:61//U81400

F-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds.//1.2e-138:664:98//AF059617

F-PLACE1011962//HS_3212_B2_G12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3212 Col=24 Row=N, genomic survey sequence.//2.4e-07:154:74//AQ175369

15 F-PLACE1011964//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 322P7, WORKING DRAFT SEQUENCE.//3.7e-22:369:69//AL023799

F-PLACE1011982//HS-1041-A1-B01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 823 Col=1 Row=C, genomic survey sequence.//0.44:309:58//B36529

F-PLACE1011995//Homo sapiens Xq28 BAC RPC11-382P7 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//8.8e-53:687:71//AC006054

20 F-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds.//1.2e-146:690:98//AB018256

F-PLACE2000003//Homo sapiens chromosome 17, clone hRPK.318_A_15, complete sequence.//1.7e-62:293:88//AC005837

F-PLACE2000006//Homo sapiens chromosome 12p13.3 clone HPC11-96H9, WORKING DRAFT SEQUENCE, 66 unordered pieces.//1.4e-116:261:91//AC006057

25 F-PLACE2000007

F-PLACE2000011//Homo sapiens chromosome 19, cosmid F20887, complete sequence.//5.2e-102:489:99//AC005578

F-PLACE2000014//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1111N9, WORKING DRAFT SEQUENCE.//0.0095:307:62//AL022574

30 F-PLACE2000015//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.0e-36:316:81//AC005069

F-PLACE2000017//HS_3042_A1_F08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3042 Col=15 Row=K, genomic survey sequence.//1.0:184:61//AQ098074

35 F-PLACE2000021//Homo sapiens TRF1-interacting ankyrin-related ADP-ribose polymerase mRNA, complete cds.//4.6e-84:844:72//AF082556

F-PLACE2000030//Human Chromosome 11 Cosmid cSRL16b6, complete sequence.//2.3e-22:233:77//U73638

F-PLACE2000033//C.capitata mRNA for chorion protein s18.//0.0019:342:62//Y08913

F-PLACE2000034//Rattus norvegicus transmembrane receptor Robo1 mRNA, complete cds.//2.8e-13:335:63//AF041082

40 F-PLACE2000039//Rattus norvegicus cytoplasmic dynein heavy chain (MAP 1C), mRNA, complete cds.//7.7e-84:489:90//L08505

F-PLACE2000047//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//5.0e-28:327:76//U95626

45 F-PLACE2000050//Homo sapiens chromosome 17, clone HRPC41C23, complete sequence.//1.1e-32:527:68//AC003101

F-PLACE2000061//CIT-HSP-2346L20.TF CIT-HSP Homo sapiens genomic clone 2346L20, genomic survey sequence.//1.1e-05:89:83//AQ059010

F-PLACE2000062//Human membrane-associated lectin type-C mRNA.//9.0e-113:662:86//M98457

50 F-PLACE2000072//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//2.2e-133:631:98//AF027219

F-PLACE2000097//Homo sapiens chromosome 12p13.3 clone RPC11-189M20, WORKING DRAFT SEQUENCE, 39 unordered pieces.//1.6e-16:119:93//AC005910

F-PLACE2000100//HS_3184_A1_D06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3184 Col=11 Row=G, genomic survey sequence.//1.5e-80:409:97//AQ150004

55 F-PLACE2000103//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 20208, WORKING DRAFT SEQUENCE.//1.0e-172:830:98//AL021848

F-PLACE2000124//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1, complete sequence//6.2e-43:362:80//AC004531

F-PLACE2000132//RPCI11-79F15.TV RPCI11 Homo sapiens genomic clone R-79F15, genomic survey sequence//5.4e-35:206:94//AQ284166

F-PLACE2000136//Human BAC clone 7E17 from 12q, complete sequence//2.7e-12:814:59//AC002070

F-PLACE2000140//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 11703, WORKING DRAFT SEQUENCE//3.6e-165:799:97//AL020995

F-PLACE2000164//Canine histamine H2 receptor gene, complete cds//0.10:392:56//M32701

F-PLACE2000170

F-PLACE2000172//Homo sapiens PAC clone DJ0811017 from 7q21-22, complete sequence//3.9e-91:552:88//AC006005

F-PLACE2000176//Homo sapiens Chromosome 22q11.2 BAC Clone b437g10 In BCRL2-GGT Region, complete sequence//0.98:201:64//AC004032

F-PLACE2000187

F-PLACE2000216

F-PLACE2000223//RPCI11-12L17.TP RPCI-11 Homo sapiens genomic clone RPCI-11-12L17, genomic survey sequence//0.00039:325:58/B75888

F-PLACE2000235//Human Chromosome 16 BAC clone CIT987SK-254P9, complete sequence//7.5e-55:237:78//AC003003

F-PLACE2000246//Homo sapiens chromosome 3p clone RPCI4-544D10, WORKING DRAFT SEQUENCE, 58 unordered pieces//2.4e-92:236:94//AC005902

F-PLACE2000264//Human DNA sequence from clone 391022 on chromosome 6p21.2-21.31 Contains pseudo-genes similar to ribosomal protein, ESTs, GSSs, complete sequence//1.4e-32:331:78//AL031577

F-PLACE2000274//Anthocidaris crassispina mRNA for B2HC, partial cds//8.5e-48:765:66//AB012308

F-PLACE2000302//Kaposi's sarcoma-associated herpes-like virus ORF73 homolog gene, complete cds//8.3e-08:662:58//US2064

F-PLACE2000305//Homo sapiens clone DJ1129L24, WORKING DRAFT SEQUENCE, 5 unordered pieces//2.4e-08:95:81//AC006021

F-PLACE2000317//HS_3183_B2_F05_MR CIT Approved Human Genomic Sperm-Library D Homo sapiens genomic clone Plate=3183 Col=10 Row=L, genomic survey sequence//2.5e-71:346:99//AQ172747

F-PLACE2000335//Homo sapiens clone DJ1032D07, WORKING DRAFT SEQUENCE, 3 unordered pieces//3.7e-14:402:65//AC004952

F-PLACE2000341//Rattus norvegicus sodium-dependent multi-vitamin transporter (SMVT) mRNA, complete cds//4.5e-77:555:82//AF026554

F-PLACE2000342//Suid herpesvirus 1 UL5 gene, partial cds, UL6 and UL7 genes, complete cds, UL8 gene, partial cds//1.8e-14:259:71//U66829

F-PLACE2000347//Human DNA from overlapping chromosome 19-specific cosmids R32543,, and F15613 containing ZNF gene family member, genomic sequence, complete sequence//6.0e-34:376:74//AC003006

F-PLACE2000359//RPCI11-23J20.TKBR RPCI-11 Homo sapiens genomic clone RPCI-11-23J20, genomic survey sequence//8.4e-21:288:69//AQ013849

F-PLACE2000366//Human Tigger1 transposable element, complete consensus sequence//5.0e-114:692:80//U49973

F-PLACE2000371//Homo sapiens 12p13.3 PAC RPCI1-29K11 (Roswell Park Cancer Institute Human PAC Library) complete sequence//0.38:356:58//AC005182

F-PLACE2000373//RPCI11-49C18.TJ RPCI11 Homo sapiens genomic clone R-49C18, genomic survey sequence//0.064:132:68//AQ051776

F-PLACE2000379//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Human BAC library) complete sequence//1.6e-130:776:88//AC003658

F-PLACE2000394//Homo sapiens chromosome 18 BAC RPCI11-128D14 (Roswell Park Cancer Institute Human BAC Library) complete sequence//5.4e-113:808:83//AC005909

F-PLACE2000398//Mouse hexamer repeat sequence (117) homologous to Drosophila 'period' gene//0.87:286:63//X06967

F-PLACE2000399

F-PLACE2000404//Caenorhabditis elegans cosmid R74, complete sequence//2.9e-59:532:68//Z36238

F-PLACE2000411//Acanthamoeba castellanii transformation-sensitive protein homolog mRNA, complete cds//1.1e-55:563:82283

F-PLACE2000414//Homo sapiens chromosome 11 cosmid R100, complete sequence//1.1e-55:563:82283

F-PLACE2000428//Homo sapiens chromosome 11 cosmid R100, complete sequence//1.1e-55:563:82283

nomic clone Plate=3047 Col=9 Row=O, genomic survey sequence.//2.8e-42:224:97//AQ126949

F-PLACE2000427

F-PLACE2000433//Homo sapiens chromosome 17, clone hRPK.156_L_14, complete sequence.//1.1e-19:363:67//AC005821

5 F-PLACE2000435//HS_3036_B1_F11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3036 Col=21 Row=L, genomic survey sequence.//3.1e-06:184:66//AQ096999

F-PLACE2000438//Caenorhabditis elegans cosmid Y45F10D, complete sequence.//4.6e-23:550:62//AL021492

F-PLACE2000450//Homo sapiens PAC clone DJ1188N21 from 7q11.23-q21.1, complete sequence.//1.0e-78:604:80//AC006025

10 F-PLACE2000455//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//8.2e-05:330:63//AC002300

F-PLACE2000458//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//5.7e-168:816:97//AC005740

15 F-PLACE2000465//Human Chromosome 11 Overlapping Cosmids cSRL72g7 and cSRL140b8, complete sequence.//4.3e-33:296:79//AC002037

F-PLACE2000477//Homo sapiens clone RG052H06, WORKING DRAFT SEQUENCE, 11 unordered pieces.//3.4e-59:598:74//AC005057

F-PLACE3000004//Human EYA3 homolog (EYA3) mRNA, complete cds.//7.6e-49:361:84//U81602

F-PLACE3000009//Human placenta (Diff48) mRNA, complete cds.//3.0e-58:713:69//U49187

20 F-PLACE3000020//R.norvegicus type III adenylyl cyclase mRNA, complete cds.//6.1e-103:600:89//M55075

F-PLACE3000029

F-PLACE3000059//Mus musculus mRNA for ubiquitin conjugating enzyme.//4.4e-115:718:86//Y17267

F-PLACE3000070//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.//1.8e-17:250:74//AC005368

25 F-PLACE3000103//Caenorhabditis elegans cosmid C13F10.//4.6e-07:408:61//U97006

F-PLACE3000119//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0190L06; HTGS phase 1, WORKING DRAFT SEQUENCE, 21 unordered pieces.//1.5e-58:291:86//AC004670

F-PLACE3000121//Rattus norvegicus rsec15 mRNA, complete cds.//8.1e-81:837:71//AF032668

F-PLACE3000124//Homo sapiens chromosome 17, clone hRPK.85_B_7, complete sequence.//1.8e-48:330:79//AC005695

30 F-PLACE3000136

F-PLACE3000142//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 349A12, WORKING DRAFT SEQUENCE.//0.011:294:62//AL033520

F-PLACE3000145//Gallus gallus tensin mRNA, 3' end.//6.9e-52:659:68//L06662

35 F-PLACE3000147//Human DNA sequence from clone 267M20 on chromosome Xq22.2-22.3. Contains part of the DIAPH2 gene and a pseudogene, ESTs, STSs and GSSs, complete sequence.//5.1e-37:305:81//AL031053

F-PLACE3000148//Homo sapiens chromosome Y, clone 47511, complete sequence.//4.7e-32:766:63//AC004474

F-PLACE3000155//Homo sapiens chromosome 17, clone hRPK.597_M_12, complete sequence.//7.4e-173:822:98//AC005277

40 F-PLACE3000156//Homo sapiens chromosome 19, overlapping cosmids F18547, F11133, R27945, R28830 and R32804, complete sequence.//2.2e-81:783:74//AC003682

F-PLACE3000157

F-PLACE3000158//, complete sequence.//1.0e-180:845:97//AC005500

F-PLACE3000160//CIT978SK-152K7.TV CIT978SK Homo sapiens genomic clone 152K7, genomic survey sequence.//0.080:259:59//B50878

45 F-PLACE3000169//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//9.8e-158:749:98//AC006130

F-PLACE3000194

F-PLACE3000197//F.rubripes GSS sequence, clone 075N04bB7, genomic survey sequence.//1.4e-08:164:68//AL003352

50 F-PLACE3000199//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 424J12, WORKING DRAFT SEQUENCE.//0.0019:277:58//Z82207

F-PLACE3000207//Homo sapiens BAC clone GS165L15 from 7p15, complete sequence.//6.6e-21:312:67//AC005013

55 F-PLACE3000208//Homo sapiens (clones: CW52-2, CW27-6, CW15-2, CW26-5, 11-67) collagen type VII inter-

genic region and (CC) 7A1 gene, complete cds.//1.7e-41:1000:1000

Sequence data from this project have been deposited in the GenBank database under accession number F0408.

- F-PLACE3000220//RPCI11-54B4.TV RPCI11 Homo sapiens genomic clone R-54B4, genomic survey sequence//2.4e-36:381:76//AQ082056
- F-PLACE3000221//Homo sapiens clone DJ1186P10, WORKING DRAFT SEQUENCE, 6 unordered pieces//7.2e-135:721:91//AC005231
- 5 F-PLACE3000226
F-PLACE3000230//Homo sapiens c1cr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence//3.3e-80:498:78//U95626
- F-PLACE3000242//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene
10 and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032, complete sequence//2.6e-54:254:92//Z98046
- F-PLACE3000244//M.musculus mRNA for 200 kD protein//1.4e-139:850:86//X80169
- F-PLACE3000254//Ateline herpesvirus 3 complete genome//1.3e-10:399:61//AF083424
- F-PLACE3000271//Human Chromosome 16 BAC clone CIT987SK-A-815A9, complete sequence//1.8e-21:350:
15 68//AF001548
- F-PLACE3000276//HS_2026_B1_H11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026 Col=21 Row=P, genomic survey sequence//5.7e-45:376:81//AQ231147
- F-PLACE3000304//Homo sapiens chromosome 19, cosmid R26660, complete sequence//1.6e-138:650:99//AC005328
- 20 F-PLACE3000310
F-PLACE3000320//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE//1.9e-41:379:77//AL034379
- F-PLACE3000322//Homo sapiens chromosome 17, clone hRPK.209_J_20, complete sequence//3.3e-35:419:68//AC005822
- 25 F-PLACE3000331//CIT-HSP-2347D24.TR CIT-HSP Homo sapiens genomic clone 2347D24, genomic survey sequence//2.7e-20:119:99//AQ061543
- F-PLACE3000339//Rhodobacter sphaeroides magnesium chelatase subunits Bchl (bchl) and BchD (bchD) genes, complete cds; and BchO (bchO) gene, partial cds//0.99:310:58//AF017642
- F-PLACE3000341//Homo sapiens 3p22 Contig 7 PAC RPCI4-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence//7.5e-159:752:98//AC006055
- 30 F-PLACE3000350//Rattus norvegicus serine/threonine protein kinase TAO1 mRNA, complete cds//2.3e-107:592:92//AF084205
- F-PLACE3000352//Human DNA sequence from PAC 293L6 on chromosome 22, complete sequence//2.1e-37:480:70//Z83732
- 35 F-PLACE3000353
F-PLACE3000362//Homo sapiens chromosome 17, clone hRPK.215_P_18, complete sequence//0.00011:373:60//AC005969
- F-PLACE3000363
F-PLACE3000365//Human DNA sequence from PAC 227P17, between markers DXS6791 and DXS8038 on chromosome X contains CpG island, EST//0.074:279:61//Z81007
- 40 F-PLACE3000373//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat//2.8e-118:653:92//Z92545
- F-PLACE3000388//Homo sapiens PAC clone DJ0777023 from 7p14-p15, complete sequence//2.2e-25:288:71//AC005154
- 45 F-PLACE3000399//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 466N1, WORKING DRAFT SEQUENCE//2.3e-69:303:86//Z97630
- F-PLACE3000400//Caenorhabditis elegans cosmid H03A11, complete sequence//0.0063:435:58//Z93239
- F-PLACE3000401//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces//5.8e-25:292:73//AC006023
- 50 F-PLACE3000402//RPCI11-20D6.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-20D6, genomic survey sequence//1.1e-10:154:74//AQ008761
- F-PLACE3000405//Homo sapiens chromosome 17, clone hRPK.628_E_12, complete sequence//2.9e-41:515:72//AC005701
- 55 F-PLACE3000406//cSRL-179E11-u cSRL flow sorted Chromosome 11 specific cosmid Homosapiens genomic
- F-PLACE3000407//Homo sapiens chromosome 11, clone hRPK.628_E_12, complete sequence//2.9e-41:515:72//AC005701
- F-PLACE3000408//Arabidopsis thaliana genomic clone hRPK.628_E_12, complete sequence//2.9e-41:515:72//AC005701

0.0018:664:55//B11305

F-PLACE3000425//Human DNA sequence from clone 231L4 on chromosome Xq27.1-27.3 Contains GSS, STS, complete sequence//1.1e-16:284:70//AL022719

F-PLACE3000455//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 469D22, WORKING DRAFT SEQUENCE//3.6e-146:732:96//AL031284

F-PLACE3000475//HS_2164_A2_H10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2164 Col=20 Row=O, genomic survey sequence//1.5e-07:159:71//AQ132983

F-PLACE3000477//Human DNA sequence from PAC 368A4 on chromosome X. Contains ESTs, CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP) like gene and STSs//2.9e-11:213:70//Z83843

F-PLACE4000009//Sequence 93 from patent US 5616500//9.9e-08:692:60//I39845

F-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds//1.1e-116:331:100//AB018352

F-PLACE4000034//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12, complete sequence//5.0e-05:244:63//AC004131

F-PLACE4000049//Homo sapiens Xp22-171-173 BAC GSHB-312I4 (Genome Systems Human BAC Library) complete sequence//1.2e-37:385:74//AC005926

F-PLACE4000052//M.musculus abcl mRNA//1.5e-110:671:88//X75926

F-PLACE4000063

F-PLACE4000089//M.musculus BOX DNA for regulatory element and promoter region related to EC cell differentiation//3.7e-12:114:85//X74311

F-PLACE4000093//CIT-HSP-2380K5.TF CIT-HSP Homo sapiens genomic clone 2380K5, genomic survey sequence//0.11:245:60//AQ108342

F-PLACE4000100//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 20208, WORKING DRAFT SEQUENCE//2.9e-19:384:65//AL031848

F-PLACE4000106//Homo sapiens mRNA for KIAA0462 protein, partial cds//1.2e-145:684:99//AB007931

F-PLACE4000128//Mus musculus putative transcription factor mRNA, complete cds//3.7e-62:541:78//AF091234

F-PLACE4000129

F-PLACE4000131//HS_3139_B2_F12_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3139 Col=24 Row=L, genomic survey sequence//2.3e-14:221:70//AQ183207

F-PLACE4000147//Human DNA sequence from clone 740A11 on chromosome Xq22.2-23. Contains part of the COL4A5 gene for Collagen Alpha 5(IV) Chain Precursor. Contains GSSs, complete sequence//0.28:412:58//AL031622

F-PLACE4000156//Human zinc finger protein ZNF136//7.2e-88:764:76//U09367

F-PLACE4000192

F-PLACE4000211

F-PLACE4000222//344J1.TVB CIT978SKA1 Homo sapiens genomic clone A-344J01, genomic survey sequence//1.2e-14:177:76//B17158

F-PLACE4000230//Mus musculus semaphorin VIa mRNA, complete cds//9.8e-116:662:89//AF030430

F-PLACE4000233//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence//5.2e-54:363:70//AC003973

F-PLACE4000247

F-PLACE4000250//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence//0.0053:229:65//AC004673

F-PLACE4000252

F-PLACE4000259//H.sapiens gene for U5 snRNP-specific 200kD protein//2.0e-25:191:87//Z70200

F-PLACE4000261//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds//2.6e-23:314:71//AF084259

F-PLACE4000269//Rattus norvegicus rexo70 mRNA, complete cds//5.5e-122:734:88//AF032667

F-PLACE4000270

F-PLACE4000300

F-PLACE4000320//Human FKBP-rapamycin associated protein (FRAP) mRNA, complete cds//1.4e-21:135:96//L34075

F-PLACE4000323//HS_2165_B1_B02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2165 Col=3 Row=D, genomic survey sequence//4.3e-08:170:71//AQ125036

F-PLACE4000326//Mouse DNA with homology to EBV IR3 repeat, segment 1, clone Mu2//2.8e-06:311:63//M10296

F-PLACE4000341//H.sapiens

1.5e-06:114:85//X74311

3.7e-12:114:85//X74311

F-PLACE4000369

F-PLACE4000379//CIT-HSP-2350B9.TF CIT-HSP Homo sapiens genomic clone 2350B9, genomic survey sequence.//9.2e-46:282:86//AQ062661

F-PLACE4000387//CIT-HSP-2382F11.TR CIT-HSP Homo sapiens genomic clone 2382F11, genomic survey sequence.//0.96:102:70//AQ080649

F-PLACE4000392//Rattus norvegicus polymorphic marker D20UIA1 sequence.//1.2e-05:222:68//AF054088

F-PLACE4000401//Homo sapiens mRNA for KIAA0640 protein, partial cds.//9.6e-46:605:71//AB014540

F-PLACE4000411//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 173D1, WORKING DRAFT SEQUENCE.//3.2e-29:179:79//AL031984

F-PLACE4000431//H.sapiens gene for U5 snRNP-specific 200kD protein.//4.0e-44:263:92//Z70200

F-PLACE4000445//HS-1053-B1-D02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 775 Col=3 Row=H, genomic survey sequence.//0.070:47:100//B41346

F-PLACE4000450

F-PLACE4000465//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//2.3e-07:273:65//AC005065

F-PLACE4000487//Homo sapiens chromosome 17, clone hRPK.156_L_14, complete sequence.//4.1e-34:351:70//AC005821

F-PLACE4000489//HS_3012_B1_G05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3012 Col=9 Row=N, genomic survey sequence.//2.0e-36:220:92//AQ095537

F-PLACE4000494//Homo sapiens 12p13.3 PAC RPCI5-1063M23 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.3e-57:395:79//AC005865

F-PLACE4000521//Homo sapiens *** SEQUENCING IN PROGRESS *** , WORKING DRAFT SEQUENCE.//1.6e-163:770:98//AJ011929

F-PLACE4000522//Feline leukemia virus Notch2 gene, clone FeLV/Notch2-C, partial cds.//4.0e-124:686:90//U47645

F-PLACE4000548

F-PLACE4000558//Bothrops atrox batroxobin gene (EC 3.4.21.29).//0.049:435:59//X12747

F-PLACE4000581

F-PLACE4000590//Homo sapiens chromosome Y, clone 475I1, complete sequence.//3.6e-20:747:59//AC004474

F-PLACE4000593//Caenorhabditis elegans cosmid F25D7, complete sequence.//5.6e-16:326:65//Z78418

F-PLACE4000612//Homo sapiens PAC clone DJ0722F20 from 7q31.1-q31.3, complete sequence.//1.7e-163:785:97//AC005281

F-PLACE4000638//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//8.7e-74:707:74//AC006039

F-PLACE4000650

F-PLACE4000654//Mus musculus mRNA for ubiquitin conjugating enzyme.//1.1e-145:840:89//Y17267

F-PLACE4000670//Sequence 13 from patent US 5712381.//1.0:311:59//I82816

F-SKNMC1000011//Gallus gallus bone sialoprotein II mRNA, complete cds.//0.014:92:73//U10577

F-SKNMC1000013//Orang-utan involucrin gene, complete cds.//0.021:417:59//M25312

F-SKNMC1000046//Homo sapiens mRNA for KIAA0654 protein, partial cds.//7.6e-147:706:98//AB014554

F-SKNMC1000050//Sequence 5 from patent US 5789181.//1.6e-52:330:90//AR020616

F-SKNMC1000091//Human NK homeobox protein (Nkx6.1) gene, exon 1.//0.0018:375:60//U66797

F-THYRO1000017//Rattus norvegicus pyridoxine 5'-phosphate oxidase mRNA, complete cds.//6.6e-97:542:84//U91561

F-THYRO1000026//Human DNA sequence from clone 833B7 on chromosome 22q12.3-13.2 Contains genes for NCF4 (P40PHOX) protein, cytokine receptor common beta chain precursor CSF2RB (partial), ESTs, CA repeat, STS, GSS, complete sequence.//3.5e-46:353:82//AL008637

F-THYRO1000034//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 90L6, WORKING DRAFT SEQUENCE.//0.83:227:61//Z97353

F-THYRO1000035//Human Chromosome X clone bWXD187, complete sequence.//1.2e-39:303:83//AC004383

F-THYRO1000040

F-THYRO1000070//Homo sapiens chromosome 10 clone CIT987SK-1144G6 map 10q25.1, complete sequence.//1.3e-05:613:58//AC005383

F-THYRO1000072//Homo sapiens mRNA for KIAA0657 protein, partial cds.//2.7e-84:722:77//AB014557

F-THYRO1000085

F-THYRO1000085
F-THYRO1000085
F-THYRO1000085

F-THYRO1000111//Human genomic DNA sequence from clone 308O1 on chromosome Xp11.3-11.4. Contains EST, CA repeat, STS, GSS, CpG island.//6.4e-110:690:87//Z93403

F-THYRO1000121//Rattus norvegicus CTD-binding SR-like protein rA8 mRNA, complete cds.//1.4e-127:816:85//U49055

5 F-THYRO1000124//H.sapiens CpG island DNA genomic MseI fragment, clone 72a7, forward read cpg72a7.ft1a.//9.5e-26:169:94//Z62724

F-THYRO1000129//Homo sapiens TED protein (TED) mRNA, complete cds.//8.5e-154:732:98//AF087142

F-THYRO1000132//Homo sapiens chromosome 9q34, clone 63G10, complete sequence.//3.7e-39:315:82//AC002096

10 F-THYRO1000156//Human DNA sequence from clone 113J7 on chromosome Xp11.22-11.4. Contains part of a putative Homeobox (pseudo?) gene, ESTs and an STS, complete sequence.//1.2e-21:335:71//AL023574

F-THYRO1000163//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-A-218C7, complete sequence.//8.4e-52:301:88//AC002331

F-THYRO1000173//Mouse clathrin-associated protein (AP47) mRNA, complete cds.//4.0e-89:821:74//M62419

15 F-THYRO1000186//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 424J12, WORKING DRAFT SEQUENCE.//7.2e-39:293:85//Z82207

F-THYRO1000187//Clostridium tetani gene for tetanus toxin.//0.041:473:57//X06214

F-THYRO1000190//Homo sapiens chromosome 17, clone hRPK.332_H_18, complete sequence.//0.38:184:64//AC005746

20 F-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease.//7.5e-174:805:99//AJ005698

F-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds.//1.2e-86:616:84//AB014552

F-THYRO1000206//HS_3047_A1_A05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=9 Row=A, genomic survey sequence.//0.51:331:63//AQ099134

25 F-THYRO1000221//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.092:738:56//AC004157

F-THYRO1000241//Gallus gallus genome fragment with pentamer tandem repeats.//0.43:191:62//X00186

F-THYRO1000242//Human zinc finger gene HZF7.//2.8e-43:534:64//X60156

F-THYRO1000253//Homo sapiens 3p22 Contig 7 PAC RPCI4-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.95:139:68//AC006055

30 F-THYRO1000270

F-THYRO1000279//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 531H16, WORKING DRAFT SEQUENCE.//1.4e-174:826:98//AL031664

F-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds.//3.9e-179:848:98//AB016068

35 F-THYRO1000320//Mus musculus sphingosine-1-phosphate lyase mRNA, complete cds.//1.0e-44:331:83//AF036894

F-THYRO1000327//Homo sapiens autocrine motility factor receptor (AMFR) mRNA, complete cds.//5.7e-112:641:91//L35233

F-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds.//2.2e-162:763:98//AB018333

F-THYRO1000358//Human selenium-binding protein (hSBP) mRNA, complete cds.//2.2e-32:177:84//U29091

40 F-THYRO1000368//Caenorhabditis elegans cosmid W09G3, complete sequence.//0.97:206:60//Z82080

F-THYRO1000381//Arthrobacter sp. glcI gene for beta-1,3-glucanase, complete cds.//0.27:427:62//D23668

F-THYRO1000387//Homo sapiens PAC clone DJ1048B16 from 7q34-q36, complete sequence.//9.7e-147:698:98//AC006019

F-THYRO1000394//HS_2061_A2_C04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2061 Col=8 Row=E, genomic survey sequence.//1.6e-29:202:91//AQ247672

45 F-THYRO1000395//Drosophila melanogaster ring canal protein and ORF2 mRNA, complete cds.//4.3e-15:512:59//L08483

F-THYRO1000401 3.2e-116:504:80//AF051908

F-THYRO1000438//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.4e-09:539:59//AC005308

50 F-THYRO1000452//RPCI11-1C19.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-1C19, genomic survey sequence.//0.27:132:64//B49573

F-THYRO1000471//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete sequence.//1.3e-38:332:81//AC005229

55 F-THYRO1000484//Homo sapiens BAC378, complete sequence.//2.2e-37:254:76//U85196

F-THYRO1000488//Homo sapiens BAC378, complete sequence.//2.2e-37:254:76//U85196

Sequence data from

GenBank accession numbers: F000000000, F000000001, F000000002, F000000003, F000000004, F000000005, F000000006, F000000007, F000000008, F000000009, F000000010, F000000011, F000000012, F000000013, F000000014, F000000015, F000000016, F000000017, F000000018, F000000019, F000000020, F000000021, F000000022, F000000023, F000000024, F000000025, F000000026, F000000027, F000000028, F000000029, F000000030, F000000031, F000000032, F000000033, F000000034, F000000035, F000000036, F000000037, F000000038, F000000039, F000000040, F000000041, F000000042, F000000043, F000000044, F000000045, F000000046, F000000047, F000000048, F000000049, F000000050, F000000051, F000000052, F000000053, F000000054, F000000055, F000000056, F000000057, F000000058, F000000059, F000000060, F000000061, F000000062, F000000063, F000000064, F000000065, F000000066, F000000067, F000000068, F000000069, F000000070, F000000071, F000000072, F000000073, F000000074, F000000075, F000000076, F000000077, F000000078, F000000079, F000000080, 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F-THYRO1000502//Human DNA sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked, juvenile) 1 (XLR51). Contains ESTs, an STS and GSSs, complete sequence.//0.076:380:59//Z94056

F-THYRO 1000505

F-THYRO1000558//Human PAC clone 127H14 from 12q, complete sequence.//2.4e-27:412:69//AC002563

F-THYRO1000569//HS_2178_B2_E03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2178 Col=6 Row=J, genomic survey sequence.//1.9e-27:326:74//AQ307499

F-THYRO1000570

F-THYRO1000585//Homo sapiens protein associated with Myc mRNA, complete cds.//7.4e-167:808:97//

AF075587

F-THYRO1000596//Human Chromosome 16 BAC clone CIT987SK-A-972D3, complete sequence.//0.99:280:61//U91323

F-THYRO1000602//HS_3037_B2_E04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3037 Col=8 Row=J, genomic survey sequence.//1.2e-05:109:75//AQ097057

F-THYRO1000605//Homo sapiens map 2p11.2; 83cM from GATA85A06 repeat region, complete sequence.//1.0:84:70//AF067777

F-THYRO1000625//Homo sapiens chromosome 19, cosmid R29425, complete sequence.//3.4e-174:820:98//AC005546

F-THYRO1000637//Human DNA sequence from clone 91J24 on chromosome 6q24 Contains part of utrophin Gene, part of cytochrome C oxidase gene, EST, CpG island, complete sequence.//3.6e-38:289:84//AL024474

F-THYRO1000641//Plasmodium falciparum MAL3P7, complete sequence.//6.8e-07:540:56//AL034559

F-THYRO1000658//Homo sapiens chromosome 17, clone hRPK.74_E_22, complete sequence.//1.1e-68:468:84//AC005696

F-THYRO1000662//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K23L20, complete sequence.//0.0072:141:70//AB016874

F-THYRO1000666//Mus musculus mRNA for motor domain of KIF9, partial cds.//4.7e-58:367:87//AB001437

F-THYRO1000676//Homo sapiens chromosome 19, cosmid F22676, complete sequence.//1.2e-36:396:71//AC005778

F-THYRO1000684//Fugu rubripes cosmid 165K09 DNA for GRM7, TRIP, Sand, PRGFR3 genes.//6.6e-13:236:69//AJ010317

F-THYRO1000699//RPC111-50D4.TK RPC111 Homo sapiens genomic clone R-50D4, genomic survey sequence.//2.7e-09:135:78//AQ052641

F-THYRO1000712//Homo sapiens BAC clone RG041D11 from 7q21, complete sequence.//5.2e-17:290:67//AC005053

F-THYRO1000715//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//8.6e-08:517:60//L14320

F-THYRO1000734//HS_3233_B1_B04_T7 CIT Approved Human Genomic Sperm Library D-Homo sapiens genomic clone Plate=3233 Col=7 Row=D, genomic survey sequence.//6.0e-72:463:89//AQ182143

F-THYRO1000748//Homo sapiens KIAA0411 mRNA, complete cds.//9.7e-34:339:74//AB007871

F-THYRO1000756//M.musculus mRNA for Gal beta1, 3GalNAc alpha2,3-sialyltransferase.//0.00034:349:60//X73523

F-THYRO1000777//S.griseus strO gene and sts gene cluster.//8.2e-05:625:59//Y08763

F-THYRO1000783//Xenopus laevis tail-specific thyroid hormone up-regulated (gene 5) mRNA, complete cds.//4.0e-70:860:69//U37373

F-THYRO1000787//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 366D1, WORKING DRAFT SEQUENCE.//5.3e-09:221:66//Z97986

F-THYRO1000793

F-THYRO1000796//Cristatella mucedo clone 5.9 microsatellite sequence.//0.34:173:63//AF085422

F-THYRO1000805//Homo sapiens Xp21 PAC RPC11-37A12 containing exons 10 to 16 of the Duchenne Muscular Dystrophy gene, complete sequence.//7.8e-43:677:66//AC004468

F-THYRO1000815//Homo sapiens chromosome 5, Bac clone 189 (LBNL H135), complete sequence.//5.5e-43:405:77//AC005914

F-THYRO1000829//CIT-HSP-2387C10.TF.1 CIT-HSP Homo sapiens genomic clone 2387C10, genomic survey sequence.//2.0e-20:159:88//AQ240053

F-THYRO1000843

F-THYRO1000843

F-THYRO1000843

F-THYRO1000843//Mus musculus mRNA for KIF9, partial cds.//4.7e-58:367:87//AB001437

64//AF008573

F-THYRO1000865//Homo sapiens PAC clone DJ0283M22 from 14, complete sequence.//1.9e-30:286:74//AC005477

F-THYRO1000895//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 385E7, WORKING DRAFT SEQUENCE.//2.8e-18:186:80//AL031720

F-THYRO1000916//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.6e-78:432:93//AC006015

F-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//9.2e-178:839:98//AF079529

F-THYRO1000934//Human pyrroline 5-carboxylate reductase mRNA, complete cds.//3.5e-32:759:63//M77836

F-THYRO1000951//Homo sapiens Chromosome 11q12 pac pDJ57114, WORKING DRAFT SEQUENCE, 29 unordered pieces.//4.9e-76:224:93//AC004229

F-THYRO1000952

F-THYRO1000974//HS_3238_B2_F01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=2 Row=L, genomic survey sequence.//12.4e-26:154:96//AQ219846

F-THYRO1000975//Plasmodium falciparum TopoII gene.//0.32:491:58//X79345

F-THYRO1000983//Mvfwf9A3 exon amplification products from BACs in Mvfwf region Mus musculus genomic, genomic survey sequence.//7.0e-16:112:94//AQ010457

F-THYRO1000984//CIT-HSP-2167O17.TR CIT-HSP Homo sapiens genomic clone 2167O17, genomic survey sequence.//0.00015:186:66//B91313

F-THYRO1000988//Human Chromosome 11q12.2 PAC clone pDJ756b9 containing human ferritin heavy chain mRNA (FTH), WORKING DRAFT SEQUENCE, 19 unordered pieces.//0.024:267:63//AC004588

F-THYRO1001003

F-THYRO1001031//Homo sapiens chromosome 17, clone hRPC.859_O_20, complete sequence.//1.1e-55:543:72//AC003695

F-THYRO1001033//Methanobacterium thermoautotrophicum from bases 48264 to 58328 (section 5 of 148) of the complete genome.//0.94:445:58//AE000799

F-THYRO1001062//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 199H16, WORKING DRAFT SEQUENCE.//4.4e-45:441:75//AL022320

F-THYRO1001093//Homo sapiens chromosome 9, clone hRPK.202_H_3, complete sequence.//4.9e-34:353:76//AC006241

F-THYRO1001100//Human DNA-binding protein mRNA, 3'end.//1.1e-72:742:74//L14787

F-THYRO1001120//Homo sapiens clone DJ1129E22, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.2e-76:521:86//AC005522

F-THYRO1001121//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 671O14, WORKING DRAFT SEQUENCE.//0.00078:594:58//AL031595

F-THYRO1001133//Homo sapiens PAC clone DJ1200I23 from 7p15, complete sequence.//4.0e-35:349:76//AC004996

F-THYRO1001134//Homo sapiens clone DJ1070G24, WORKING DRAFT SEQUENCE, 12 unordered pieces.//1.0:154:66//AC005486

F-THYRO1001142//Human DNA sequence from clone B79B4 on chromosome 22 Contains CA repeat and GSS, complete sequence.//1.4e-44:374:80//Z82178

F-THYRO1001173

F-THYRO1001177//Human pigment epithelium-derived factor gene, complete cds.//1.9e-42:250:86//U29953

F-THYRO1001189//HS_3171_B2_F10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3171 Col=20 Row=L, genomic survey sequence.//1.8e-28:246:83//AQ302330

F-THYRO1001204//Drosophila melanogaster DNA repair protein (mei-41) gene, complete cds, and TH1 gene, partial cds.//4.9e-39:657:64//U34925

F-THYRO1001213//, complete sequence.//1.7e-45:257:84//AC005300

F-THYRO1001262//Homo sapiens genomic DNA, chromosome 21q11.1, segment 7/28, WORKING DRAFT SEQUENCE.//1.5e-40:274:87//AP000036

F-THYRO1001271//Streptomyces coelicolor cosmid 1A6.//0.033:364:61//AL023496

F-THYRO1001287//Drosophila melanogaster cosmid clone 86E4.119.6e-49:586:69//AL021086

F-THYRO1001290//HS_2045_B1_H09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2045 Col=17 Row=P, genomic survey sequence.//4.4e-13:156:78//AQ248237

F-THYRO1001313//S. lavendulae bla gene for beta-lactamase, complete cds.//1.7e-22:64:10//U10000

F-THYRO1001314//Homo sapiens chromosome 12, clone hRPC.859_O_20, complete sequence.//1.1e-55:543:72//AC003695

F-THYRO1001315//Homo sapiens chromosome 12, clone hRPC.859_O_20, complete sequence.//1.1e-55:543:72//AC003695

- F-THYRO1001321//Human PAC clone DJ527C21 from Xq23, complete sequence.//1.2e-115:740:87//AC000114
- F-THYRO1001322//HS_3205_B2_C12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3205 Col=24 Row=F, genomic survey sequence.//0.00031:285:61//AQ304025
- F-THYRO1001347//Homo sapiens mRNA for KIAA0745 protein, partial cds.//2.2e-43:638:64//AB018288
- 5 F-THYRO1001363//Homo sapiens PAC clone DJ0845I21 from 7q11.21-q11.23, complete sequence.//1.0e-09:189:74//AC004905
- F-THYRO1001365//Homo sapiens chromosome 10 clone CIT987SK-1163G10 map-10q25, complete sequence.//7.6e-168:821:97//AC005660
- F-THYRO1001374//Homo sapiens mRNA for KIAA0707 protein, partial cds.//2.3e-155:740:97//AB014607
- 10 F-THYRO1001401//Homo sapiens chromosome 19, cosmid F23149, complete sequence.//3.2e-07:138:73//AC005239
- F-THYRO1001403//Homo sapiens chromosome 12p13.3 clone RPCI3-454B23, WORKING DRAFT SEQUENCE, 48 unordered pieces.//3.6e-70:360:86//AC005845
- F-THYRO1001405//Bos taurus mRNA for NDP52, complete cds.//2.6e-14:559:63//AB008852
- 15 F-THYRO1001406//Mus musculus putative steroid dehydrogenase (KIK-I) mRNA, complete cds.//1.0e-91:631:82//AF064635
- F-THYRO1001411//Homo sapiens chromosome 19, cosmid F18718, complete sequence.//5.5e-42:509:71//AC006126
- F-THYRO1001426//*** SEQUENCING IN PROGRESS *** Homo sapiens genomic DNA (PAC 1118i22) from chromosome 11; HTGS phase 1, WORKING DRAFT SEQUENCE.//2.7e-31:172:81//AJ002553
- 20 F-THYRO1001434//Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.0:98:70//AC000384
- F-THYRO1001458//Bos taurus non-muscle myosin heavy chain mRNA, partial cds.//1.9e-58:653:71//U87265
- F-THYRO1001480//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//7.5e-42:357:80//AC006001
- 25 F-THYRO1001487//H.sapiens DNA sequence.//0.92:160:64//Z22449
- F-THYRO1001534//Homo sapiens chromosome 17, clone hCIT.468_F_23, WORKING DRAFT SEQUENCE, 3 unordered pieces.//4.8e-47:266:80//AC004666
- F-THYRO1001537//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 998H6, WORKING DRAFT SEQUENCE.//1.3e-79:479:89//AL031687
- 30 F-THYRO1001541//Human DNA sequence from clone 399M14 on chromosome Xq26.1-26.3. Contains ESTs, an STS and GSSs, complete sequence.//0.0034:106:77//Z96074
- F-THYRO1001559//Rattus norvegicus simple sequence repeat D18Mco6.//1.6e-09:351:63//AF006056
- F-THYRO1001570//RPCI11-49B23.TJ RPCI11 Homo sapiens genomic clone R-49B23, genomic survey sequence.//1.4e-65:384:91//AQ052105
- 35 F-THYRO1001573//Homo sapiens clone 24778 unknown mRNA.//8.2e-104:546:95//AF070572
- F-THYRO1001584//CIT-HSP-2365J21.TF CIT-HSP Homo sapiens genomic clone 2365J21, genomic survey sequence.//1.3e-24:180:88//AQ080498
- F-THYRO1001595//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING DRAFT SEQUENCE.//8.7e-145:779:93//AL023808
- 40 F-THYRO1001602//Homo sapiens chromosome 17, clone hRPK.786_O_4, complete sequence.//2.9e-26:393:68//AC005863
- F-THYRO1001605//Dictyostelium discoideum filopodin (talA) gene, complete cds.//0.0012:436:58//U14576
- F-THYRO1001617//Homo sapiens full-length insert cDNA clone ZD69D05.//8.6e-43:342:82//AF086381
- 45 F-THYRO1001637//Homo sapiens clone DJ1019E05, WORKING DRAFT SEQUENCE, 10 unordered pieces.//6.2e-15:318:66//AC004950
- F-THYRO1001656//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.//1.5e-05:147:68//AC004827
- F-THYRO1001661
- 50 F-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform.//2.5e-164:780:98//AJ225089
- F-THYRO1001673//Homo sapiens clone RG161A02, complete sequence.//4.4e-40:770:64//AC005071
- F-THYRO1001703//S.coelicolor plasmid SCP2 transfer region DNA.//0.14:414:59//X72857
- F-THYRO1001706//Homo sapiens BAC clone RG281B09 from 7q21.1-q31.1, complete sequence.//2.6e-43:308:75//AC004745
- 55 F-THYRO1001707//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001708//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001709//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001710//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001711//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001712//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001713//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001714//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001715//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001716//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001717//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001718//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001719//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001720//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001721//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001722//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001723//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001724//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001725//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001726//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001727//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001728//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001729//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001730//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001731//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001732//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001733//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001734//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001735//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001736//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001737//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001738//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001739//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001740//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001741//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001742//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001743//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001744//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001745//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001746//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001747//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001748//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001749//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001750//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001751//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001752//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001753//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001754//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001755//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001756//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001757//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001758//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001759//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001760//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001761//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001762//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001763//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001764//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001765//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001766//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001767//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001768//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001769//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001770//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001771//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001772//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001773//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001774//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001775//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001776//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001777//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001778//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001779//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001780//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001781//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001782//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001783//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001784//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001785//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001786//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001787//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001788//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001789//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001790//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001791//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001792//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001793//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001794//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001795//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001796//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001797//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001798//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001799//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745
- F-THYRO1001800//Homo sapiens genomic DNA sequence.//1.1e-11:11:11//AC004745

F-THYRO1001745

F-THYRO1001746

F-THYRO1001772//HS_3069_B1_C05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3069 Col=9 Row=F, genomic survey sequence.//1.5e-61:360:91//AQ171021

5 F-THYRO1001793//B.taurus mRNA for beta-subunit of rod photoreceptor CNG-channel.//0.028:446:58//X89626

F-THYRO 1001809

F-THYRO1001828//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 110F11, WORKING DRAFT SEQUENCE.//1.3e-175:841:98//AL033526

10 F-THYRO1001854//Homo sapiens chromosome 17, clone hCIT54K19, complete sequence.//7.9e-07:445:59//AC003664

F-THYRO1001895

4.4e-13:248:68//AB012576

F-THYRO1001907//Homo sapiens BAC clone RG054D04 from 7q31, complete sequence.//2.9e-15:144:77//AC005058

15 F-VESEN1000122//HS_3075_B1_C09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=17 Row=F, genomic survey sequence.//1.1e-16:130:90//AQ143749

F-Y79AA1000013

F-Y79AA1000033//Homo sapiens BAC clone GS114I09 from 7p14-p15, complete sequence.//2.9e-95:300:94//AC006027

20 F-Y79AA1000037//Human prot-oncogene (BMI-1) mRNA, complete cds.//2.4e-19:230:66//L13689

F-Y79AA1000059//Homo sapiens immunophilin homolog ARA9 mRNA, complete cds.//2.2e-38:629:64//U78521

F-Y79AA1000065//Human DNA sequence from cosmid J256K24, between markers DXS6791 and DXS8038 on chromosome X contains EST.//5.3e-10:117:83//Z72005

F-Y79AA1000131//Homo sapiens LERK-6 (EPLG6) gene, exon 1.//7.6e-10:381:64//U92893

25 F-Y79AA1000181//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//1.4e-165:732:99//AL031864

F-Y79AA1000202//Drosophila melanogaster DNA sequence (P1 DS06882 (D310)), complete sequence.//9.1e-20:339:65//AC005115

30 F-Y79AA1000214//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//3.7e-72:397:93//AC004854

F-Y79AA1000230

F-Y79AA1000231//Mus musculus SIK similar protein mRNA, complete cds.//8.5e-151:833:90//AF053232

35 F-Y79AA1000258//Leishmania donovani histidine secretory acid phosphatase (SACP-1) gene, complete cds.//0.0099:547:58//U78522

F-Y79AA1000268//Mus musculus Nip21 mRNA, complete cds.//4.0e-11:424:62//AF035207

F-Y79AA1000313

F-Y79AA1000328//CIT-HSP-386A20.TF CIT-HSP Homo sapiens genomic clone 386A20, genomic survey sequence.//5.9e-07:173:69//B55085

40 F-Y79AA1000342//RPC111-57J6.TK.1 RPC111 Homo sapiens genomic clone R-57J6, genomic survey sequence.//5.2e-27:151:99//AQ115511

F-Y79AA1000346//B.primigenius mRNA for coat protein gamma-cop.//5.7e-69:694:71//X92987

F-Y79AA1000349//M.musculus Spnr mRNA for RNA binding protein.//1.8e-98:535:92//X84692

45 F-Y79AA1000355//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.6e-21:129:85//AC005484

F-Y79AA1000368//H.sapiens CpG island DNA genomic Mse1 fragment, clone 12f1, reverse read cpg12f1.rt1c.//0.00016:53:98//Z56610

F-Y79AA1000405//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P4, WORKING DRAFT SEQUENCE.//0.069:366:59//AL031747

50 F-Y79AA1000410//Human DNA sequence from PAC 117P19 on chromosome X.//1.0e-25:235:80//Z86061

F-Y79AA1000420//H.sapiens CpG island DNA genomic Mse1 fragment, clone 82c3, forward read cpg82c3.ft1a.//2.0e-36:194:98//Z63378

F-Y79AA1000469//Mus musculus ancient ubiquitous 46 kDa protein AUP1 precursor (Aup1) mRNA, complete cds.//8.5e-121:696:89//U41736

55 F-Y79AA1000480//HS_2175_A2_H11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2175 Col=22 Row=C, genomic survey sequence.//2.5e-26:178:89//AQ007897

F-Y79AA1000498//H.sapiens CpG island DNA genomic Mse1 fragment, clone 12f1, reverse read cpg12f1.rt1c.//0.00016:53:98//Z56610

F-Y79AA1000539//HS_2237_B2_F10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=20 Row=L, genomic survey sequence//1.2e-14:168:77//AQ153503

F-Y79AA1000540//Homo sapiens clone DJ0655N24, WORKING DRAFT SEQUENCE, 8 unordered pieces//0.94:127:67//AC005193

5 F-Y79AA1000560//Mouse mRNA for alpha-adaptin (C)//1.7e-114:776:84//X14972

F-Y79AA1000574//M.musculus tex23 mRNA (5'region)//1.8e-23:291:75//X80424

F-Y79AA1000589//Homo sapiens clone 614 unknown mRNA, complete sequence//8.6e-153:755:97//AF091080

F-Y79AA1000627//Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds//5.2e-135:644:98//AF060503

F-Y79AA1000705//M.musculus mRNA of enhancer-trap-locus 1//6.9e-148:902:86//X69942

10 F-Y79AA1000734//Homo sapiens PEX11 beta mRNA for peroxisome assembly factor, complete cds//4.8e-180:850:98//AB018080

F-Y79AA1000748//Caenorhabditis elegans cosmid F25B5//0.00019:308:60//U23172

F-Y79AA1000752//Oryctolagus cuniculus mRNA for hnRNP-E1 protein//1.7e-40:513:68//AJ003023

F-Y79AA1000774

15 F-Y79AA1000782

F-Y79AA1000784//Homo sapiens RanBP7/importin 7 mRNA, complete cds//3.5e-177:847:97//AF098799

F-Y79AA1000794//H.sapiens CpG island DNA genomic Mse1 fragment, clone 45a4, forward read cpg45a4.ft1a.//2.5e-13:104:92//Z61120

F-Y79AA1000800//Homo sapiens GABA-B receptor mRNA, complete cds//0.98:244:60//AF056085

20 F-Y79AA1000802

F-Y79AA1000805//Human Chromosome 11 Cosmid cSRL30h11, complete sequence//9.3e-76:528:85//U73642

F-Y79AA1000824//RPCI11-26B4.TP RPCI-11 Homo sapiens genomic clone RPCI-11-26B4, genomic survey sequence//4.4e-14:99:95//B84538

F-Y79AA1000827//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 117715, WORKING

25 DRAFT SEQUENCE//1.5e-08:249:69//AL022315

F-Y79AA1000833//Macaca fascicularis mRNA for alpha-tubulin//1.8e-103:603:89//X04757

F-Y79AA1000850

F-Y79AA1000962//Human DNA sequence from PAC 360E18 on chromosome X contains EST, CpG island and polymorphic CA repeat//0.038:468:59//Z82203

30 F-Y79AA1000966//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, complete cds//9.7e-150:865:89//AF071314

F-Y79AA1000968//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds//6.4e-122:717:88//U38253

F-Y79AA1000969//Mouse chromosome 6 BAC-284H12 (Research Genetics mouse BAC library) complete sequence//1.0:155:63//AC002397

35 F-Y79AA1000976//Caenorhabditis elegans cosmid F54C1//4.3e-06:130:73//U88165

F-Y79AA1000985//Mus musculus pericentrin mRNA, complete cds//2.4e-44:428:77//U05823

F-Y79AA1001023

F-Y79AA1001041//Human mutY homolog (hMYH) gene, complete cds//2.3e-13:90:100//U63329

40 F-Y79AA1001048//Human mRNA for very-long-chain acyl-CoA dehydrogenase (VLCAD), complete cds//2.6e-28:772:60//D43682

F-Y79AA1001061//Homo sapiens chromosome 4 clone B331M8 map 4q25, complete sequence//9.4e-36:292:82//AC004701

F-Y79AA1001068//tipAL-AS complex: tipA=TipAL-AS [Streptomyces lividans, Genomic, 1146 nt]//0.17:537:59//S64314

45 F-Y79AA1001077//Zea mays mRNA for aldehyde oxidase-2, complete cds//0.17:231:64//D88452

F-Y79AA1001078

F-Y79AA1001105//Zebrafish otx2 mRNA for otx homeoprotein, complete cds//3.1e-63:529:77//D26173

F-Y79AA1001145//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces//1.3e-23:228:76//AC005015

50 F-Y79AA1001167

F-Y79AA1001177//M.musculus mRNA for NfiX1-protein//4.0e-10:398:64//Y07688

F-Y79AA1001185//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 16915, WORKING

DRAFT SEQUENCE//1.1e-113:666:90//Z93015

55 F-Y79AA1001211//HS_3124_B2_H08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3124 Col=16 Row=D, genomic survey sequence//1.1e-14:168:77//AQ153503

AL021841

F-Y79AA1001233//Human placental 17-beta-hydroxysteroid dehydrogenase mRNA, complete cds //3.5e-24:731:60//M36263

F-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110I133Q7 (RZPD Berlin)).//1.2e-133.441:97//AJ005892

F-Y79AA1001281//HS_2241_B2_F09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2241 Col=18 Row=L, genomic survey sequence//5.0e-27;169:94//AQ217497

F-Y79AA1001299//Human Ini1 mRNA, complete cds//6.7e-115:323:93//U04847

F-Y79AA1001312

F-Y79AA1001323

F-Y79AA1001384

F-Y79AA1001391//Mus musculus transcription factor HOXA13 (Hoxa13) gene, complete cds.//5.8e-42:245:74//U59322

F-Y79AA1001394//Caenorhabditis elegans cosmid F54B3, complete sequence//7.8e-18:636:58//Z48583

F-Y79AA1001402//Homo sapiens Chr.14 PAC RPC14-794B2 (Roswell Park Cancer Institute Human PAC Library)
complete sequence//1.2e-110:738:85//AC005924

F-Y79AA1001493//H.sapiens DNA sequence.//2.0e-27:254:82//Z22497

F-Y79AA1001511//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs, complete sequence//1.1e-158:804:95//AL034430

F-Y79AA1001533//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.//1.7e-100:820:78//D14336

F-Y79AA1001541//HS_3197_A2_G11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3197 Col=22 Row=M, genomic survey sequence.//5.1e-28:218:86//AQ150183

F-Y79AA1001548//Homo sapiens chromosome 19, cosmid R28738, complete sequence.//5.4e-21:167:86//AC004151

F-Y79AA1001555//R.norvegicus mRNA for drebrin A.//0.88:463:59//X59267

F-Y79AA1001581//FMR1 {CGG repeats} [human, Fragile X syndrome patient, Genomic, 429 nt]//0.00051:252:65//S74494

F-Y79AA1001585//Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds //7.2e-33:375:76//M26434

F-Y79AA1001594

F-Y79AA1001603//Homo sapiens PAC 128M19 derived from chromosome 21q22.3, containing the HMG-14 and CHD5 genes, complete cds, complete sequence.//4.2e-06:338:66//AF064861

F-Y79AA1001613//Homo sapiens mRNA for KIAA0683 protein, complete cds.//0.024:520:57//AB014583

F-Y79AA1001647//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y53F4, WORK-
ING DRAFT SEQUENCE//0.014:331:61//Z92860

F-Y79AA1001665//Human DNA sequence from clone 299D3 on chromosome 22q13.3, complete sequence //0.99:
273:63//Z84468

F-Y79AA1001679//O.cuniculus lambda-crystallin mRNA, complete cds//1.2e-97:682:81//M22743

F-Y79AA1001692//insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1292 nt, segment 1 of 4]//5.6e-05:426:59//S37712

F-Y79AA1001696//Rice endogenous double-stranded RNA encoding polyprotein (containing putative helicase and putative RNA-dependent RNA polymerase domains), complete cds.//1.0:437:60/D32136

F-Y79AA1001705//M.musculus fkh-5 gene.//0.18:153:64//X71943

F-Y79AA1001711//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 328E19, WORKING DRAFT SEQUENCE.//5.4e-76:191:98//AL022240

F-Y79AA1001781//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 10/15,
WORKING DRAFT SEQUENCE.//0.99:227:63//AP000017

F-Y79AA1001805//H.sapiens CpG island DNA genomic Mse1 fragment, clone 13d12, reverse read
cpg13d12.rt1c.//2.6e-13:88:100//Z64565

F-Y79AA1001827//*Oryctolagus cuniculus* PiUS mRNA, complete cds.//3.7e-130:775:88//U74297

F-Y79AA1001846//CIT-HSP-2300M6.TR CIT-HSP Homo sapiens genomic clone 2300M6, genomic survey sequence.//8.3e-17:218:76//AQ012369

F-Y79AA1001848//Human mRNA for KIAA0390 gene, complete cds.//4.2e-10:378:62//AB002388

F-Y79AA1001866//Rattus norvegicus Cys2/His2 zinc finger protein (rKr1) mRNA, complete cds.//6 9e-41 441 71//
141164

TABLE 1. *Effect of the addition of a small amount of water to the reaction mixture on the polymerization of styrene initiated by benzoyl peroxide in benzene at 60°C.*

076 005 - 00000000 AF02977

F-Y79AA1001875//CTT-HSP-2317G18.TR CIT-HSP Homo sapiens genomic clone 2317G18, genomic survey sequence.//1.9e-09:271:67//AQ042654

F-Y79AA1001923//H.sapiens CpG island DNA genomic MseI fragment, clone 193c12, forward read cpg193c12.ft1a.//0.0031:108:75//Z60186

5 F-Y79AA1001963//CITBI-E1-2510J4.TR CITBI-E1 Homo sapiens genomic clone 2510J4, genomic survey sequence.//1.8e-05:56:100//AQ261184

F-Y79AA1002027//Arabidopsis thaliana ubiquitin-conjugating enzyme 17 (UBC17) mRNA, complete cds.//3.3e-13:451:62//AF028340

10 F-Y79AA1002083//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 526I14, WORKING DRAFT SEQUENCE.//0.91:134:65//Z82214

F-Y79AA1002089

F-Y79AA1002093//Mus musculus transcription factor like protein 4 TCFL4 mRNA, partial cds.//1.2e-112:678:88//U43548

F-Y79AA1002103//HS_3052_B1_H08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3052 Col=15 Row=P, genomic survey sequence.//6.5e-18:238:72//AQ135014

15 F-Y79AA1002115

F-Y79AA1002125//H.sapiens (D8S135) DNA segment containing GT repeat.//1.5e-14:99:96//X61693

F-Y79AA1002139//Saccharomyces cerevisiae dnaJ homolog Hlj1p (HLJ1) gene, complete cds.//2.5e-07:208:64//U19358

20 F-Y79AA1002204//HS_2235_B2_D12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2235 Col=24 Row=H, genomic survey sequence.//2.9e-13:89:98//AQ154260

F-Y79AA1002208//CIT-HSP-2006M21.TV CIT-HSP Homo sapiens genomic clone 2006M21, genomic survey sequence.//3.7e-27:154:98//B56397

F-Y79AA1002209//E.coli tyrS gene coding for tyrosyl-tRNA synthetase.//2.8e-05:143:70//J01719

25 F-Y79AA1002210//Homo sapiens chromosome 19, cosmid R28058, complete sequence.//8.3e-22:229:78//AC005615

F-Y79AA1002211//Homo sapiens chromosome 17, clone HRPC1067M6, complete sequence.//1.0e-06:241:67//AC003043

F-Y79AA1002220//CIT-HSP-2374P23.TR CIT-HSP Homo sapiens genomic clone 2374P23, genomic survey sequence.//1.3e-68:375:95//AQ109738

30 F-Y79AA1002229//Human mRNA for KIAA0086 gene, complete cds.//0.12:203:63//D42045

F-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds.//1.3e-174:821:98//AB014592

F-Y79AA1002246//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.50:470:60//AC005015

35 F-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds.//6.8e-159:748:98//AB014555

F-Y79AA1002298//Human density enhanced phosphatase-1 mRNA, complete cds.//0.036:278:62//U10886

F-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds.//6.4e-129:622:97//AB014534

F-Y79AA1002311//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//2.0e-116:693:82//X67877

F-Y79AA1002351//S.clavuligerus pah and cas genes.//1.0:369:58//X84101

40 F-Y79AA1002361//Rattus norvegicus mRNA for protein phosphatase 1 (GL-subunit).//5.4e-105:762:80//Y18208

F-Y79AA1002399//Homo sapiens chromosome 17, clone hRPK.700_H_6, complete sequence.//1.0e-159:411:100//AC005920

F-Y79AA1002407//Homo sapiens chromosome 17, clone hRPC.842_A_23, complete sequence.//1.1e-118:609:84//AC004662

45 F-Y79AA1002416//Mus musculus CTP synthetase homolog (CTPsH) mRNA, complete cds.//4.4e-90:529:88//U49385

F-Y79AA1002431//Chlamydomonas reinhardtii novel protein kinase mRNA, complete cds.//1.0:166:66//U36196

F-Y79AA1002433//CIT-HSP-384K8.TF CIT-HSP Homo sapiens genomic clone 384K8, genomic survey sequence.//0.24:85:72//B51917

50 F-Y79AA1002472//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//1.9e-13:242:69//AC006116

F-Y79AA1002482//Homo sapiens full-length insert cDNA clone ZC18H06.//1.2e-35:462:71//AF088022

F-Y79AA1002487//Bovine herpesvirus type 1 genes for UL[27,28,29,30,31].//0.93:215:60//X94677

55 Homology Search Result Data 3.

the name of clone,
 definition of the top hit data,
 the P-value: the length of the compared sequence: identity (%), and
 the Accession No. of the top hit data, as in the order separated by //.

5

[0305] Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone.

[0306] Data are not shown for the clones in which the P-value was higher than 1.

10

R-HEMBA1000005//Mouse tumor cell dnaJ-like protein 1 mRNA, complete cds.//3.6e-60:504:78//L16953
 R-HEMBA1000030//F.rubripes GSS sequence, clone 063K10bD3, genomic survey sequence.//0.28:117:68//
 Z88864

R-HEMBA1000042//RPC11-77G23.TV RPC11 Homo sapiens genomic clone R-77G23, genomic survey se-
 quence.//1.3e-56:292:97//AQ268240

15

R-HEMBA1000046//Homo sapiens chromosome X map Xq28, complete sequence.//9.8e-56:401:82//U82696

R-HEMBA1000050//Human cosmid insert containing polymorphic marker DXS455.//0.0010:175:68//L31948

R-HEMBA1000076//Homo sapiens clone DJ1021I20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//4.9e-
 41:364:79//AC005520

R-HEMBA1000111//Homo sapiens Xp22 BAC GSHB-519E5 (Genome Systems Human BAC library) complete
 sequence.//4.7e-30:229:84//AC003684

20

R-HEMBA1000129//Homo sapiens chromosome 17, clone HCIT48C15, complete sequence.//2.4e-93:503:93//
 AC003104

R-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds.//6.5e-99:514:94//AB018340

R-HEMBA1000150//Homo sapiens clone RG086D03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.7e-
 37:289:83//AC005060

25

R-nnnnnnnnnnnnn//Homo sapiens scaffold attachment factor B (SAF-B) mRNA, partial cds.//3.1e-21:417:64//
 L43631

R-HEMBA1000158

R-nnnnnnnnnnnnn

R-HEMBA1000180//Plasmodium falciparum encoding Pfg27/25.//0.073:292:56//X84904

30

R-HEMBA1000185//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces.//
 5.3e-40:286:85//AC006146

R-HEMBA1000193

R-HEMBA1000201//Homo sapiens SNF5/INI1 gene, exon 9.//2.0e-24:137:99//Y17126

R-HEMBA1000213//Caenorhabditis elegans cosmid C44C8.//0.025:192:68//AF100655

35

R-HEMBA1000216//Human Chromosome 16 BAC clone CIT987SK-A-815A9, complete sequence.//2.5e-31:269:
 79//AF001548

R-nnnnnnnnnnnnn

R-HEMBA1000231//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1p35. Contains delta opiate
 receptor, CpG island, CA repeat.//4.3e-24:400:68//AL009181

40

R-HEMBA1000243//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence.//1.3e-19:
 319:69//AC004526

R-HEMBA1000244

R-HEMBA1000251//Meloidogyne hapla mitochondrial COII gene, 3' end of cds; transfer RNA-His gene; 16S ri-
 bosomal RNA gene; ND3 gene, complete cds; cytochrome b (cytb) gene, 5' end of cds.//0.16:338:60//L76262

45

R-HEMBA1000264//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 5/15,
 WORKING DRAFT SEQUENCE.//0.00093:300:66//AP000012

R-nnnnnnnnnnnnn//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete
 sequence.//3.5e-10:238:70//AC003037

R-HEMBA1000282//Arabidopsis thaliana BAC IG002P16.//0.71:344:60//AF007270

50

R-HEMBA1000288//Homo sapiens Xp22 PACs RPC11-263P4 and RPC11-164K3 complete sequence.//4.8e-33:
 267:82//AC003046

R-HEMBA1000290//Homo sapiens chromosome 17, clone HRPC837J1, complete sequence.//2.2e-15:249:69//
 AC004223

R-HEMBA1000302//CIT-HSP-2173N10.TF CIT-HSP Homo sapiens genomic clone 2173N10, genomic survey se-
 quence.//1.0:215:61//B95105

55

R-nnnnnnnnnnnnn

R-nnnnnnnnnnnnn//Mouse tumor cell dnaJ-like protein 1 mRNA, complete cds.//3.6e-60:504:78//L16953
 (in 40) L16953

R-HEMBA1000307//Mus musculus mRNA for CDV-1 protein//3.8e-36:315:68/Y10496
 R-nnnnnnnnnnn//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING
 DRAFT SEQUENCE, 8 unordered pieces//0.078:379:59//AC005505
 R-HEMBA1000338//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 620E11, WORKING
 5 DRAFT SEQUENCE//2.0e-33:399:72//AL031667
 R-HEMBA1000351//Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing
 Familial Mediterranean Fever gene disease//1.7e-39:272:87//AJ003147
 R-HEMBA1000355//Human primary Alu transcript//0.0045:67:85//U67829
 R-HEMBA1000357//Homo sapiens (subclone 9_h8 from PI H16) DNA sequence//8.7e-93:426:88//L42086
 10 R-HEMBA1000366//Homo sapiens PAC clone DJ0942116 from 7q11, complete sequence//1.7e-12:130:83//
 AC006012
 R-HEMBA1000369//Human DNA sequence from clone 1039K5 on chromosome 22q12.3-13.2 Contains gene sim-
 ilar to PICK1 perinuclear binding protein, gene similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS
 and a CpG island, complete sequence//1.9e-69:355:97//AL031587
 15 R-HEMBA1000376//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence//3.7e-
 66:410:89//AC006116
 R-HEMBA1000387//Homo sapiens chromosome 17, clone HCIT169H9, WORKING DRAFT SEQUENCE, 6 un-
 ordered pieces//2.0e-43:363:81//AC002993
 R-HEMBA1000390//Homo sapiens BAC clone RG041D11 from 7q21, complete sequence//4.6e-23:417:69//
 20 AC005053
 R-HEMBA1000392//Human Chromosome 11p14.3 PAC clone pDJ59m18, complete sequence//6.2e-05:174:68//
 AC004582
 R-HEMBA1000396//Homo sapiens DNA sequence from PAC 159A15 on chromosome Xp11.21-p11.23. Contains
 inter-alpha-trypsin inhibitor heavy chain H3 precursor-like protein//1.4e-62:564:77//AL022575
 25 R-HEMBA1000411
 R-HEMBA1000418//Liverwort Marchantia polymorpha chloroplast genome DNA//0.94:210:60//X04465
 R-HEMBA1000422//CIT-HSP-2382A6.TR CIT-HSP Homo sapiens genomic clone 2382A6, genomic survey se-
 quence//4.4e-12:98:92//AQ078233
 R-HEMBA1000428//Human DNA sequence from clone 393P23 on chromosome Xq21.1-21.33. Contains GSSs,
 30 complete sequence//2.0e-93 :526:90//Z95400
 R-HEMBA1000434//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE, 12 unordered pieces//
 2.7e-07:452:60//AC004826
 R-HEMBA1000442//E.caballus microsatellite DNA, clone HMB4//0.39:135:62//Y07733
 R-HEMBA1000456//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-52, com-
 35 plete sequence//2.6e-05:174:70//AL010226
 R-HEMBA1000459//Arabidopsis thaliana putative transmembrane protein G1p (AtG1), putative nuclear DNA-bind-
 ing protein G2p (AtG2), Em1 protein (ATEM1), putative chlorophyll synthetase (AtG4), putative transmembrane
 protein G5p (AtG5), putative acyl-coA dehydrogenase (AtG6), and calcium dependent protein kinase genes, com-
 plete cds; and unknown genes//0.013:212:63//AF049236
 40 R-HEMBA1000460//Homo sapiens PAC clone DJ0593H12 from 7p31, complete sequence//8.6e-114:556:98//
 AC004839
 R-HEMBA1000464//Caenorhabditis elegans cosmid C34B7, complete sequence//0.086:334:61//Z83220
 R-HEMBA1000469//Homo sapiens BAC clone RG442F18 from 2, complete sequence//1.8e-52:472:79//
 AC005104
 45 R-HEMBA1000488//, complete sequence//3.3e-68:200:99//AC005500
 R-HEMBA1000490//Caenorhabditis elegans cosmid Y53C12B, complete sequence//0.97:233:61//Z99278
 R-HEMBA1000491
 R-HEMBA1000504//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-64, com-
 plete sequence//1.7e-08:440:60//AL009014
 50 R-HEMBA1000505//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and
 non-small cell lung cancer, segment 1/11 //0.37:189:62//AB020858
 R-HEMBA1000508//Human DNA sequence from cosmid V210E9, between markers DXS366 and DXS87 on chro-
 mosome X//1.1e-25:248:80//Z70280
 R-HEMBA1000518//RPCI11-6022.TV RPCI-11 Homo sapiens genomic clone RPCI-11-6022, genomic survey se-
 55 quence//0.0035:293:61//B49544
 R-HEMBA1000521//Arabidopsis thaliana putative transmembrane protein G1p (AtG1), putative nuclear DNA-bind-
 ing protein G2p (AtG2), Em1 protein (ATEM1), putative chlorophyll synthetase (AtG4), putative transmembrane
 protein G5p (AtG5), putative acyl-coA dehydrogenase (AtG6), and calcium dependent protein kinase genes, com-
 plete cds; and unknown genes//0.013:212:63//AF049236

R-HEMBA1000523//Human cleavage stimulation factor 77kDa subunit mRNA, complete cds.//1.2e-53:203:92//U15782

R-HEMBA1000531//CIT-HSP-388J17.TR CIT-HSP Homo sapiens genomic clone 388J17, genomic survey sequence.//2.7e-24:137:99//B55638

5 R-HEMBA1000540//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 510D11, WORKING DRAFT SEQUENCE.//0.00014:329:60//Z98044

R-HEMBA1000545//Homo sapiens Xp22 BAC GS-619J3 (Genome Systems Human BAC library) complete sequence.//6.9e-87:552:87//AC004103

10 R-HEMBA1000557//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 134019, WORKING DRAFT SEQUENCE.//8.9e-121:584:98//AL034555

R-HEMBA1000557//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence.//5.7e-45:307:87//AC004381

R-HEMBA1000561//Mus musculus clone OST20235, genomic survey sequence.//1.3e-43:279:90//AF046762

15 R-HEMBA1000563//Plasmodium falciparum chromosome 2, section 5 of 73 of the complete sequence.//3.8e-05:506:56//AE001368

R-HEMBA1000568//RPCI11-49P8.TK.1 RPCI11 Homo sapiens genomic clone R-49P8, genomic survey sequence.//1.7e-101:498:97//AQ116293

R-HEMBA1000575//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 754E20, WORKING DRAFT SEQUENCE.//1.3e-47:458:75//AL022335

20 R-HEMBA1000588//Mus musculus FLI-LRR associated protein-1 mRNA, complete cds.//2.9e-62:447:81//AF045573

R-HEMBA1000591//Homo sapiens mRNA for E1B-55kDa-associated protein.//1.2e-111:9411:AJ007509

R-HEMBA1000592//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-10, complete sequence.//3.5e-09:421:60//AL010216

25 R-HEMBA1000594//Homo sapiens clone RG004N09, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.1e-15:421:66//AC005044

R-HEMBA1000604//HS_2220_A1_G10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2220 Col=19 Row=M, genomic survey sequence.//1.0e-51:306:92//AQ151991

30 R-HEMBA1000608

R-HEMBA1000622//H.sapiens CpG island DNA genomic Mse1 fragment, clone 155e4, reverse read cpg155e4.r1a.//4.5e-16:105:98//Z56962

R-HEMBA1000636//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 1/15, WORKING DRAFT SEQUENCE.//4.8e-62:421:86//AP000008

35 R-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds.//1.2e-97:443:97//AB014590

R-HEMBA1000655//Homo sapiens chromosome 19, cosmid R26349, complete sequence.//9.8e-61:311:90//AC005953

R-HEMBA1000657

R-HEMBA1000662

40 R-HEMBA1000673//Human DNA sequence from PAC 448E20 on chromosome Xq26.1 contains ESTs and STS.//1.0e-13:351:63//Z97196

R-HEMBA1000682//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.2e-50:298:79//AC005377

R-HEMBA1000686//HS_3018_B1_H10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=19 Row=P, genomic survey sequence.//0.00048:210:62//AQ093513

45 R-HEMBA1000702//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces.//9.7e-54:317:88//AC005000

R-HEMBA1000705//Glossonotus uhivittatus 12S mitochondrial ribosomal RNA, small subunit, mitochondrial gene, partial sequence.//0.080:138:65//U77850

50 R-HEMBA1000719//Rattus norvegicus mRNA for TESK1, complete cds.//0.96:291:58//D50864

R-HEMBA1000722

R-HEMBA1000726//Homo sapiens PAC clone DJ0701016 from 7q33-q36, complete sequence.//4.4e-26:284:77//AC005531

R-HEMBA1000727//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-89, complete sequence.//9.1e-05:351:60//AL010266

55 R-HEMBA1000731//Homo sapiens chromosome 19, cosmid R26349, complete sequence.//9.8e-61:311:90//AC005953

R-HEMBA1000749//Human Chromosome 16 BAC clone CIT987SK-327O24, complete sequence.//2.8e-32:298:79//AC003108

R-HEMBA1000752//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//2.8e-90:542:90//Z92545

5 R-HEMBA1000769//Homo sapiens P1 clone GSP13996 from 5q12, complete sequence.//2.7e-36:405:75//AC005031

R-HEMBA1000773//HS_3050_A2_B08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3050 Col=16 Row=C, genomic survey sequence.//0.00053:268:60//AQ105619

10 R-HEMBA1000774//Homo sapiens PAC clone DJ0630C24 from 7q31-q32, complete sequence.//4.7e-46:338:85//AC004690

R-HEMBA1000791//***ALU WARNING: Human Alu-Sc subfamily consensus sequence.//5.3e-47:279:91//U14571

R-HEMBA10008177//Sequence 1 from Patent WO 8904839.//0.86:148:67//I09339

R-HEMBA1000822//T.brucei kinetoplast maxicircle variable region DNA.//0.00061:246:61//Z15118

15 R-HEMBA1000827//Homo sapiens Ser/Arg-related nuclear matrix protein (SRM160) mRNA, complete cds.//6.9e-43:228:98//AF048977

R-HEMBA1000843//Homo sapiens DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 PLC-II, PLC-148), the KIAA0395 gene for a probable Zinc Finger Homeobox protein and a 60S Ribosomal Protein L23 LIKE pseudogene. Contains a predicted CpG island, ESTs, STSs and GSSs, complete sequence.//1.7e-41:319:84//AL022394

20 R-HEMBA1000851//Arabidopsis thaliana chromosome I BAC T14N5 genomic sequence, complete sequence.//0.40:168:67//AC004260

R-HEMBA1000852//Homo sapiens Xp22 bins 3-5 PAC RPCI4-617A9 (Roswell Park Cancer Institute Human PAC Library) containing Arylsulfatase D and E genes, complete sequence.//1.5e-112:572:96//AC005295

25 R-HEMBA1000867//Homo sapiens clone DJ0971C03, WORKING DRAFT SEQUENCE, 18 unordered pieces.//0.11:121:71//AC004938

R-HEMBA1000869//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-A-180G2, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.2e-22:186:76//AC002042

30 R-HEMBA1000870//Human BAC clone GS542D18 from 7q31-q32, complete sequence.//0.0060:283:63//AC002528

R-HEMBA1000872//Rattus norvegicus polymorphic satellite repetitive elements.//3.8e-05:269:61//M98801

R-HEMBA1000876//Homo sapiens chromosome 12p13.3 clone RPCI1-96H9, WORKING DRAFT SEQUENCE, 66 unordered pieces.//6.5e-38:327:77//AC006057

35 R-HEMBA1000908//CIT-HSP-237314.TR CIT-HSP Homo sapiens genomic clone 237314, genomic survey sequence.//5.0e-34:221:90//AQ108658

R-HEMBA1000910//T.pigmentosa UM1060 macronuclear rDNA telomeric region 3' term.//0.19:280:61//X04205

R-HEMBA1000918//RPCI11-68E14.TK RPCI11 Homo sapiens genomic clone R-68E14, genomic survey sequence.//1.3e-32:172:100//AQ267293

40 R-HEMBA1000919

R-HEMBA1000934//Homo sapiens DNA sequence from PAC 874C20 on chromosome 6p22.1-22.3. Contains a Zinc Finger Protein ZFP47 LIKE gene, a Zinc Finger Protein pseudogene and a Zinc Finger Protein SRE-ZBP pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.6e-18:284:71//AL021997

R-HEMBA1000942//Homo sapiens clone RG350L10, WORKING DRAFT SEQUENCE, 15 unordered pieces.//1.4e-17:217:76//AC005098

45 R-HEMBA1000943//Homo sapiens chromosome 17, clone hRPK.640_I_15, complete sequence.//9.0e-113:586:95//AC005324

R-HEMBA1000946//T5N8TFB TAMU Arabidopsis thaliana genomic clone T5N8, genomic survey sequence.//0.030:369:59//B26224

50 R-HEMBA1000960//Homo sapiens clone RG339C12, WORKING DRAFT SEQUENCE, 10 unordered pieces.//2.5e-52:494:77//AC005096

R-HEMBA1000968//Homo sapiens P1 clone 797a11 containing MHC class II DQ-beta (HLA-DQB) and MHC class II DC-alpha (HLA-DCA) genes, complete cds.//3.5e-77:568:83//U92032

R-HEMBA1000971//RPCI11-54D1.TJ RPCI11 Homo sapiens genomic clone R-54D1, genomic survey sequence.//2.3e-27:153:98//AQ081552

55 R-HEMBA1000972//Homo sapiens clone DJ0630C24 from 7q31-q32, complete sequence.//4.7e-46:338:85//AC004690

R-HEMBA1000973//Homo sapiens clone DJ0630C24 from 7q31-q32, complete sequence.//4.7e-46:338:85//AC004690

R-HEMBA1000975//Human DNA sequence from clone 105D16 on chromosome Xp11.3-11.4 Contains pseudogene similar to laminin-binding protein, CA repeat, STS, complete sequence.//8.0e-22:352:68//AL031311

R-HEMBA1000985//Homo sapiens PAC clone DJ0797C05 from 7q31, complete sequence.//8.5e-05:306:63//AC004888

5 R-HEMBA1000986//Homo sapiens clone RG031N19, WORKING DRAFT SEQUENCE, 1 unordered pieces.//5.7e-37:296:83//AC005632

R-HEMBA1000991//RPCI11-22017.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-22017, genomic survey sequence.//6.5e-44:162:90//AQ008952

R-HEMBA1001007

10 R-HEMBA1001008//Homo sapiens chromosome 16, P1 clone 79-2A (LANL), complete sequence.//0.082:313:60//AC005365

R-HEMBA1001009//O.sativa osr40g2 gene.//0.99:203:62//Y08987

R-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds.//1.0e-113:587:95//AB007937

15 R-HEMBA1001019//Bos taurus cyclin-dependent kinase 1 (cdk1/cdc2) mRNA, complete cds.//7.4e-24:215:82//L26547

R-HEMBA1001020//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 732E4, WORKING DRAFT SEQUENCE.//2.8e-18:449:64//AL008722

R-HEMBA1001022

20 R-HEMBA1001024//Homo sapiens BAC clone 393I22 from 8q21, complete sequence.//6.6e-48:536:74//AF070717

R-HEMBA1001026//T33H14TF TAMU Arabidopsis thaliana genomic clone T33H14, genomic survey sequence.//0.013:180:66//B97363

R-nnnnnnnnnnnn//Caenorhabditis elegans cosmid R10H10, complete sequence.//1.2e-25:438:65//Z70686

25 R-HEMBA1001051//Homo sapiens 12q24.1 PAC RPCI3-521E19 (Roswell Park Cancer Institute Human PAC library) complete sequence.//7.3e-38:188:89//AC004217

R-HEMBA1001052//Rabbit alpha-1-globin gene to theta-1-globin pseudogene region.//2.4e-24:279:74//X04751

R-HEMBA1001060//HS_2056_B1_C01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2056 Col=1 Row=F, genomic survey sequence.//4.1e-14:137:83//AQ245004

R-HEMBA1001071//M.musculus COL3A1 gene for collagen alpha-1.//6.9e-38:513:70//X52046

30 R-HEMBA1001077//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 150C2, WORKING DRAFT SEQUENCE.//1.9e-22:507:61//AL022318

R-HEMBA1001080

R-HEMBA1001085//Human Chromosome 15q26.1 PAC clone pDJ290i21 containing fur, fes, and alpha mannosidase IIx genes, WORKING DRAFT SEQUENCE, 9 unordered pieces.//2.2e-43:317:83//AC004586

35 R-HEMBA1001088//Caenorhabditis elegans cosmid C18H7.//0.46:301:60//AF067607

R-HEMBA1001094//Homo sapiens clone RG491N20, complete sequence.//5.3e-98:501:96//AC005105

R-HEMBA1001099

R-HEMBA1001109//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 118J21, WORKING DRAFT SEQUENCE.//3.1e-39:335:80//AL033527

40 R-HEMBA1001121//Human cosmid LL12NC01-132B11A, ETV6 gene, intron 2.//9.8e-11:122:81//U81833

R-HEMBA1001122//Plasmodium falciparum MAL3P6, complete sequence.//0.0024:284:63//Z98551

R-HEMBA1001123//Human NFE genomic fragment.//3.6e-26:318:72//M98511

R-HEMBA1001133

R-HEMBA1001137//Homo sapiens full-length insert cDNA clone ZD29F04.//4.2e-88:426:98//AF086241

45 R-HEMBA1001140//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//4.0e-41:304:84//AC005077

R-HEMBA1001172//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 54B20, WORKING DRAFT SEQUENCE.//3.7e-36:261:85//Z98304

50 R-HEMBA1001174//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//1.0:219:58//AE001398

R-HEMBA1001197

R-HEMBA1001208//HS_2233_A1_G10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2233 Col=19 Row=M, genomic survey sequence.//0.083:174:68//AQ170789

55 R-HEMBA1001226//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.1e-59:553:75//AC005377

R-HEMBA1001235//RPCI11-11555.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-11555, genomic survey sequence.//1.0e-113:587:95//AB007937

R-HEMBA1001236//RPCI11-11555.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-11555, genomic survey sequence.//1.0e-113:587:95//AB007937

R-HEMBA1001237//Caenorhabditis elegans cosmid C18H7.//0.46:301:60//AF067607

R-HEMBA1001446//HS_3207_A1_A08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3207 Col=15 Row=A, genomic survey sequence.//8.9e-06:119:73//AQ175385

R-HEMBA1001450//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//0.0043:266:63//AC005065

5 R-HEMBA1001454//Homo sapiens PAC clone DJ0673011 from 7q31, complete sequence.//7.1e-25:210:82//AC004855

R-HEMBA1001455//Homo sapiens chromosome 17, clone hRPK.640_I_15, complete sequence.//2.7e-08:316:62//AC005324

10 R-HEMBA1001463//Homo sapiens chromosome 17, clone hRPK.1064_E_11, complete sequence.//0.57:219:60//AC005208

R-HEMBA1001476//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12 unordered pieces.//9.3e-50:252:80//AC004840

R-HEMBA1001478

R-HEMBA1001497

15 R-HEMBA1001510//Human HLA class III region containing cAMP response element binding protein-related protein (CREB-RP) and tenascin X (tenascin-X) genes, complete cds, complete sequence.//3.5e-41:282:86//U89337

R-HEMBA1001515//Human DNA sequence from PAC 238J17 on chromosome 6q22. Contains EST and STS.//1.9e-79:529:86//Z98753

20 R-HEMBA1001517//Homo sapiens BAC clone RG459N13 from 7p15, complete sequence.//4.3e-18:335:71//AC004549

R-HEMBA1001522

R-HEMBA1001526//Human DNA sequence from cosmid 444G9 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contains ESTs and CpG islands, //5.6e-08:265:67//Z98258

R-HEMBA1001533//Human DNA sequence from PAC 179M20 on chromosome 20q12-13.1. Contains adenosine deaminase (ADA), placental protein Diff33, CA repeat, ESTs, STS.//7.8e-16:235:72//Z97053

25 R-HEMBA1001557

R-HEMBA1001566//Human Chromosome X clone bWXD187, complete sequence.//2.2e-44:416:78//AC004383

R-HEMBA1001569//Sequence 15 from patent US 5693476.//1.8e-59:389:88//I77040

R-HEMBA1001570//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence.//1.1e-44:316:87//AC004453

30 R-HEMBA1001579//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.0047:437:60//AC005506

R-HEMBA1001581//P.falciparum complete gene map of plastid-like DNA (IR-B) //2.3e-07:491:58//X95276

R-HEMBA1001585//Caenorhabditis elegans cosmid C06A6 //0.68:224:62//U41012

35 R-HEMBA1001589

R-HEMBA1001595//CIT-HSP-2349G19. TF CIT-HSP Homo sapiens genomic clone 2349G19, genomic survey sequence.//8.0e-69:337:99//AQ060483

R-HEMBA1001608//Homo sapiens chromosome 17, clone HCIT462L7, complete sequence.//9.5e-59:514:78//AC005177

40 R-HEMBA1001620//S.polyrrhiza mRNA for D-myo-inositol-3-phosphate synthase.//4.5e-12:289:65//Z11693

R-nnnnnnnnnnnn//HS_2195_A1_E09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2195 Col=17 Row=I, genomic survey sequence.//5.8e-09:358:58//AQ292688

R-HEMBA1001636//Human putative potassium channel subunit (h-erg) mRNA, complete cds.//0.77:225:59//U04270

45 R-HEMBA1001640//Human DNA sequence from PAC 50J22 on chromosome 6p21. Contains ETS related protein TEL like and GS2 like genes, ESTs and an STS //6.0e-49:404:79//Z84484

R-nnnnnnnnnnnn

R-HEMBA1001655//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.//1.1e-103:532:95//AC005368

50 R-HEMBA1001658//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING DRAFT SEQUENCE.//1.0:197:64//AL023808

R-HEMBA1001661//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//1.5e-100:457:93//AC005740

R-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds.//1.2e-90:496:91//AF072247

55 R-HEMBA1001675

R-HEMBA1001681//CIT-HSP-2345M7.TF CIT-HSP Homo sapiens genomic clone 2345M7, genomic survey sequence.//0.21:124:68//AQ056593

R-HEMBA1001702//Homo sapiens 12q13.1 PAC RPC11-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//8.3e-06:279:63//AC004801

5 R-HEMBA1001709//Homo sapiens mRNA for KIAA0698 protein, complete cds.//1.9e-96:483:96//AB014598

R-HEMBA1001711//Human HepG2 3' region cDNA, clone hmd2b02.//2.3e-31:169:100//D16886

R-HEMBA1001712//HS-1015-B1-E01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 790 Col=1 Row=J, genomic survey sequence.//0.0025:200:65/B32577

10 R-HEMBA1001714//Rattus norvegicus mitochondrial ATPase inhibitor gene, complete cds.//6.6e-27:316:75//U12250

R-HEMBA1001718//CIT-HSP-2171J2.TR CIT-HSP Homo sapiens genomic clone 2171J2, genomic survey sequence.//3.1e-41:167:87//B89781

R-HEMBA1001723//Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds.//0.53:275:61//AF018261

15 R-HEMBA1001731//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 322P7, WORKING DRAFT SEQUENCE.//2.9e-48:292:84//AL023799

R-HEMBA1001734//Homo sapiens Chromosome 15q22.3-23 PAC 88m3, WORKING DRAFT SEQUENCE, 2 ordered pieces.//3.2e-33:290:81//AC005959

R-HEMBA1001744//Human DNA sequence from clone 134E15 on chromosome 6q21 Contains Blimp-1, apoptosis specific protein similar to yeast APG5 ESTs, GSSs and retroviral sequence, complete sequence.//0.98:203:62//AL022067

20 R-HEMBA1001745//Homo sapiens BAC clone RG298G08 from 7p15-p21, complete sequence.//0.00019:312:59//AC005084

R-HEMBA1001746//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.045:457:61//AC004153

25 R-HEMBA1001761//Homo sapiens chromosome X, clone hCIT.200_L_4, complete sequence.//3.8e-39:331:80//AC006121

R-HEMBA1001781//Homo sapiens Xp22 BAC GSHB-590J6 (Genome Systems Human BAC library) complete sequence.//0.0062:245:60//AC004554

30 R-HEMBA1001784//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//2.1e-22:370:63//AC005740

R-HEMBA1001791//Human DNA sequence from clone 931E15 on chromosome Xq25. Contains STSs, GSSs and genomic marker DXS8098, complete sequence.//3.0e-50:408:80//AL023575

R-HEMBA1001800//CIT-HFP-2049N5.TF CIT-HSP Homo sapiens genomic clone 2049N5, genomic survey sequence.//9.0e-37:335:77//AQ009222

35 R-HEMBA1001803//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.86:536:56//AC005506

R-nnnnnnnnnnnn//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//2.9e-93:553:89//M21977

R-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500.//2.8e-112:548:98//AB007969

40 R-HEMBA1001809

R-HEMBA1001815//Homo sapiens Xp22 BAC GS-321G17 (Genome Systems Human BAC library) complete sequence.//2.6e-48:363:84//AC004025

R-HEMBA1001819//Homo sapiens *** SEQUENCING IN PROGRESS *** from PAC 1577, WORKING DRAFT SEQUENCE.//1.1e-15:275:68//AJ009612

45 R-HEMBA1001820//HS_3022_B1_A09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3022 Col=17 Row=B, genomic survey sequence.//0.00054:335:59//AQ165107

R-nnnnnnnnnnnn//Xenopus laevis intersectin mRNA, complete cds.//1.4e-19:533:63//AF032118

R-HEMBA1001824//S.clavuligerus linear plasmid pSCL (complete sequence).//0.62:189:65//X54107

50 R-HEMBA1001835//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 191J18, WORKING DRAFT SEQUENCE.//1.0:450:60//AL024507

R-HEMBA1001844//Human familial Alzheimer's disease (STM2) gene, complete cds.//1.6e-07:170:68//U50871

R-HEMBA1001847

R-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds.//3.3e-108:553:96//AB014517

55 R-HEMBA1001864//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463

R-HEMBA1001865//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463

R-HEMBA1001866//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463

R-HEMBA1001867//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463

R-HEMBA1001868//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463

R-HEMBA1001869//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463

R-HEMBA1001870//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463

R-HEMBA1001871//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463

R-HEMBA1001872//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463

R-HEMBA1001873//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463

R-HEMBA1001874//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463

R-HEMBA1001875//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463

R-HEMBA1001876//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463

R-HEMBA1001877//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463

R-HEMBA1001878//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463

R-HEMBA1001879//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463

R-HEMBA1001880//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463

R-HEMBA1001881//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463

R-HEMBA1001882//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463

R-HEMBA1001883//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463

R-HEMBA1001884//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463

R-HEMBA1001885//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463

R-HEMBA1001886//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463

R-HEMBA1001887//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463

R-HEMBA1001888//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463

R-HEMBA1001889//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463

R-HEMBA1001890//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463

R-HEMBA1001891//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463

R-HEMBA1001892//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463

R-HEMBA1001893//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463

R-HEMBA1001894//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463

R-HEMBA1001895//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463

R-HEMBA1001896//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463

R-HEMBA1001897//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463

R-HEMBA1001898//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463

R-HEMBA1001899//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463

R-HEMBA1001900//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence.//1.7e-14:245:67//AG002463

R-HEMBA1002113//Human chromosome 12p13 sequence, complete sequence//1.6e-64:550:80//U47924
 R-HEMBA1002119//Human Chromosome 11 pac pDJ1173a5, complete sequence//1.2e-92:435:92//AC000378
 R-HEMBA1002125
 R-HEMBA1002139//Human nebulin mRNA, partial cds//0.056:68:88//U35637
 5 R-HEMBA1002144//Homo sapiens Chromosome 11p14.3 PAC clone 6-130a9 containing tryptophan hydroxylase gene, complete sequence//2.0e-26:323:70//AC005728
 R-HEMBA1002150//Human DNA sequence from clone 742C19 on chromosome 22q12.3-13.1. Contains a pseudogene similar to Cytochrome C Oxidase Polypeptide VB and (parts of) up to four novel genes, two with homology to Phorbolins and one a novel Chromobox protein gene. Contains ESTs, an STS, GSSs and putative CpG islands, complete sequence//1.0:371:61//AL031846
 10 R-HEMBA1002151
 R-HEMBA1002153//Human BAC 367D17 from chromosome 18, complete sequence//2.4e-21:322:70//AC003971
 R-HEMBA1002160//Human DNA sequence from PAC 339A18 on chromosome Xp11.2. Contains KIAA0178 gene, similar to mitosis-specific chromosome segregation protein SMC1 of *S.cerevisiae*, DNA binding protein similar to URE-B1, ESTs and STS//2.5e-38:216:84//Z97054
 15 R-HEMBA1002161//CIT-HSP-2163F10.TF CIT-HSP Homo sapiens genomic clone 2163F10, genomic survey sequence//3.1e-58:284:80//B89969
 R-HEMBA1002162//Caenorhabditis elegans cosmid F48C11, complete sequence//0.0079:286:57//Z80789
 R-HEMBA1002166//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library) complete sequence//5.9e-53:326:80//AC002980
 20 R-HEMBA1002177
 R-HEMBA1002185//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 745I14, WORKING DRAFT SEQUENCE//9.5e-37:356:76//AL033532
 R-HEMBA1002189//Homo sapiens Xp22 BAC GSHB-519E5 (Genome Systems Human BAC library) complete sequence//3.4e-43:244:77//AC003684
 25 R-HEMBA1002191//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces//4.3e-37:323:78//AC005077
 R-HEMBA1002199//Human Cosmid g5129g124 from 7q31.3, complete sequence//1.4e-89:564:87//AC002498
 R-HEMBA1002204//Homo sapiens Chromosome 22q11.2 Cosmid Clone 817g In IGLC Region, complete sequence//1.5e-31:313:71//AC000053
 30 R-HEMBA1002212//K.lactis mitochondrial COX1 and A8 genes for cytochrome oxidase subunit I and ATPase subunit 8//0.0023:346:60//X57546
 R-HEMBA1002215//M.musculus mRNA for testin//4.7e-61:414:84//X78989
 R-HEMBA1002226//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 2705, WORKING DRAFT SEQUENCE//4.6e-46:375:77//AL033529
 35 R-HEMBA1002229//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds//4.6e-46:238:98//AF089814
 R-HEMBA1002237//Homo sapiens 12q13 PAC RPC1-316M24 (Roswell Park Cancer Institute Human PAC library) complete sequence//4.3e-26:469:67//AC004242
 40 R-HEMBA1002253//Homo sapiens BAC clone GS180J15 from 7q31, complete sequence//5.1e-23:162:82//AC005016
 R-HEMBA1002257
 R-HEMBA1002267//Equus caballus dermatan sulfate proteoglycan II mRNA, complete cds//4.6e-44:300:88//AF03 8127
 45 R-HEMBA1002270//Human BAC clone RG067M09 from 7q21-7q22, complete sequence//1.9e-19:176:85//AC000057
 R-HEMBA1002321
 R-HEMBA1002328//HS_3061_A1_D06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3061 Col=11 Row=G, genomic survey sequence//1.0:151:65//AQ127617
 50 R-HEMBA1002337//Saccharomyces cerevisiae RNA polymerase II holoenzyme component (SRB7) gene, complete cds//3.7e-07:328:63//U23811
 R-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds//2.4e-128:642:96//AB018314
 R-HEMBA1002348//Human DNA sequence from clone 409O10 on chromosome 20q12 Contains CA repeat, GSS, STS, complete sequence//3.7e-07:587:58//AL031256
 55 R-HEMBA1002349//Leishmania tarentolae maxicircle DNA fragment//0.018:341:58//X02438
 R-HEMBA1002350//Homo sapiens chromosome associated factor 1 (CAF-1) mRNA, complete cds//1.0:151:65//AF03 8127

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R-HEMBA1002351//Homo sapiens chromosome associated factor 1 (CAF-1) mRNA, complete cds//1.0:151:65//AF03 8127

non-small cell lung cancer , segment 11/11//1.1e-70:559:79//AB020868
 R-HEMBA1002389//HS_3218_B2_E08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3218 Col=16 Row=J, genomic survey sequence//0.0011:122:72//AQ213602
 R-HEMBA1002417//Homo sapiens chromosome 19, cosmid R28784, complete sequence//4.2e-81:232:97//
 5 AC005954
 R-HEMBA1002419//Homo sapiens PAC clone DJ0649P17 from 7q11.23-q21, complete sequence//0.50:231:64//
 AC004848
 R-HEMBA1002430//P.falciparum complete gene map of plastid-like DNA (IR-B)//0.0023:604:56//X95276
 R-HEMBA1002439//Homo sapiens clone GS096J14, WORKING DRAFT SEQUENCE, 3 unordered pieces//3.4e-
 10 23:183:80//AC006026
 R-HEMBA1002458//Human DNA sequence from clone 146H21 on chromosome Xq22 Contains cleavage stimu-
 lation factor, 64 KD subunit, gene similar to CYTOCHROME B-245 HEAVY CHAIN. pseudogene similar to hnRNP
 A1 protein and ESTs, complete sequence//7.7e-32:161:83//Z83819
 R-HEMBA1002460//Homo sapiens clone DJ1137M13, complete sequence//2.6e-100:305:100//AC005378
 15 R-HEMBA1002462//Sequence 43 from patent US 5708157//2.0e-10:131:77//I80068
 R-nnnnnnnnnnnnn
 R-HEMBA1002477//Homo sapiens PAC clone DJ0607J23 from 7q21.2-q31.1, complete sequence//6.6e-33:279:
 80//AC004841
 R-HEMBA1002486//***ALU WARNING: Human Alu-Sq subfamily consensus sequence//2.1e-50:290:92//U14573
 20 R-HEMBA1002495//CITBI-E1-2515J10.TR CITBI-E1 Homo sapiens genomic clone 2515J10, genomic survey se-
 quence//1.0:122:68//AQ261762
 R-HEMBA1002498//Homo sapiens clone DJ1102A12, WORKING DRAFT SEQUENCE, 15 unordered pieces//
 2.8e-22:210:78//AC004963
 R-HEMBA1002503//Homo sapiens chromosome 17, clone HRPC1067M6, complete sequence//2.7e-17:435:58//
 25 AC003043
 R-HEMBA1002508//Homo sapiens, clone hRPK.15_A_1, complete sequence//3.7e-09:408:61//AC006213
 R-nnnnnnnnnnnnn/Homo sapiens mRNA for histone deacetylase-like protein (JM21)//7.1e-112:456:92//AJ011972
 R-HEMBA1002515
 R-HEMBA1002538//Homo sapiens mRNA for KIAA0454 protein, partial cds//1.6e-104:564:93//AB007923
 30 R-HEMBA1002542//HS_3197_B2_B10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3197 Col=20 Row=D, genomic survey sequence//2.8e-25:186:86//AQ188792
 R-HEMBA1002547//Mus musculus agrin gene, exon 36//0.0095:93:75//M92658
 R-HEMBA1002552//Homo sapiens clone DJ1137M13, complete sequence//4.0e-49:308:90//AC005378
 R-HEMBA1002555//Homo sapiens full-length insert cDNA clone YR87G10//8.3e-65:318:99//AF085957
 35 R-HEMBA1002558//, complete sequence//2.3e-38:264:89//AC005409
 R-HEMBA1002561//Human DNA sequence from clone 396D17 on chromosome 1p33-35.3 Contains EST, STS,
 GSS, complete sequence//7.1e-44:192:80//AL008634
 R-nnnnnnnnnnnnn/Homo sapiens protein associated with Myc mRNA, complete cds//4.5e-119:587:97//AF075587
 R-HEMBA1002583
 40 R-HEMBA1002590//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains
 the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein
 CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete se-
 quence//9.4e-42:248:88//Z95152
 R-HEMBA1002592//Homo sapiens chromosome 19, cosmid R30385, complete sequence//2.6e-56:302:84//
 45 AC004510
 R-HEMBA1002621
 R-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds//6.7e-76:380:97//AB018351
 R-HEMBA1002628//P.falciparum complete gene map of plastid-like DNA (IR-A)//8.8e-05:327:60//X95275
 R-HEMBA1002629//Mus musculus clone OST16705, genomic survey sequence//4.3e-06:205:66//AF046247
 50 R-HEMBA1002645//***ALU WARNING: Human Alu-J subfamily consensus sequence//7.1e-39:281:84//U14567
 R-HEMBA1002651//Homo sapiens PAC clone DJ0593H12 from 7p31, complete sequence//1.1e-104:500:95//
 AC004839
 R-HEMBA1002659//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs
 and GSSs, complete sequence//1.2e-61:280:92//AL022323
 55 R-HEMBA1002661//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 225E12. WORKING
 DRAFT SEQUENCE//2.2e-41:325:81//AL005174
 R-HEMBA1002666//Homo sapiens full-length insert cDNA clone YR87G10//8.3e-65:318:99//AF085957
 R-HEMBA1002678//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1137F22. WORK

ING DRAFT SEQUENCE //2.3e-107:561:94//AL034421

R-nnnnnnnnnnnnn/CIT-HSP-2287E8.TF CIT-HSP Homo sapiens genomic clone 2287E8, genomic survey sequence //5.4e-17:137:88//B99281

R-HEMBA1002688//Homo sapiens chromosome 5, P1 clone 1354A7 (LBNL H47), complete sequence //0.033:146:70//AC004503

R-HEMBA1002696

R-HEMBA1002712//Homo sapiens PAC clone 166H1 from 12q, complete sequence //6.2e-44:302:87//AC003982

R-HEMBA1002716//Mus musculus mRNA for ELM1, complete cds //1.1e-31:332:76//AB004873

R-HEMBA1002728//Homo sapiens mRNA for KIAA0621 protein, partial cds //1.2e-35:287:81//AB014521

R-HEMBA1002730//D.discoideum actin M6 gene, 5' flank //0.018:233:66//M29109

R-HEMBA1002742//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1108H3, WORKING DRAFT SEQUENCE //2.6e-13:419:62//AL033525

R-HEMBA1002746//Mus musculus chromosome 19, clone CIT282B21, complete sequence //0.019:202:65//AC003694

R-HEMBA1002748//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 404K8, WORKING DRAFT SEQUENCE //0.046:263:60//AL023883

R-HEMBA1002750//Human DNA sequence from PAC 452H17 on chromosome X contains sodium-and chloride-dependent glycine transporter 1 (GLYT-1) like, ESTs //0.052:421:58//Z96810

R-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds //1.2e-104:545:95//AB011126

R-HEMBA1002770//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces //3.0e-07:523:59//AC005140

R-HEMBA1002777

R-HEMBA1002779//Human HepG2 3' region Mbol cDNA, clone hmd1e03m3 //9.4e-25:158:93//D17139

R-HEMBA1002780//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y214H10, WORKING DRAFT SEQUENCE //1.6e-42:463:75//AL022344

R-HEMBA1002794//Plasmodium falciparum MAL3P8, complete sequence //2.2e-05:417:59//AL034560

R-HEMBA1002801//Meloidogyne javanica mitochondrial transfer RNA His, 16S ribosomal RNA (16S rRNA) genes, ND3 gene, complete cds, and cytochrome b gene, 5' end of CDS //0.00055:444:59//L76261

R-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds //4.4e-115:559:97//AF071185

R-HEMBA1002816//Homo sapiens clone NH0576N21, WORKING DRAFT SEQUENCE, 5 unordered pieces //4.3e-88:329:94//AC005043

R-HEMBA1002826//Homo sapiens genomic DNA, chromosome 21q11.1, segment 12/28, WORKING DRAFT SEQUENCE //1.9e-22:262:67//AP000041

R-HEMBA1002833//Homo sapiens chromosome 17, clone hRPC.117_B_12, complete sequence //1.3e-79:396:97//AC004707

R-HEMBA1002850//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces //0.013:393:61//AC005506

R-HEMBA1002863//Homo sapiens chromosome 17, clone hRPK.271_K_11, complete sequence //4.1e-73:489:85//AC005562

R-HEMBA1002876//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE //0.21:549:55//AL034557

R-HEMBA1002886//CIT-HSP-2013C4.TR CIT-HSP Homo sapiens genomic clone 2013C4, genomic survey sequence //0.30:431:56//B53836

R-HEMBA1002896//Homo sapiens SH3-containing adaptor molecule-1 mRNA, complete cds //3.9e-106:541:95//AF037261

R-HEMBA1002921

R-HEMBA1002924//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 7/10 //4.6e-19:139:78//AB020875

R-HEMBA1002934//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 862K6, WORKING DRAFT SEQUENCE //7.5e-45:282:89//AL031681

R-HEMBA1002935//CIT-HSP-2282P14.TFB CIT-HSP Homo sapiens genomic clone 2282P14, genomic survey sequence //1.5e-102:514:97//AQ008584

R-HEMBA1002937//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 745114, WORKING DRAFT SEQUENCE //3.3e-87:444:97//AL033532

R-HEMBA1002939

R-HEMBA1002944//HS-2107-A1-C05-11 CIT-Ap1 genomic clone 2107-A1-C05-11

R-HEMBA1002945//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 7/10 //4.6e-19:139:78//AB020875

R-HEMBA1002946//Xenopus laevis mitochondrial transfer RNA gene, 16S rRNA gene //0.228:63//AC008021

R-HEMBA1002954//HS_3246_A2_G09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3246 Col=18 Row=M, genomic survey sequence.//5.8e-42:258:91//AQ218005

R-HEMBA1002968//Homo sapiens chromosome 17, clone hRPK.112_J_9, complete sequence.//4.2e-38:300:83//AC005553

5 R-HEMBA1002970//Slime mold (D.discoideum) prestalk D11 gene, complete cds.//5.0e-05:541:57//M11012

R-HEMBA1002971//Homo sapiens mRNA for KIAA0679 protein, partial cds.//7.2e-29:162:99//AB014579

R-HEMBA1002973//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//9.1e-36:520:69//AC006128

10 R-nnnnnnnnnnnn//Homo Sapiens Chromosome X clone bWXD691, complete sequence.//0.00040:504:59//AC004386

R-HEMBA1002999//Rattus norvegicus lamina-associated polypeptide 1C (LAP1C) mRNA, complete cds.//3.7e-66:556:79//U19614

R-HEMBA1003021//Human Chromosome 11 overlapping pacs pDJ235k10 and pDJ239b22, WORKING DRAFT SEQUENCE, 17 unordered pieces.//1.6e-44:530:70//AC000406

15 R-HEMBA1003033//Homo sapiens full-length insert cDNA clone ZC34B10.//4.6e-78:414:94//AF086194

R-HEMBA1003034//Homo sapiens chromosome 19, cosmid R29351, complete sequence.//9.0e-52:322:75//AC004026

R-HEMBA1003035//HS_2008_A2_G08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2008 Col=16 Row=M, genomic survey sequence.//4.0e-68:343:97//AQ269839

20 R-HEMBA1003037//347G15.TVB CIT978SKA1 Homo sapiens genomic clone A-347G15, genomic survey sequence.//0.57:188:58//B17694

R-HEMBA1003041//Homo sapiens PAC clone DJ1163J12 from 7q21.2-q31.1, complete sequence.//6.3e-30:350:72//AC004983

25 R-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, complete cds.//4.1e-118:578:97//AF054182

R-HEMBA1003064//Human cosmid LL12NC01-N-136B11, located centromeric to the ETV6 gene, chromosome 12p12-13.//0.0018:271:60//U59962

R-HEMBA1003067//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 633019, WORKING DRAFT SEQUENCE.//5.3e-48:464:76//AL022302

30 R-HEMBA1003071//CIT-HSP-2370D6.TR CIT-HSP Homo sapiens genomic clone 2370D6, genomic survey sequence.//0.19:48:87//AQ110136

R-HEMBA1003077//Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds.//4.9e-69:494:84//U42975

35 R-HEMBA1003078//Human DNA sequence from PAC 339A18 on chromosome Xp11.2. Contains KIAA0178 gene, similar to mitosis-specific chromosome segregation protein SMC1 of S.cerevisiae, DNA binding protein similar to URE-B1, ESTs and STS.//1.1e-11:331:64//Z97054

R-HEMBA1003079//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//4.6e-116:576:98//AC004673

40 R-HEMBA1003083//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0442P12; HTGS phase 1, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.1e-43:280:83//AC005798

R-HEMBA1003086//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3-unordered pieces.//1.2e-43:281:88//AC006039

R-HEMBA1003096//Human DNA sequence from clone J506G21, WORKING DRAFT SEQUENCE.//0.00037:421:59//Z82213

45 R-HEMBA1003098//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0024K08; HTGS phase 1, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.4e-30:303:78//AC005598

R-HEMBA1003117

R-HEMBA1003129//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 407F11, WORKING DRAFT SEQUENCE.//7.9e-11:109:85//AL022329

50 R-HEMBA1003133//Homo sapiens chromosome 9, P1 clone 11659, complete sequence.//3.9e-99:484:98//AC004472

R-HEMBA1003136//CIT-HSP-2281L22.TF CIT-HSP Homo sapiens genomic clone 2281L22, genomic survey sequence.//2.0e-10:93:92//B99861

R-HEMBA1003142//Homo sapiens 12q24.2 PAC RPCI1-128M12 (Roswell Park Cancer Institute Human PAC library) complete sequence.//9.8e-40:270:87//AC004024

55 R-HEMBA1003148//Homo sapiens mRNA for Cerebral Glycine Decarboxylase, partial cds.//1.1e-37:100:100//U19614

R-HEMBA1003149//Human DNA sequence from PAC 339A18 on chromosome Xp11.2. Contains ESTs and STS.//1.1e-11:331:64//Z97054

R-HEMBA1003175//Human IFNAR gene for interferon alpha/beta receptor.//1.9e-30:282:77//X60459
 R-HEMBA1003197
 R-HEMBA1003199//HS_2166_A1_E12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=2166 Col=23 Row=I, genomic survey sequence.//0.00026:271:61//AQ164162
 5 R-HEMBA1003202//Homo sapiens clone DJ0592G07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//
 5.4e-44:291:83//AC005480
 R-HEMBA1003204//Human BAC clone RG072E11 from 7q21-7q22, complete sequence.//3.1e-10:293:62//
 AC000118
 10 R-HEMBA1003212//Homo sapiens clone DJ0902E20, WORKING DRAFT SEQUENCE, 1 unordered pieces.//1.0:
 118:69//AC006148
 R-HEMBA1003220//HS_3092_B1_F09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3092 Col=17 Row=L, genomic survey sequence.//0.00014:59:91//AQ128202
 R-HEMBA1003222//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y43F8,
 WORKING DRAFT SEQUENCE.//0.84:214:62//Z95393
 15 R-HEMBA1003229//RPCI11-16F15.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-16F15, genomic survey
 sequence.//0.42:167:64//B83610
 R-HEMBA1003235//CIT-HSP-2320G19.TF CIT-HSP Homo sapiens genomic clone 2320G19, genomic survey se-
 quence.//3.6e-36:195:81//AQ037231
 20 R-HEMBA1003250//HS_2168_A2_C09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=2168 Col=18 Row=E, genomic survey sequence.//1.4e-22:158:89//AQ125356
 R-HEMBA1003257//Human PCP4 gene, exon 3 and complete cds.//0.96:268:61//U53709
 R-HEMBA1003273//Homo sapiens Xp22 BAC GS-377014 (Genome Systems Human BAC library) complete se-
 quence.//1.0e-32:255:84//AC002549
 25 R-HEMBA1003276//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING
 DRAFT SEQUENCE, 5 unordered pieces.//0.0044:212:60//AC005308
 R-HEMBA1003278//Homo sapiens 12q24.1 PAC RPCI1-315L5 (Roswell Park Cancer Institute Human PAC library)
 complete sequence.//1.1e-34:286:74//AC002395
 R-HEMBA1003281//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1
 ordered pieces.//1.8e-53:428:83//AC005840
 30 R-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds.//3.0e-115:551:99//AB011109
 R-HEMBA1003296//CIT-HSP-2196L16.TR CIT-HSP Homo sapiens genomic clone 2196L16, genomic survey se-
 quence.//2.9e-20:337:65//AQ003073
 R-HEMBA1003304//Sequence 23 from patent US 5552281.//1.8e-31:179:97//I25662
 R-HEMBA1003309//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E20, complete se-
 35 quence.//0.00019:334:60//AB017061
 R-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds.//2.8e-111:545:97//
 AB001872
 R-HEMBA1003322//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS,
 GSS, complete sequence.//0.60:274:61//AL022153
 40 R-HEMBA1003327//Homo sapiens BAC clone RG351J01 from 7q22-q31, complete sequence.//0.00028:172:65//
 AC005099
 R-HEMBA1003328//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//
 2.2e-44:268:90//AC005081
 45 R-HEMBA1003330//Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds.//2.7e-61:312:97//
 AF026029
 R-HEMBA1003348//***ALU WARNING: Human Alu-J subfamily consensus sequence.//7.2e-38:186:83//U14567
 R-HEMBA1003369//Caenorhabditis elegans cosmid F59C6, complete sequence.//0.00012:465:59//Z79600
 R-HEMBA1003370//Homo sapiens chromosome 17, clone hRPC867C24, complete sequence.//3.2e-42:301:87//
 AC002558
 50 R-HEMBA1003373//Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alter-
 natively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a
 PUTATIVE ZNF127 LIKE gene, and the PPARD for Peroxisome Proliferator Activated Receptor Delta (PPAR-Delta,
 PPAR-Beta, Nuclear Hormone Receptor 1, NUC1, NUCI, PPARG). Contains three putative CpG islands, ESTs,
 STSs, GSSs and a ca repeat polymorphism, complete sequence.//7.4e-34:375:74//AL022721
 55 R-HEMBA1003376//Homo sapiens chromosome 16, cosmid clone RT102 (LANL), complete sequence.//1.6e-46:
 309:88//AC004651
 R-HEMBA1003380//HS_2166_A1_E12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=2166 Col=23 Row=I, genomic survey sequence.//1.0e-35:237:88//AQ189144

R-HEMBA1003645//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 32B1, WORKING DRAFT SEQUENCE.//1.7e-33:297:82//AL023693

R-HEMBA1003646//Plasmodium falciparum MAL3P7, complete sequence.//0.44:319:59//AL034559

R-HEMBA1003656//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence.//6.9e-36:242:80//AC004382

R-HEMBA1003662//Homo sapiens chromosome 17, clone hRPK.332_H_18, complete sequence.//8.6e-117:588:96//AC005746

R-HEMBA1003667//Sequence 8 from patent US 5420245.//1.8e-21:170:88//I12222

R-HEMBA1003679//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//1.6e-22:180:87//AC005065

R-HEMBA1003680//C. elegans cosmid ZK353.//1.1e-06:270:61//L15313

R-HEMBA1003684//Colias alexandra alexandra cytochrome oxidase subunit I (cox1) gene, mitochondrial gene encoding mitochondrial protein, partial cds.//0.77:171:66//AF044872

R-HEMBA1003690//Homo sapiens 12q13.1 PAC RPCI5-1057I20 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.6e-104:523:97//AC004466

R-HEMBA1003692//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 508I15, WORKING DRAFT SEQUENCE.//1.7e-41:414:77//AL021707

R-HEMBA1003711//Human Chromosome 11 overlapping pacs pDJ235k10 and pDJ239b22, WORKING DRAFT SEQUENCE, 17 unordered pieces.//1.6e-29:304:77//AC000406

R-HEMBA1003714

R-HEMBA1003715//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-A-685D8, WORKING DRAFT SEQUENCE, 16 unordered pieces.//1.4e-63:578:77//AC005136

R-HEMBA1003720//Homo sapiens, WORKING DRAFT SEQUENCE, 135 unordered pieces.//2.4e-36:350:78//AC002353

R-HEMBA1003725//Homo sapiens chromosome 19, cosmid R31973, complete sequence.//6.3e-42:250:75//AC004699

R-HEMBA1003729//RPCI11-22D14.TV RPCI-11 Homo sapiens genomic clone RPCI-11-22D14, genomic survey sequence.//1.0:234:62//B86158

R-HEMBA1003733//Human DNA sequence from clone 396D17 on chromosome 1p33-35.3 Contains EST, STS, GSS, complete sequence.//7.7e-80:558:83//AL008634

R-HEMBA1003742//HS_3080_B2_H06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3080 Col=12 Row=P, genomic survey sequence.//3.4e-55:331:91//AQ139179

R-HEMBA1003758//Human DNA sequence from PAC 295C6 on chromosome 1q24. Contains ESTs, CA repeat, STS and CpG island.//4.5e-59:521:75//Z97876

R-HEMBA1003760

R-HEMBA1003773//Mus musculus signal recognition particle receptor beta subunit mRNA, complete cds.//2.6e-72:467:86//U17343

R-HEMBA1003783//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//1.0e-77:557:81//AF084259

R-HEMBA1003784

R-HEMBA1003799//Homo sapiens PAC clone DJ1032B10 from 7p15.3-p21, complete sequence.//2.1 e-49:390:72//AC004455

R-HEMBA1003803

R-HEMBA1003804//Homo sapiens chromosome 17, clone hCIT.175_E_5, complete sequence.//9.4e-99:359:99//AC004596

R-HEMBA1003805//Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.//8.0e-113:567:96//AL031781

R-HEMBA1003807//Bovine dinucleotide microsatellite HUJII77.//5.4e-18:194:78//M96348

R-HEMBA1003836//Human DNA from overlapping chromosome 19 cosmids R31396, F2545L and R31076 containing COX6B and UPKA, genomic sequence, complete sequence.//3.4e-40:256:85//AC002115

R-HEMBA1003838//CIT-HSP-2380F18.TF CIT-HSP Homo sapiens genomic clone 2380F18, genomic survey sequence.//9.7e-25:150:96//AQ196624

R-HEMBA1003856//Human DNA sequence from clone 272E8 on chromosome Xp22.13-22.31. Contains a pseudogene similar to MDM2 like P53 binding site.

complete sequence.//4.6e-33:486:68//Z93925

R-HEMBA1003864 complete sequence.//4.4e-100:351:94//AC005300

R-HEMBA1003866//HS_3203_B2_C01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3203 Col=2 Row=F, genomic survey sequence.//2.6e-05:206:64//AQ180298

R-HEMBA1003879//Homo sapiens chromosome 10 clone CIT987SK-1119P3 map 10q25.1, WORKING DRAFT SEQUENCE, 1 ordered pieces.//4.7e-17:170:79//U82207

R-HEMBA1003880//Homo sapiens genomic DNA, chromosome 21q11.1, segment 7/28, WORKING DRAFT SEQUENCE.//7.8e-103:526:96//AP000036

R-HEMBA1003885//Human apolipoprotein apoC-IV (APOC4) gene, complete cds.//3.5e-45:299:87//U32576

R-HEMBA1003893//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1137F22, WORKING DRAFT SEQUENCE.//1.1e-41:386:77//AL034421

R-HEMBA1003902//HS_3031_B2_E07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3031 Col=14 Row=J, genomic survey sequence.//5.3e-50:293:93//AQ165549

R-HEMBA1003908//CIT-HSP-2367K7.TR CIT-HSP Homo sapiens genomic clone 2367K7, genomic survey sequence.//1.2e-32:220:92//AQ076795

R-HEMBA1003926//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.//3.1e-58:294:85//AC005368

R-HEMBA1003937//Homo sapiens chromosome 3 subtelomeric region.//8.0e-111:590:93//AF109718

R-HEMBA1003939

R-HEMBA1003942//Homo sapiens clone DJ0828F13, complete sequence.//2.2e-08:474:58//AC004904

R-HEMBA1003950//Plasmodium vivax from Brazil cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds.//0.034:258:62//AF069619

R-HEMBA1003953//Plasmodium falciparum MAL3P8, complete sequence.//0.096:492:57//AL034560

R-HEMBA1003958//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 64K7, WORKING DRAFT SEQUENCE.//7.3e-40:382:78//AL031668

R-HEMBA1003959//Amaranthus hypochondriacus betaine aldehyde dehydrogenase (ahybadh4) gene, complete cds.//0.11:428:60//AF000132

R-HEMBA1003976//Homo sapiens PAC clone DJ0724E13 from 7p11.2-p12, complete sequence.//1.0:222:62//AC004414

R-HEMBA1003978//Sequence 31 from patent US 5708157.//1.9e-14:159:77//I80060

R-HEMBA1003985//Homo sapiens 12p13.3 PAC RPCI5-927J10 (Roswell Park Cancer Institute Human PAC library) complete sequence.//5.6e-14:136:83//AC004804

R-HEMBA1003987//Human chromosome 12p13 sequence, complete sequence.//3.2e-26:268:79//U47924

R-HEMBA1003989//RPCI11-52K22.TJ RPCI11 Homo sapiens genomic clone R-52K22, genomic survey sequence.//2.2e-86:443:95//AQ052484

R-HEMBA1004000

R-HEMBA1004011

R-HEMBA1004012//Homo sapiens chromosome 17, clone hRPK.63_A_1, complete sequence.//4.7e-38:284:85//AC005670

R-HEMBA1004015//Human DNA sequence from clone 931E15 on chromosome Xq25. Contains STSs, GSSs and genomic marker DXS8098, complete sequence.//0.48:460:58//AL023575

R-HEMBA1004024//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//2.5e-21:159:80//AC005081

R-HEMBA1004038//Homo sapiens Xq28 BAC RPCI11-382P7 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//7.9e-10:231:66//AC006054

R-HEMBA1004042//Homo sapiens clone DJ0968I16, complete sequence.//0.00071:263:68//AC006016

R-HEMBA1004045//Homo sapiens PAC clone DJ0074M20 from X, complete sequence.//8.8e-23:196:69//AC006143

R-HEMBA1004048//CIT-HSP-2288N20.TF CIT-HSP Homo sapiens genomic clone 2288N20, genomic survey sequence.//0.013:162:67//AQ007283

R-HEMBA1004049//Human hsp 70 gene 3' region for 70 kDa heat shock protein.//7.7e-30:176:96//X04677

R-HEMBA1004055//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//8.4e-05:395:63//AC005504

R-HEMBA1004056//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.5e-61:551:77//AC005484

R-HEMBA1004074//Homo sapiens clone DJ1032D07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.98:275:63//AC004952

R-HEMBA1004086//Se1

R-HEMBA1004087//Mus musculus Estrogen-Responsive Factor mRNA, complete cds

R-HEMBA1004101//Human mRNA for KIAA0128 gene, partial cds.//9.3e-42:534:69//D50918

R-HEMBA1004132//Homo sapiens chromosome 17, clone hCIT.211_P_7, complete sequence.//6.0e-49:491:76//AC003665

R-HEMBA1004133//HS_3229_B2_E09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3229 Col=18 Row=J, genomic survey sequence.//1.1e-72:374:97//AQ192003

R-HEMBA1004138//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 417M14, WORKING DRAFT SEQUENCE.//3.1e-09:277:66//AL024498

R-HEMBA1004143//Plasmodium falciparum MAL3P4, complete sequence.//0.53:239:61//AL008970

R-HEMBA1004146//Homo sapiens clone DJ0038110, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.0e-35:165:88//AC004820

R-HEMBA1004150//CITBI-E1-251712.TR CITBI-E1 Homo sapiens genomic clone 251712, genomic survey sequence.//0.56:379:59//AQ277616

R-HEMBA1004164//Human BAC clone GS200K05 from 7q21-q22, complete sequence.//4.6e-49:448:77//AC002429

R-HEMBA1004168//Homo sapiens geminin mRNA, complete cds.//2.4e-110:563:96//AF067855

R-HEMBA1004199//S.pombe chromosome I cosmid c8A4.//0.73:187:64//Z66569

R-HEMBA1004200//Homo sapiens Xp22 BAC GSHB-184P14 (Genome Systems Human BAC library) complete sequence.//6.3e-30:293:77//AC004552

R-HEMBA1004202//rah=ras-related homolog [mice, HT4 neural cell line, mRNA, 993 nt].//3.0e-64:517:80//S72304

R-HEMBA1004203//Homo sapiens clone NH0313P13, WORKING DRAFT SEQUENCE, 15 unordered pieces.//1.0e-97:303:98//AC005488

R-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, complete cds.//3.6e-116:573:97//U50748

R-HEMBA1004225//Drosophila melanogaster mitochondrial DNA with 12 tRNAs and 7 genes.//5.4e-11:493:60//M37275

R-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, complete cds.//6.1e-76:443:86//AF095927

R-HEMBA1004238//Homo sapiens chromosome 19, cosmid R28341, complete sequence.//1.1e-42:330:83//AC005763

R-HEMBA1004241

R-HEMBA1004246//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 4/15, WORKING DRAFT SEQUENCE.//1.1e-45:288:85//AP000011

R-HEMBA1004248//Homo sapiens PAC clone DJ0828B12 from 7q11.23-q21.1, complete sequence.//5.2e-09:516:61//AC004903

R-HEMBA1004264

R-HEMBA1004267//HS_2255_A2_H12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2255 Col=24 Row=O, genomic survey sequence.//8.6e-59:318:95//AQ068854

R-HEMBA1004272//Homo sapiens 12p13.3 PAC RPCIS-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.1e-113:576:96//AC005831

R-nnnnnnnnnnnnn//Homo sapiens clone 617 unknown mRNA, complete sequence.//4.4e-110:553:96//AF091081

R-HEMBA1004276

R-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds.//1.9e-106:538:97//AF022795

R-HEMBA1004289//RPCI11-74010.TJ RPCI11 Homo sapiens genomic clone R-74O10, genomic survey sequence.//2.3e-37:248:76//AQ266668

R-HEMBA1004295//Baboon apolipoprotein A-VI mRNA, 3' end.//0.0016:273:64//L13174

R-HEMBA1004306//HS_3175_B2_F01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3175 Col=2 Row=L, genomic survey sequence.//1.6e-28:190:77//AQ169206

R-HEMBA1004312//Human BAC clone RG119P24 from 7q31, complete sequence.//6.3e-36:267:82//AC003088

R-HEMBA1004321//Homo sapiens *** SEQUENCING IN PROGRESS *** from PAC 10155, WORKING DRAFT SEQUENCE.//4.1e-111:576:95//AJ009611

R-HEMBA1004323//CIT-HSP-2374C8.TR CIT-HSP Homo sapiens genomic clone 2374C8, genomic survey sequence.//2.7e-42:136:91//AQ114933

R-HEMBA1004327//CIT-HSP-2303L24.TF CIT-HSP Homo sapiens genomic clone 2303L24, genomic survey sequence.//1.0:78:67//AQ017600

R-HEMBA1004330//Homo sapiens clone DJ1173120, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.3e-119:580:98//AC004987

R-HEMBA1004334//Homo sapiens 12p13.3 PAC RPCIS-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete cds.//1.1e-113:576:96//AF091081

R-HEMBA1004335//Homo sapiens chromosome 16 BAC clone G1987SK-A-116A10, complete sequence.//1.1e-42:330:83//AC005763

21:291:71//AC004638

R-HEMBA1004341

R-HEMBA1004353//Homo sapiens mRNA for c-myc binding protein, complete cds.//4.1e-74:444:90//D89667

R-HEMBA1004354//Human DNA from overlapping chromosome 19-specific cosmids R29515 and R28253, genomic sequence, complete sequence.//7.0e-38:287:82//AC003002

R-HEMBA1004356//Sequence 2 from patent US 5652144.//3.7e-108:588:92//I58611

R-HEMBA1004366//WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.8e-14:446:63//AC005949

R-HEMBA1004372//CIT-HSP-2005C13.TF CIT-HSP Homo sapiens genomic clone 2005C13, genomic survey sequence.//0.010:334:61//B55811

R-HEMBA1004389//Homo sapiens full-length insert cDNA clone ZE09A11.//1.5e-19:170:83//AF086540

R-HEMBA1004394//Human (D21S198) DNA segment containing (TG)₂₃ repeat.//1.0:50:84//X58124

R-HEMBA1004396//Homo sapiens chromosome 4 clone B240N9 map 4q25, complete sequence.//8.2e-34:459:69//AC004057

R-HEMBA1004405//Homo sapiens BAC clone GS589P19 from 7p13-p14, complete sequence.//2.8e-42:314:84//AC005030

R-HEMBA1004408

R-HEMBA1004429//M.musculus of DNA encoding DNA-binding protein.//1.6e-66:449:82//Z54200

R-HEMBA1004433//Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1..333303.//7.2e-32:460:68//AJ011930

R-HEMBA1004460//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//3.9e-113:581:96//AC004846

R-HEMBA1004461//HS_3244_A2_F12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3244 Col=24 Row=K, genomic survey sequence.//8.0e-83:397:99//AQ220876

R-HEMBA1004479//Homo sapiens PAC clone DJ0942I16 from 7q11, complete sequence.//1.7e-40:485:70//AC006012

R-HEMBA1004482//Plasmodium falciparum chromosome 2, section 7 of 73 of the complete sequence.//2.2e-11:513:59//AE001370

R-HEMBA1004502//Homo sapiens chromosome 17, clone hRPK.372_K_20, complete sequence.//2.0e-08:245:66//AC005951

R-HEMBA1004506//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 34606, WORKING DRAFT SEQUENCE.//4.2e-81:582:83//Z84487

R-HEMBA1004507//Caenorhabditis elegans cosmid C40C9, complete sequence.//0.56:235:64//Z70266

R-HEMBA1004509

R-HEMBA1004534//Sequence 58 from patent US 5691147.//1.9e-61:430:83//I76230

R-HEMBA1004538//HS_3189_B2_C03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3189 Col=6 Row=F, genomic survey sequence.//6.1e-21:140:92//AQ170330

R-HEMBA1004554//CIT-HSP-712K9.TP CIT-HSP Homo sapiens genomic clone 712K9, genomic survey sequence.//1.7e-16:116:93//B73329

R-HEMBA1004560//Human mRNA for KIAA0281 gene, complete cds.//2.2e-14:213:71//D87457

R-HEMBA1004573

R-HEMBA1004577//Human DNA sequence from cosmid L247F6, Huntington's Disease Region, chromosome 4p16.3 contains protein similar to Mouse SH3 binding protein 3BP2, multiple ESTs and a CpG island.//1.0:352:60//Z68279

R-HEMBA1004586

R-nnnnnnnnnnnn//Plasmodium falciparum MAL3P6, complete sequence.//0.0012:359:60//Z98551

R-HEMBA1004610//S.pombe chromosome II cosmid c354.//0.0011:362:62//AL022071

R-HEMBA1004617//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501.//1.4e-50:327:85//AB007970

R-HEMBA1004629//Homo sapiens Xp22 bins 16-17 BAC GSHB-531I17 (Genome Systems Human BAC Library) complete sequence.//4.4e-13:527:63//AC004805

R-HEMBA1004631//Rattus norvegicus Nclone10 mRNA.//2.9e-24:364:71//U31866

R-HEMBA1004632

R-HEMBA1004637//Homo sapiens clone DJ0982E09, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.7e-117:573:98//AC005534

R-HEMBA1004638//H.sapiens mRNA for DGCR2.//3.8e-19:118:99//X84076

R-HEMBA1004666//Arabidopsis thaliana chromosome 1, clone B1-1111111111

R-HEMBA1004669//Human DNA sequence from cosmid L247F6, Huntington's Disease Region, chromosome 4p16.3 contains two novel

genes, ESTs, GSSs and CpG islands, complete sequence.//1.5e-120:571:98//AL031432
 R-HEMBA1004670//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 222E13, WORKING
 DRAFT SEQUENCE.//4.4e-12:110:88//Z93241
 R-HEMBA1004672//Human DNA sequence from PAC 308I13 on chromosome 1p35-1p36.3.//3.4e-38:324:81//
 5 Z99291
 R-HEMBA1004693//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPO12, complete sequence.//
 0.86:309:57//AB006702
 R-HEMBA1004697//T33B22TF TAMU Arabidopsis thaliana genomic clone T33B22, genomic survey sequence.//
 0.29:331:61//B97342
 10 R-HEMBA1004705//Plasmodium falciparum MAL3P7, complete sequence.//0.051:424:58//AL034559
 R-HEMBA1004709//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-116A10, complete sequence.//1.7e-
 49:497:76//AC004638
 R-HEMBA1004711//Homo sapiens chromosome 17, clone hRPK.271_K_11, complete sequence.//1.6e-38:362:
 79//AC005562
 15 R-HEMBA1004725
 R-HEMBA1004730//Homo sapiens Chromosome 17p13 Cosmid Clone cos26, complete sequence.//1.1e-58:489:
 79//AC002085
 R-HEMBA1004733
 R-HEMBA1004734//Human DNA sequence from clone 273N12 on chromosome 6q16.1-16.3. Contains the gene
 20 for the N-Oct5a (N-Oct3, N-Oct5b) POU domain proteins and an unknown gene. Contains a putative CpG island,
 ESTs, STS; and GSSs, complete sequence.//0.0030:362:61//AL022395
 R-HEMBA1004736//Homo sapiens clone DJ0981O07, complete sequence.//1.9e-58:282:87//AC006017
 R-HEMBA1004748//Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete sequence.//3.6e-34:287:
 81//AC004953
 25 R-HEMBA1004751//Human DNA sequence from PAC 507I15 on chromosome Xq26.3-27.3. Contains 60S ribos-
 omal protein L44 (L41, L36) like gene, ESTs, STSs and a polymorphic CA repeat.//5.3e-40:266:89//Z98950
 R-HEMBA1004752//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 495010, WORKING
 DRAFT SEQUENCE.//3.3e-39:281:85//AL031121
 R-HEMBA1004753//Homo sapiens ribosomal protein S20 (RPS20) mRNA, complete cds.//2.6e-65:475:84//
 30 L06498
 R-HEMBA1004756//Homo sapiens DNA sequence from PAC 86C11 on chromosome 6p21.31-22.1. Contains his-
 tone genes H2A/1, H2B.1A, H4, H2A.1b, H3 pseudogene, pheromone receptor pseudogene, ESTs, STS and CpG
 island.//1.8e-08:516:59//AL021807
 R-HEMBA1004758//Homo sapiens chromosome 4 clone B240N9 map 4q25, complete sequence.//5.1e-45:577:
 35 72//AC004057
 R-HEMBA1004763
 R-HEMBA1004768//Human DNA sequence from clone 395P12 on chromosome 1q24-25. Contains the TXGP1
 gene for tax-transcriptionally activated glycoprotein 1 (34kD) (OX40 ligand, OX40L) and a GOT2 (Aspartate Ami-
 notransferase, mitochondrial precursor, EC 2.6.1.1, Transaminase A, Glutamate Oxaloacetate Transaminase-2)
 40 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//4.1e-60:435:78//AL022310
 R-HEMBA1004770//Plasmodium falciparum chromosome 2, section 8 of 73 of the complete sequence.//8.7e-05:
 476:61//AE001371
 R-HEMBA1004771//Homo sapiens Xp22 Cosmid U152D7 (Lawrence Livermore human cosmid library) complete
 sequence.//5.0e-08:113:80//AC003047
 45 R-HEMBA1004776
 R-HEMBA1004778//***ALU WARNING: Human Alu-J subfamily consensus sequence.//1.1e-35:288:84//U14567
 R-nnnnnnnnnnnn/HS_3192_B1_F09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic
 clone Plate=3192 Col=17 Row=L, genomic survey sequence.//1.9e-44:233:98//AQ155855
 R-HEMBA1004803//Homo sapiens minisatellite ms31 repeat region.//3.0e-67:318:87//AF048728
 50 R-HEMBA1004806
 R-HEMBA1004807//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.6e-
 20:333:69//AC005015
 R-HEMBA1004816//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE
 LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs.
 55 Contains polymorphic CA repeat.//6.3e-13:148:77//Z92545
 R-HEMBA1004820//Homo sapiens chromosome 17, clone hRPK.271_K_11, complete sequence.//1.6e-38:362:
 79//AC005562

R-HEMBA1004850

R-HEMBA1004863//Human DNA sequence from PAC 345P10 on chromosome 22q12-qter contains ESTs and STS and polymorphic CA repeat D22S927.//2.0e-14:159:79//Z82201

R-HEMBA1004864

R-HEMBA1004865//Homo sapiens Xp22-149 BAC RPC111-466O4 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.90:76:76//AC005297

R-HEMBA1004880//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE, 12 unordered pieces.//1.9e-49:551:73//AC004826

R-HEMBA1004889//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 223B1, WORKING DRAFT SEQUENCE.//0.0021:189:65//AL031943

R-HEMBA1004900//Homo sapiens chromosome 17, clone hRPK.180_P_8, complete sequence.//6.6e-11:144:7711AC005972

R-HEMBA1004909//Human DNA sequence from clone 505B13 on chromosome 1p36.2-36.3 Contains CA repeat and GSSs, complete sequence.//7.6e-46:341:83//Z98052

R-HEMBA1004918//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 994L9, WORKING DRAFT SEQUENCE.//1.6e-54:301:89//AL034554

R-HEMBA1004923//Homo sapiens 47kB DNA fragment from Xq28, proximal to MTM1 gene.//2.0e-07:182:69//Y15994

R-HEMBA1004929

R-HEMBA1004930//Homo sapiens chromosome 11 clone CIT987SK-1012F4, WORKING DRAFT SEQUENCE, 6 unordered pieces.//7.7e-66:547:79//AC005848

R-HEMBA1004933//H.sapiens Humig mRNA.//0.13:233:62//X72755

R-HEMBA1004934//CIT-HSP-2021116.TF CIT-HSP Homo sapiens genomic-clone 2021116, genomic survey sequence.//0.66:268:62//B65345

R-HEMBA1004944//CIT-HSP-2281L12.TR CIT-HSP Homo sapiens genomic clone 2281L12, genomic survey sequence.//3.8e-20:104:82//B99849

R-HEMBA1004954//Homo sapiens chromosome 17, clone hRPK.146_P_2, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.00082:385:60//AC005341

R-HEMBA1004956//CIT-HSP-2305H22.TF CIT-HSP Homo sapiens genomic clone 2305H22, genomic survey sequence.//1.6e-84:411:99//AQ020408

R-HEMBA1004960//Human DNA sequence from PAC 358H7 on chromosome X.//3.3e-22:249:74//Z77249

R-HEMBA1004972//nbxb0003aF01f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0003K01f, genomic survey sequence.//0.52:171:64//AQ049982

R-HEMBA1004973//*** SEQUENCING IN PROGRESS *** EPM1/APECED region of chromosome 21, clones A68E8, B127P21, B173L3, B23N8, C1242C9, C579E2, A70B6, B159G9, B175D10, B52C10, C124G1 Note: Sequencing in this region has been discontinued by the Stanford Human Genome Center, WORKING DRAFT SEQUENCE, 50 unordered pieces.//0.69:179:64//AC003656

R-HEMBA1004977//Caenorhabditis elegans cosmid F08G2, complete sequence.//7.6e-07:492:58//Z81495

R-HEMBA1004978//Human DNA sequence from clone 522P13 on chromosome 6p21.31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous Nuclear Riboprotein A3, FBRNP) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.20:427:60//AL024509

R-HEMBA1004980//CIT-HSP-2379K5.TF CIT-HSP Homo sapiens genomic clone 2379K5, genomic survey sequence.//1.6e-53:331:88//AQ108614

R-HEMBA1004983//Genomic sequence from Human 17, complete sequence.//0.00061:473:58//AC000389

R-HEMBA1004995//Homo sapiens chromosome 16, cosmid clone 306E5 (LANL), complete sequence.//1.6e-90:527:89//AC004224

R-HEMBA1005008//Human DNA sequence from clone 461P17 on chromosome 20q12-13.2. Contains four novel (pseudo)genes for proteins with Kunitz/Bovine pancreatic trypsin inhibitor and/or WAP-type (Whey Acidic Protein) 'four-disulfide core' domains, COX6C (Cytochrome C Oxidase Polypeptide VIC, EC 1.9.3.1) and RPL5 (60S Ribosomal Protein L5) pseudogenes, a pseudogene similar to part of the HSPD1 (HSP60, Mitochondrial Matrix Protein P1 precursor, Heat Shock Protein 60, GROEL protein, HUCHA60) gene, and the Major Epididymis-specific protein E4 precursor (HE4, Epididymis Secretory protein E4, WAP-type (Whey Acidic Protein) 'four-disulfide core' domain) gene. Contains ESTs, an STS, GSSs and a putative CpG island, complete sequence.//5.4e-65:357:83//AL031663

R-HEMBA1005009//Homo sapiens BAF53a (BAF53a) mRNA, complete cds.//5.6e-107:550:96//AF041474

R-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein (putative).//1.1e-107:111:111//AF041475

R-HEMBA1005020//Homo sapiens chromosome 17p11.2-11.1 contains a new pseudogene, a Ribosomal protein L21 pseudogene and histone genes H2BFC (H2B/c).

H4FFP (H4/f pseudogene), H2AFC (H2A/c), H3F1K (H3.1/k) and a tRNA-Val pseudogene and tRNA-Thr gene. Contains ESTs, STSs, GSSs and genomic marker D6S464, complete sequence.//3.1e-67:493:83//AL009179
 R-HEMBA1005035//Homo sapiens chromosome 17, clone hCIT.175_E_5, complete sequence.//7.4e-101:537:94//AC004596

5 R-HEMBA1005039//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018D12, WORKING DRAFT SEQUENCE.//9.5e-30:446:68//AL031650

R-HEMBA1005047//Mus musculus mRNA for Rab24 protein.//1.4e-34:229:88//Z22819

R-HEMBA1005050//Human Chromosome X PAC RPC11-290C9 from the Pieter de Jong Human PAC library; complete sequence.//4.0e-43:371:80//AC002404

10 R-HEMBA1005062//Homo sapiens chromosome 17, clone hCIT.186_H_2, complete sequence.//2.3e-15:269:66//AC004675

R-HEMBA1005066//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//4.0e-30:305:74//AC006030

R-HEMBA1005075

15 R-HEMBA1005079//Homo sapiens clone HS 19.11 Alu-Ya5 sequence.//6.5e-48:245:91//AF015156

R-HEMBA1005083//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1185N5, WORKING DRAFT SEQUENCE.//1.3e-15:142:83//AL034423

R-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds.//5.3e-110:545:96//AF080561

20 R-HEMBA1005113//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y53C10, WORKING DRAFT SEQUENCE.//0.026:252:64//Z93340

R-HEMBA1005123//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//7.1e-55:306:82//AL022336

25 R-HEMBA1005133//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y738F9, WORKING DRAFT SEQUENCE.//6.4e-45:309:87//AL022345

R-HEMBA1005149//Human cosmid LL12NC01-95H4, ETV6 gene, exon 2 and partial cds.//3.2e-31:310:76//U81834

R-HEMBA1005152//Homo sapiens DNA sequence from PAC 13D10 on chromosome 6p22.3-23. Contains CpG island.//1.4e-33:361:79//AL021407

30 R-HEMBA1005159//Human DNA sequence from clone 163016 on chromosome 1p35.1-36.13 Contains CA repeat, STS, complete sequence.//2.7e-22:440:66//AL031279

R-HEMBA1005185//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y105E8, WORKING DRAFT SEQUENCE.//0.0017:381:58//AL022594

35 R-HEMBA1005201//P.falciparum complete gene map of plastid-like DNA (IR-B).//8.5e-05:457:57//X95276

R-HEMBA1005202//Human 18S ribosomal RNA.//4.7e-38:236:91//X03205

R-HEMBA1005219

R-HEMBA1005223//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//1.0:209:65//AC004854

40 R-HEMBA1005232//Homo-sapiens chromosome Y, clone 264,M,20, complete sequence.//0.0040:439:58//AC004617

R-HEMBA1005241//Homo sapiens PAC clone DJ0777023 from 7p14-p15, complete sequence.//4.2e-111:568:96//AC005154

R-HEMBA1005244//HS_3092_B2_C11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3092 Col=22 Row=F, genomic survey sequence.//4.9e-12:116:84//AQ127947

45 R-HEMBA1005251//Homo sapiens PAC clone DJ1182N03 from 7q11.23-q21.1, complete sequence.//3.2e-27:210:84//AC004548

R-HEMBA1005252//Homo sapiens chromosome 17, clone hRPK.318_A_15, complete sequence.//4.6e-105:437:97//AC005837

50 R-HEMBA1005274//Slime mold mitochondrial DNA, binding region to the membrane system.//0.011:339:59//D86630

R-HEMBA1005275//Homo sapiens PAC clone DJ0886O08 from 7q32-q35, complete sequence.//3.4e-17:269:71//AC004914

R-HEMBA1005293//Human DNA sequence from PAC 130N4, BRCA2 gene region chromosome 13q12-13 contains xs7 mRNA, ESTs.//6.9e-20:193:73//Z75887

55 R-HEMBA1005296//HS_3037_B1_D01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3037 Col=1 Row=D, genomic survey sequence.//0.25:184:64//AQ111111

R-HEMBA1005304//Homo sapiens clone DJ0693M15, WORKING DRAFT SEQUENCE, 7 unordered pieces.

1.5e-58:445:78//AC006146

R-HEMBA1005311//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 796E4, WORKING DRAFT SEQUENCE.//9.3e-42:383:78//AL022337

R-HEMBA1005314//Caenorhabditis elegans cosmid F23H11.//0.80:179:65//AF003389

R-HEMBA1005315//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.4e-40:409:71//AC006030

R-HEMBA1005318//S.pombe chromosome I cosmid c2E11.//0.97:370:61//AL031181

R-HEMBA1005331//Homo sapiens chromosome 17, clone hRPK.214_C_8, complete sequence.//1.9e-112:577:95//AC005803

R-HEMBA1005353//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 429E7, WORKING DRAFT SEQUENCE.//8.9e-80:406:97//AL031722

R-HEMBA1005359//Homo sapiens chromosome 17, clone hRPK.22_N_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//3.2e-50:320:84//AC005412

R-HEMBA1005367//RPC111-85E23.TV RPC111 Homo sapiens genomic clone R-85E23, genomic survey sequence.//0.39:148:67//AQ281915

R-HEMBA1005372//Homo sapiens full-length insert cDNA YH93B03.//2.6e-108:557:95//AF074997

R-HEMBA1005374//Homo sapiens full-length insert cDNA clone ZA95D11.//1.9e-110:531:98//AF086142

R-HEMBA1005389//Human DNA sequence from clone 245G19 on chromosome Xp22.11-22.2 Contains serine-threonine kinase (Tpx3) gene, a pseudogene similar to ALPHA-1 PROTEIN ((CONNEXIN 43, CX43, GAP JUNCTION 43 KD HEART PROTEIN)), and the 3' end of the RS (X-linked juvenile retinoschisis precursor protein) gene. Contains ESTs, STSs and GSSs, complete sequence.//6.0e-41:432:75//Z92542

R-HEMBA1005394//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 681N20, WORKING DRAFT SEQUENCE.//4.9e-107:585:93//AL031670

R-HEMBA1005403//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE.//5.1e-118:586:97//AL034379

R-HEMBA1005408//Bos taurus retina membrane guanylate cyclase ROS-GC2 mRNA, complete cds.//1.6e-06:204:68//U95958

R-HEMBA1005410//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 732E4, WORKING DRAFT SEQUENCE.//1.2e-23:452:66//AL008722

R-HEMBA1005411//RPC111-66N19.TK RPC111 Homo sapiens genomic clone R-66N19, genomic survey sequence.//2.2e-38:222:79//AQ237442

R-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds.//5.6e-117:453:99//AF041248

R-HEMBA1005426//Human DNA sequence from PAC 448E20 on chromosome Xq26.1 contains ESTs and STS.//0.86:278:60//Z97196

R-HEMBA1005443//Homo sapiens (clone s153) mRNA fragment.//5.4e-46:305:87//L40391

R-HEMBA1005447//Human DNA sequence from clone 48G12 on chromosome Xq27.1-27.3. Contains STSs and GSSs, complete sequence.//3.3e-79:531:86//AL031054

R-HEMBA1005468//Homo sapiens PAC clone DJ0808G16 from 7q11.23-q21, complete sequence.//4.0e-27:469:66//AC004894

R-HEMBA1005469//Homo sapiens chromosome 16, P1 clone 96-4B (LANL), complete sequence.//7.2e-40:410:76//AC005212

R-HEMBA1005472//Human DNA Sequence *** SEQUENCING IN PROGRESS *** from clone 1090E8, WORKING DRAFT SEQUENCE.//3.1e-40:296:85//AL033524

R-HEMBA1005475//HS_2266_B2_C04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2266 Col=8 Row=F, genomic survey sequence.//0.49:209:61//AQ069377

R-HEMBA1005497

R-HEMBA1005500//Homo sapiens PAC clone DJ1093O17 from 7q11.23-q21, complete sequence.//4.5e-116:580:97//AC004957

R-HEMBA1005506//Arabidopsis thaliana BAC T26D22.//0.0050:442:59//AF058826

R-HEMBA1005508//Sigalphus sp. 16S ribosomal RNA gene, partial sequence.//0.020:391:59//AF003509

R-HEMBA1005511//Human DNA sequence from PAC 52D1 on chromosome Xq21. Contains CA repeats, STS.//0.44:195:63//Z96811

R-HEMBA1005517//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//0.44:470:57//L14320

R-HEMBA1005518//M. musculus

Mouse cDNA clone hRPK.214_C_8, complete sequence.//1.9e-112:577:95//AC005803

Mouse cDNA clone

R-HEMBA1005526//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 341D10, WORKING DRAFT SEQUENCE.//3.9e-40:482:73/Z97985

R-HEMBA1005528//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11.//3.8e-84:309:99//AB020860

5 R-HEMBA1005530//Homo sapiens PAC clone 946B23 SCA2 region, SP6 end, genomic sequence, genomic survey sequence.//8.1e-25:154:94//J84091

R-HEMBA1005548//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 970A17, WORKING DRAFT SEQUENCE.//5.3e-105:534:96//AL034431

10 R-HEMBA1005552//Homo sapiens PAC clone DJ0807C15 from 7q34-q36, complete sequence.//2.8e-69:432:88//AC004743

R-HEMBA1005558

R-HEMBA1005568//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete sequence.//5.9e-33:367:74//AC004087

15 R-HEMBA1005570//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudogene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//2.2e-67:399:91//AL020989

R-HEMBA1005576//Homo sapiens chromosome 16, BAC clone 97H22 (LANL), complete sequence.//1.0:156:631/AC005737

R-HEMBA1005577

R-HEMBA1005581//Homo sapiens mRNA for MEGFS, partial cds.//9.7e-27:561:64//AB011538

20 R-HEMBA1005582//Torulopsis glabrata mitochondrial intergenic region ATPase 9 -cytochrome oxidase 2 genes.//2.3e-10:404:62//X02171

R-HEMBA1005583//HS_3014_B1_D05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3014 Col=9 Row=H, genomic survey sequence.//3.0e-81:442:94//AQ154499

25 R-HEMBA1005589//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032, complete sequence.//1.8e-54:490:77//Z98046

R-HEMBA1005593//Homo sapiens chromosome 17, clone hRPK.332_H_18, complete sequence.//2.2e-28:262:79//AC005746

30 R-HEMBA1005595//HS_2224_A2_G03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2224 Col=6 Row=M, genomic survey sequence.//3.6e-48:263:95//AQ033446

R-HEMBA1005606//Human PAC clone DJ0093I03 from Xq23, complete sequence.//2.5e-08:355:63//AC003983

R-HEMBA1005609//HS_2182_B1_H06_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=11 Row=P, genomic survey sequence.//2.2e-82:400:99//AQ023130

35 R-HEMBA1005616//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 124K22, WORKING DRAFT SEQUENCE.//0.80:308:60//AL031176

R-HEMBA1005621//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 330012, WORKING DRAFT SEQUENCE.//7.4e-76:338:98//AL031731

R-HEMBA1005627//Homo sapiens full-length insert cDNA clone ZD53D02.//4.5e-72:398:93//AF086321

40 R-HEMBA1005631//Homo sapiens PAC clone DJ1086D14, complete sequence.//3.8e-17:548:60//AC004460

R-HEMBA1005632//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS, CpG island, complete sequence.//1.4e-13:172:75//AL022069

R-HEMBA1005634//RPCI11-13O15.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-13O15, genomic survey sequence.//1.0e-28:153:82//B73293

45 R-HEMBA1005666//Human DNA sequence from PAC 696H22 on chromosome Xq21.1-21.2. Contains a mouse E25 like gene, a Kinesin like pseudogene and ESTs.//4.5e-51:343:87//AL021786

R-HEMBA1005670//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 11703, WORKING DRAFT SEQUENCE.//2.5e-33:288:78//AL020995

R-HEMBA1005679//Human esterase D mRNA, 3'end.//4.2e-49:322:88//M13450

50 R-HEMBA1005680//Homo sapiens Chr. 14 PAC RPCI4-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//3.0e-36:285:83//AC005924

R-HEMBA1005685//H.sapiens (MAR8) chromosome 19 DNA, 343bp.//0.022:65:86//Z35281

R-HEMBA1005699//Human putative EPH-related PTK receptor ligand LERK-8 (Eplg8) mRNA, complete cds.//5.4e-46:376:84//U66406

55 R-HEMBA1005705//RPCI11-13O14.TP RPCI-11 Homo sapiens genomic clone RPCI-11-13O14 genomic survey sequence //0.071.182.59//B76186

R-HEMBA1005706//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete sequence.//5.9e-33:367:74//AC004087
 R-HEMBA1005707//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032, complete sequence.//1.8e-54:490:77//Z98046

Contains polymorphic CA repeat.//1.0:189:66//Z92545

R-HEMBA1005732//Human Chromosome 11q12 pac pDJ363p2, WORKING DRAFT SEQUENCE, 22 unordered pieces.//2.1e-47:449:75//AC003023

R-HEMBA1005737

5 R-nnnnnnnnnnnnn//H.sapiens DNA for repeat unit locus D18S51 (285 bp).//0.11:174:63//X91255

R-HEMBA1005755//Human DNA-sequence from clone 396D17 on chromosome 1p33-35.3 Contains EST, STS, GSS, complete sequence.//0.15:160:65//AL008634

R-HEMBA1005765//Human Xq28 cosmids U225B5 and U236A12, complete sequence.//5.2e-39:422:74//U71148

10 R-HEMBA1005780//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 3/15, WORKING DRAFT SEQUENCE.//0.037:261:61//AP000010

R-HEMBA1005813//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING DRAFT SEQUENCE.//1.7e-26:242:80//AL023808

R-HEMBA1005815//Bufo boreas MVZ 145227 c-mos gene, partial cds.//0.17:199:62//U52805

R-HEMBA1005822//Plasmodium falciparum MAL3P7, complete sequence.//0.26:437:56//AL034559

15 R-HEMBA1005829//Human Cosmid g1572c035, complete sequence.//3.8e-05:366:61//AC000124

R-HEMBA1005834//Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.//8.2e-107:551:96//AL031781

20 R-HEMBA1005852//F.rubripes GSS sequence, clone 163A22aA4, genomic survey sequence.//2.6e-17:225:72//AL018730

R-HEMBA1005853//Human Chromosome 15 pac pDJ24m8, complete sequence.//1.1e-27:314:75//AC000379

R-HEMBA1005884//Homo sapiens 12p13.3 BAC RPCI3-488H23 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//2.6e-20:328:67//AC006207

25 R-HEMBA1005891//Homo sapiens PAC clone DJ0997N05 from 7q11.23-q21.1, complete sequence.//2.0e-102:543:95//AC004945

R-HEMBA1005894

R-HEMBA1005909

30 R-HEMBA1005911//CIT-HSP-2342E5.TR CIT-HSP Homo sapiens genomic clone 2342E5, genomic survey sequence.//0.0012:315:60//AQ058081

R-HEMBA1005921//P.chrysogenum mitochondrion genes for tRNA-Arg, tRNA-Asn, tRNA-Tyr, small subunit rRNA, and ATPase subunit 6.//0.0090:445:58//Z23072

R-HEMBA1005931//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 54B20, WORKING DRAFT SEQUENCE.//1.7e-46:351:83//Z98304

35 R-HEMBA1005934//Homo sapiens chromosome 17, clone hRPK.261_A_13, complete sequence.//0.0052:179:71//AC005138

R-HEMBA1005962//Homo sapiens clone RG012D21, complete sequence.//1.1e-11:149:74//AC005045

R-HEMBA1005963//HS_3055_A1_E08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=15 Row=1, genomic survey sequence.//5.4e-79:403:97//AQ147357

40 R-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//6.9e-112:580:95//AF082516

R-HEMBA1005991//Human DNA sequence from clone 58A9 on chromosome 1q24.1-24.3. Contains STSs, GSSs, genomic marker D1S210 and a ca repeat polymorphism, complete sequence.//2.6e-39:299:82//AL031285

45 R-HEMBA1005999//Homo sapiens clone DJ0691F11, WORKING DRAFT SEQUENCE, 11 unordered pieces.//1.1e-29:260:70//AC004859

R-HEMBA1006002//Rattus norvegicus s-nexilin mRNA, complete cds.//6.3e-15:174:78//AF056035

R-HEMBA1006005//Homo sapiens MLL (MLL) gene, exons 1-3, and partial cds.//2.6e-112:574:95//AF036405

R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0725 protein, partial cds.//7.6e-27:444:67//AB018268

50 R-HEMBA1006035//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.025:373:60//AC005139

R-HEMBA1006036//Homo sapiens Chromosome 16 BAC clone CIT987SK-625P11, complete sequence.//0.0056:535:59//AC004125

R-HEMBA1006042//HS_2169_A1_B11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2169 Col=21 Row=C, genomic survey sequence.//1.7e-73:390:95//AQ132995

55 R-nnnnnnnnnnnnn

R-HEMBA1006081

R-HEMBA1006081//Homo sapiens clone DJ0691F11, WORKING DRAFT SEQUENCE, 11 unordered pieces.//1.1e-29:260:70//AC004859

R-HEMBA1006081//Homo sapiens clone DJ0691F11, WORKING DRAFT SEQUENCE, 11 unordered pieces.//1.1e-29:260:70//AC004859

R-HEMBA1006091

R-HEMBA1006100//Homo sapiens DNA sequence from PAC 212G6 on chromosome Xp11.3-p11.4. Contains syn-apsin 1, brain protein 4.1, properdin, tyrosine kinase (ELK1) oncogene, ESTs, STS, GSS, complete sequence.//1.6e-36:354:77//AL009172

R-HEMBA1006108

R-HEMBA1006121

R-HEMBA1006124//Human DNA sequence from BAC 175E3 on chromosome 22q11.2-qter. Contains ESTs, STSs and polymorphic CA repeat.//1.3e-12:327:64//Z95113

R-HEMBA1006130//WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.60:326:62//AC005948

R-nnnnnnnnnnnn//Homo sapiens chromosome 19, cosmid F16403, complete sequence.//4.3e-52:321:80//AC005777

R-HEMBA100614211, complete sequence.//1.0e-13:160:78//AC005500

R-HEMBA1006155//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.0013:389:60//AC004688

R-HEMBA1006158//Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds.//1.4e-119:574:98//AF048693

R-HEMBA1006173//Mus musculus protein tyrosine phosphatase STEP61 mRNA, complete cds.//4.1e-43:307:86//U28217

R-HEMBA1006182//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//1.7e-30:300:71//AC004491

R-HEMBA1006198//***ALU WARNING: Human Alu-J subfamily consensus sequence.//1.3e-36:284:85//U14567

R-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence.//2.1e-110:545:97//AF070557

R-HEMBA1006248//Homo sapiens mRNA for KIAA0667 protein, partial cds.//0.46:365:58//AB014567

R-HEMBA1006252//Human Chromosome 16 BAC clone CIT987SK-A-972D3, complete sequence.//2.8e-41:438:71//U91323

R-HEMBA1006253//Homo sapiens 45kDa splicing factor mRNA, complete cds.//1.8e-28:179:91//AF083384

R-HEMBA1006259//RPC11-44N14.TJ RPC11 Homo sapiens genomic clone R-44N14, genomic survey sequence.//1.5e-48:348:85//AQ203161

R-HEMBA1006268

R-HEMBA1006272//Human DNA sequence from clone 1198H6 on chromosome 1p36.11-36.31. Contains two Melanoma Preferentially Expressed Antigen PRAME LIKE genes. Contains GSSs and ESTs, complete sequence.//2.8e-73:273:87//AL023753

R-nnnnnnnnnnnn//H.sapiens PAP mRNA.//1.6e-54:585:71//X76770

R-HEMBA1006283//Sequence 7 from patent US 5776683.//9.7e-18:113:98//AR016240

R-HEMBA1006284//Homo sapiens chromosome 17, clone hRPC.1028_K_7, complete sequence.//0.97:447:59//AC004585

R-HEMBA1006291//Homo sapiens full-length insert cDNA clone ZB76B10.//2.9e-94:454:98//AF086161

R-HEMBA1006293//Sequence 8 from patent US 5721351.//8.1e-10:111:72//I89415

R-HEMBA1006309//Homo sapiens chromosome 17, clone hRPK.22_N_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//8.6e-37:288:84//AC005412

R-HEMBA1006310//Rattus norvegicus cytosolic sorting protein PACS-1a (PACS-1) mRNA, complete cds.//6.5e-29:132:81//AF076183

R-HEMBA1006328//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 894K16, WORKING DRAFT SEQUENCE.//3.3e-50:340:75//AL034429

R-HEMBA1006334

R-HEMBA1006344//Rattus norvegicus nitzin mRNA, partial cds.//8.7e-22:259:72//AF087945

R-HEMBA1006347//Human prostaticin gene, complete cds.//1.8e-78:170:100//U33446

R-HEMBA1006349//Rat brain calcium channel alpha-1 subunit mRNA, complete cds.//0.00051:120:73//M57682

R-HEMBA1006359//CITBI-E1-2516C16.TR CITBI-E1 Homo sapiens genomic clone 2516C16, genomic survey sequence.//4.7e-74:576:82//AQ277951

R-HEMBA1006364//G.gallus gene for transforming growth factor-beta2, exons 5-7.//2.5e-21:118:85//X59080

R-HEMBA1006377//Homo sapiens chromosome 19, cosmid F23149, complete sequence.//5.7e-68:367:85//AC005239

R-HEMBA1006380//Human BAC clone RG007J15 from 7q31, complete sequence.//6.1e-47:300:83//AC003989

R-HEMBA1006381//Homo sapiens chromosome 5, Bac clone 189 (LBNL H135) complete sequence.//1.5e-47:336:86//AC005914

R-HEMBA1006386//Homo sapiens chromosome 19, cosmid F23149, complete sequence.//5.7e-68:367:85//AC005239

R-HEMBA1006416//Homo sapiens chromosome 17, clone 347_H_5, complete sequence//4.4e-37:319:76//AC002119

R-HEMBA1006419//Homo sapiens chromosome 17, clone HCIT542B22, complete sequence//2.9e-50:502:75//AC004253

5 R-HEMBA1006421//Homo sapiens chromosome 14q24.3 clone BAC270M14 transforming growth factor-beta 3 (TGF-beta 3) gene, complete cds; and unknown genes//4.1e-116:572:97//AF107885

R-HEMBA1006424//Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence//9.4e-117:578:97//AL031781

10 R-HEMBA1006426//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 291J10, WORKING DRAFT SEQUENCE//2.2e-08:353:63//Z93017

R-HEMBA1006438//HS_2008_A1_D04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2008 Col=7 Row=G, genomic survey sequence//1.2e-29:194:91//AQ245162

15 R-HEMBA1006445//Homo sapiens clone RG219E16, WORKING DRAFT SEQUENCE, 3 unordered pieces//0.011:330:60//AC005075

R-HEMBA1006446//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence//0.032:256:61//AE001398

20 R-HEMBA1006461//Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12, U115B9 (Lawrence Livermore human cosmid library) complete sequence//5.6e-35:229:77//AC002364

R-HEMBA1006467//Homo sapiens Chromosome 9p22 Cosmid clone 34a5, complete sequence//11.1e-14:354:63//AC002052

R-HEMBA1006471

25 R-HEMBA1006474//p40, p24 [Borna disease virus BDV, WT-1, Halle B1/91, horse brain, field isolate, Genomic RNA, 1138 nt, segment 1 of 3]//1.1e-14:442:60//S67502

R-HEMBA1006483//Human chromosome 16p13.1 BAC clone CIT987SK-551G9 complete sequence//3.7e-37:290:82//U95742

R-HEMBA1006485//H.sapiens mRNA for aminopeptidase//7.6e-91:517:91//Y07701

30 R-HEMBA1006486//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces//1.1e-33:289:81//AC005089

R-HEMBA1006489//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudogene similar to rat Plasmolipin, ESTs and GSSs, complete sequence//6.0e-07:485:60//AL020989

R-HEMBA1006492//Homo sapiens chromosome 17, clone hRPK.269_G_24, complete sequence//4.3e-112:572:95//AC005828

35 R-HEMBA1006494//Homo sapiens chromosome 17, clone HRPC987K16, complete sequence//2.3e-10:186:67//AC002994

R-HEMBA1006497//RPCI11-16L10.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-16L10, genomic survey sequence//1.5e-10:75:100//B88015

40 R-HEMBA1006502//Human DNA sequence from clone 272E8 on chromosome Xp22.13-22.31. Contains a pseudogene similar to MDM2-Like P53-binding protein gene. Contains STSs, GSSs and a CA repeat polymorphism, complete sequence//3.3e-36:516:70//Z93929

R-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds//1.2e-115:570:96//AB014566

R-HEMBA1006521//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 54B20, WORKING DRAFT SEQUENCE//2.2e-20:266:71//Z98304

45 R-HEMBA1006530//RPCI11-52M1.TJ RPCI11 Homo sapiens genomic clone R-52M1, genomic survey sequence//0.00015:227:64//AQ052526

R-HEMBA1006535//HS_2234_B1_B07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2234 Col=13 Row=D, genomic survey sequence//7.5e-33:191:95//AQ129525

R-HEMBA1006540//Homo sapiens clone GS051M12, complete sequence//0.026:497:58//AC005007

50 R-HEMBA1006546//Homo sapiens chromosome 19, cosmid R33496, complete sequence//5.2e-41:289:86//AC004603

R-HEMBA1006559//Mus musculus PRAJA1 (Praja1) mRNA, complete cds//3.4e-64:551:78//U06944

R-HEMBA1006562//Human Chromosome 11p11.2 PAC clone pDJ404m15, complete sequence//5.7e-09:266:66//AC002554

55 R-HEMBA1006566//HS_2171_B1_B04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2171 Col=7 Row=D, genomic survey sequence//7.5e-33:191:95//AQ129525

R-HEMBA1006570//Homo sapiens mRNA for KIAA0666 protein, partial cds//3.8e-71:529:82//U03935

R-HEMBA1006570//Homo sapiens mRNA for KIAA0666 protein, partial cds//3.8e-71:529:82//U03935

R-HEMBA1006583//CIT-HSP-2377M16.TR CIT-HSP Homo sapiens genomic clone 2377M16, genomic survey sequence.//1.7e-31:271:76//AQ111875

R-HEMBA1006595//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.093:270:61//AC004709

R-HEMBA1006597//Homo sapiens P1 clone GSP13996 from 5q12, complete sequence.//2.7e-45:371:80//AC005031

R-HEMBA1006612

R-nnnnnnnnnnnn//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 8B22, WORKING DRAFT SEQUENCE.//2.1e-20:229:77//AL031737

R-HEMBA1006624//Human DNA sequence from clone 406A7 on chromosome 6q23-24. Contains three pseudogenes similar to Elongation Factor 1-Alpha (EF-1-ALPHA, Statin S1), 60S Acidic Ribosomal Protein P1 and NADH-Ubiquinone Oxidoreductase 15 kDa subunit, and part of the Microtubule Associated Protein E-MAP-115 gene. Contains ESTs, STSs and GSSs, complete sequence.//4.8e-40:321:83//AL023284

R-HEMBA1006631//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 20208, WORKING DRAFT SEQUENCE.//1.5e-45:477:77//AL031848

R-HEMBA1006635//***ALU WARNING: Human Alu-Sp subfamily consensus sequence.//8.0e-40:245:91//U14572

R-HEMBA1006639

R-HEMBA1006643

R-HEMBA1006648//Homo sapiens integrin-linked kinase (ILK) mRNA, complete cds.//2.5e-106:567:94//U40282

R-HEMBA1006652//Human BAC clone RG308B22 from 7q22-q31, complete sequence.//8.7e-54:334:76//AC002089

R-HEMBA1006653//Homo sapiens 7q telomere, complete sequence.//5.0e-36:207:89//AF027390

R-HEMBA1006665//HS_3213_B2_D04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=8 Row=H, genomic survey sequence.//1.2e-21:235:67//AQ175625

R-HEMBA1006674//H.sapiens telomeric DNA sequence, clone 9QTELO23, read 9QTELOO23.seq.//2.6e-32:212:83//Z96776

R-HEMBA1006676//Plasmodium falciparum MAL3P6, complete sequence.//1.9e-10:436:60//Z98551

R-HEMBA1006682//Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds.//6.1e-06:477:59//L40608

R-HEMBA1006695//Homo sapiens clone RG339C12, WORKING DRAFT SEQUENCE, 10 unordered pieces.//1.8e-30:266:80//AC005096

R-HEMBA1006696

R-HEMBA1006708

R-HEMBA1006709//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 715N11, WORKING DRAFT SEQUENCE.//6.8e-14:139:82//AL031674

R-HEMBA1006717

R-HEMBA1006737//Homo sapiens chromosome 17, clone hRPK.269_G_24, complete sequence.//9.9e-18:365:66//AC005828

R-HEMBA1006744//Human Chromosome 16 BAC clone CIT987SK-327O24, complete sequence.//1.3e-37:380:75//AC003108

R-HEMBA1006754//Homo sapiens chromosome 5, P1 clone 962c5 (LBNL H87), complete sequence.//2.1e-75:338:85//AC003951

R-HEMBA1006758//Homo sapiens chromosome 5, BAC clone 182a8 (LBNL H161), complete sequence.//1.2e-112:579:95//AC005752

R-HEMBA1006767//Plasmodium falciparum MAL3P6, complete sequence.//0.00022:528:58//Z98551

R-HEMBA1006779//Homo sapiens chromosome 17, clone hRPK.628_E_12, complete sequence.//2.3e-46:305:87//AC005701

R-HEMBA10067801//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs and GSSs, complete sequence.//7.2e-39:305:82//AL022323

R-HEMBA1006789//Streptomyces coelicolor cosmid 6G4.//0.0085:449:61//AL031317

R-HEMBA1006795//Homo sapiens chromosome 17, clone hRPK.346_K_10, complete sequence.//4.1e-43:355:801//AC006120

R-HEMBA1006796//HS_3038_B2_H11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3038 Col=22 Row=P, genomic survey sequence.//0.99:158:63//AQ102483

R-HEMBA1006807//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE 33 unordered pieces.//8.4e-47:481:75//AC004854

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SEQUENCE

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R-HEMBA1006824//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//3.7e-54:496:76//Z93023

R-HEMBA1006832//Homo sapiens chromosome 17, clone hRPK.243_K_12, complete sequence.//0.70:206:65//AC005668

5 R-HEMBA1006849//Homo sapiens 12q24.1 PAC RPCI3-521E19 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.2e-46:281:91//AC004217

R-HEMBA1006865//Mus musculus clone 101 B1 repeat region sequence.//0.61:115:70//AF056074

R-nnnnnnnnnnn//Mus musculus mRNA for oxysterol-binding protein, complete cds.//3.3e-102:618:87//AB017026

R-HEMBA1006885 4.2e-14:379:63//AG006839

10 R-HEMBA1006900//CIT-HSP-2006M20.TR CIT-HSP Homo sapiens genomic clone 2006M20, genomic survey sequence.//2.6e-07:230:66//B56395

R-HEMBA1006921//Homo sapiens PAC clone DJ0777O23 from 7p14-p15, complete sequence.//2.1e-68:267:86//AC005154

R-HEMBA1006926

15 R-HEMBA1006929//HS_3244_A2_C01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3244 Col=2 Row=E, genomic survey sequence.//6.9e-21:191:83//AQ207500

R-HEMBA1006936

R-HEMBA1006938//Colias philodice eriphyle large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs.//0.11:309:59//AF044853

20 R-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein.//2.0e-75:371:98//AJ010841

R-HEMBA1006949//Homo sapiens PAC clone DJ0777G09 from 7q34-q36, complete sequence.//0.47:240:63//AC005518

R-HEMBA1006973//HS_2009_A2_A12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2009 Col=24 Row=A, genomic survey sequence.//9.6e-05:407:60//AQ232302

25 R-HEMBA1006976//RPCI11-49L11.TJ RPCI11 Homo sapiens genomic clone R-49L11, genomic survey sequence.//0.0018:184:63//AQ051701

R-HEMBA1006993//Human thymopoietin (TMPO) gene, partial exon 6, complete exon 7, partial exon 8, and partial cds for thymopoietin beta.//1.9e-47:394:79//U18271

30 R-HEMBA1006996//CIT-HSP-2172D17.TF CIT-HSP Homo sapiens genomic clone 2172D17, genomic survey sequence.//1.8e-07:365:62//B93406

R-HEMBA1007002//Plasmodium falciparum MAL3P2, complete sequence.//0.0012:505:56//AL034558

R-HEMBA1007017//Homo sapiens chromosome 17, clone hRPK.597_M_12, complete sequence.//5.6e-41:437:71//AC005277

35 R-HEMBA1007018//G.gallus mRNA for dynein light chain-A.//8.2e-73:556:80//X79088

R-HEMBA1007045

R-HEMBA1007051//Human DNA sequence from cosmid N69F4 on chromosome 22q11.2-qter contains EST.//9.9e-27:342:71//Z72006

R-HEMBA1007052//Homo sapiens FSHD-associated repeat DNA, proximal region.//5.4e-85:558:87//U85056

40 R-HEMBA1007062

R-HEMBA1007066

R-HEMBA1007073//Homo sapiens chromosome 17, clone hRPK.421_E_14, complete sequence.//2.0e-66:476:85//AC006141

R-HEMBA1007078//Homo sapiens chromosome 17, clone hRPK.60_A_24, complete sequence.//1.0e-38:179:82//AC005325

45 R-HEMBA1007085//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.2e-49:551:73//AC006015

R-HEMBA1007087//Human Chromosome 11 pac pDJ392a17, complete sequence.//1.0:261:61//AC000385

R-HEMBA1007112//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 37 unordered pieces.//0.043:295:62//AC004803

50 R-HEMBA1007113//Homo sapiens (subclone 6_a8 from P1 H16) DNA sequence.//1.4e-52:307:87//L43392

R-HEMBA1007129//Human DNA sequence from PAC 863K19 on chromosome X. Contains STS.//1.2e-08:131:75//Z92547

R-HEMBA1007147//H.sapiens CpG island DNA genomic Mse1 fragment, clone 65f1, reverse read cpg65f1.rt1a.//0.16:187:64//Z62246

55 R-HEMBA1007149//H.sapiens DNA sequence from PAC 863K19 on chromosome X. Contains STS.//1.2e-08:131:75//Z92547

R-HEMBA1007149//H.sapiens DNA sequence from PAC 863K19 on chromosome X. Contains STS.//1.2e-08:131:75//Z92547

AC004875

R-nnnnnnnnnnnr//Homo sapiens epsin 2a mRNA, complete cds//5.1e-103:529:94//AF062085

R-HEMBA1007178//Homo sapiens chromosome 12p13.3 clone RPC11-372B4, WORKING DRAFT SEQUENCE, 129 ordered pieces//5.4e-106:537:96//AC005911

5 R-HEMBA1007194//Homo sapiens Xp22 bins 87-93 PAC RPC11-122K4 (Roswell Park Cancer Institute Human PAC Library) complete sequence//4.1e-39:262:80//AC003035

R-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds//5.3e-61:332:95//D86987

R-HEMBA1007206//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island//1.9e-50:436:81//Z93023

10 R-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds//2.3e-96:471:97//AB018340

R-HEMBA1007251//Homo sapiens chromosome 5, PAC clone 247f3 (LBNL H85), complete sequence//0.011:349:62//AC004777

R-HEMBA1007256//Homo sapiens PAC clone DJ0676L20 from 7q35-q36, complete sequence//2.8e-10:224:70//AC004856

15 R-HEMBA1007267//Homo sapiens Chr.14 PAC RPC14-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence//3.4e-53:362:86//AC005924

R-HEMBA1007273

R-HEMBA1007279//Rickettsia prowazekii strain Madrid E, complete genome; segment 4/4//0.042:454:57//AJ235273

20 R-HEMBA1007281//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4//0.99:288:60//AJ235272

R-HEMBA1007288//Human DNA sequence from clone 422G23 on chromosome 6q24 Contains EST, STS, GSS, CpG island, complete sequence//7.4e-107:554:95//AL031003

R-HEMBA1007300//Caenorhabditis elegans cosmid C48C5//0.22:474:59//U39994

25 R-HEMBA1007301

R-HEMBA1007319//Campylobacter jejuni repetitive DNA, clone pINT//4.9e-08:524:58//Y14425

R-HEMBA1007320//Homo sapiens genomic DNA, chromosome 21q11.1, segment 14/28, WORKING DRAFT SEQUENCE//3.4e-16:244:71//AP000043

R-HEMBA1007322//Homo sapiens BAC clone RG324D18 from 7p15-p21, complete sequence//3.9e-83:383:85//AC005251

30 R-HEMBA1007327//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 7706, WORKING DRAFT SEQUENCE//1.6e-38:533:71//Z96804

R-HEMBA1007341//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 268D13, WORKING DRAFT SEQUENCE//3.6e-21:394:66//AL023513

35 R-HEMBA1007342//Human BAC clone GS368F15 from 7q31, complete sequence//1.7e-15:190:73//AC003080

R-HEMBA1007347//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone N38G6, WORKING DRAFT SEQUENCE//2.2e-47:455:77//Z96802

R-HEMBA1000005//Homo sapiens 3p21.1-9 PAC RPC14-793P23 (Roswell Park Cancer Institute Human PAC Library) complete sequence//1.1e-62:539:79//AC006208

40 R-HEMBA1000008//Homo sapiens chromosome 17, clone hCIT.211_P_7, complete sequence//1.2e-36:285:83//AC003665

R-HEMBA1000018//Homo sapiens clone DJ0038I10, WORKING DRAFT SEQUENCE, 5 unordered pieces//1.2e-51:416:79//AC004820

45 R-HEMBA1000024//Human DNA sequence from BAC 175E3 on chromosome 22q11.2-qter. Contains ESTs, STSs and polymorphic CA repeat//3.9e-18:211:79//Z95113

R-HEMBA1000025//HS_3064_B2_B07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=14 Row=D, genomic survey sequence//5.9e-40:254:90//AQ132765

R-HEMBA1000030//Human DNA sequence from clone 108K11 on chromosome 6p21 Contains SRP20 (SR protein family member), Ndr protein kinase gene similar to yeast suppressor protein SRP40, EST and GSS, complete sequence//1.5e-32:452:70//Z85986

50 R-HEMBA1000036//CIT-HSP-2024L15.TF CIT-HSP Homo sapiens genomic clone 2024L15, genomic survey sequence//9.3e-63:541:77//B66264

R-HEMBA1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//7.6e-91:467:97//AF084928

55 R-HEMBA1000039//Homo sapiens chromosome 17, clone hRPK.401 O 9, complete sequence//2.4e-44:456:68//AC005291

R-HEMBA1000044//Homo sapiens chromosome 17, clone hRPK.401 O 9, complete sequence//2.4e-44:456:68//AC005291

R-HEMBA1000048//Homo sapiens chromosome 17, clone hRPK.401 O 9, complete sequence//2.4e-44:456:68//AC005291

R-HEMBA1000048//Homo sapiens chromosome 17, clone hRPK.401 O 9, complete sequence//2.4e-44:456:68//AC005291

09:330:63//AC002300

R-HEM BB1000050//Human DNA sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked, juvenile) 1 (XLRS1). Contains ESTs, an STS and GSSs, complete sequence.//6.7e-12:225:65//Z94056

R-HEM BB1000054//Human DNA sequence from clone 444C7 on chromosome 6p22.3-23. Contains an EST, an STS and GSSs, complete sequence.//8.9e-76:557:82//AL033521

R-HEM BB1000055//Human housekeeping (Q1Z 7F5) gene, exons 2 through 7, complete cds.//1.6e-88:350:86//M81806

R-HEM BB1000059//Homo sapiens clone DJ0850101, WORKING DRAFT SEQUENCE, 1 unordered pieces.//4.9e-12:356:65//AC006009

R-HEM BB1000083//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12 unordered pieces.//3.7e-41:311:82//AC004840

R-HEM BB1000089//Homo sapiens clone DJ1021120, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.6e-34:314:78//AC005520

R-HEM BB1000099//Homo sapiens DNA sequence from BAC 1216H12 on chromosome 22q12. Contains a pseudogene with similarity to part of mouse Ninein and the KIAA0609 gene for a protein similar to C. elegans K09C8.4. Contains ESTs, GSSs and a gggt repeat polymorphism, complete sequence.//8.8e-32:434:71//AL008715

R-HEM BB1000103//Human DNA sequence from BAC 445C9 on chromosome 22q12.1. Contains CRYBB1, beta B1 crystallin, CRYBA4, beta A4 crystallin, high mobility group-1 protein (HMG-1), ESTs.//2.5e-16:207:74//Z95115

R-HEM BB1000113//HS_3013_A1_B08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3013 Col=15 Row=C, genomic survey sequence.//0.94:211:63//AQ118730

R-HEM BB1000119//Homo sapiens ASMTL gene.//1.9e-106:531:96//Y15521

R-HEM BB1000136//Human Chromosome X, complete sequence.//0.00073:359:59//AC002407

R-HEM BB1000141//Homo sapiens chromosome 21q22.3 PAC 39C17, complete sequence.//6.8e-41:280:74//AF043945

R-HEM BB1000144//Homo sapiens chromosome 17, clone hCIT.507_E_2, complete sequence.//0.00083:206:66//AC004134

R-HEM BB1000173//Homo sapiens, WORKING DRAFT SEQUENCE, 97 unordered pieces.//2.5e-82:401:90//AC004085

R-HEM BB1000175

R-HEM BB1000198//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//0.91:428:56//AL021368

R-HEM BB1000215//Homo sapiens DNA sequence from PAC 69E11 on chromosome 1q23-24. Contains a NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ) LIKE pseudogene, a 60S Ribosomal protein L34 LIKE pseudogene, an unknown gene similar to yeast YPR037W and worm C02C2.6 predicted genes, a predicted CpG island, ESTs and an STS, complete sequence.//4.4e-54:298:91//AL021397

R-HEM BB1000217

R-HEM BB1000218//Homo sapiens 12q24 PAC RPC11-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//5.8e-32:517:70//AC004216

R-HEM BB1000226//Human DNA sequence from cosmid COS12 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs, Flanking sequences of 3' alpha globin HVR and CpG island.//2.5e-77:450:92//Z69706

R-HEM BB1000240//Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families.//4.1e-05:310:62//AF029308

R-HEM BB1000244//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1112F19, WORKING DRAFT SEQUENCE.//1.3e-43:278:85//AL034420

R-HEM BB1000250//Human DNA sequence from clone 34B20 on chromosome 6p21.31-22.2. Contains seventeen Histone (pseudo)genes and a 40S Ribosomal protein S10 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//3.8e-16:484:64//AL031777 R-HEM BB1000258//Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds.//4.3e-11:286:67//U91328

R-HEM BB1000264//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//1.2e-42:406:79//AF079765

Gene ID: 1000050
Accession: AF026550

R-HEM BB1000272//HS_3032_B1_H06_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3032 Col=11 Row=P, genomic survey sequence//0.0082:209:62//AQ096702

R-HEM BB1000274//Homo sapiens Chromosome 22q11.2 Cosmid Clone 817g In IGLC Region, complete sequence//1.6e-45:277:72//AC000053

5 R-HEM BB1000284//Homo sapiens full-length insert cDNA clone YY88A05//6.9e-112:572:96//AF088018

R-HEM BB1000307//Homo sapiens chromosome 17, clone hRPK.471_L_13, complete sequence//5.7e-96:523:93//AC005244

R-HEM BB1000312//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 32B1, WORKING DRAFT SEQUENCE//7.5e-21:218:67//AL023693

10 R-HEM BB1000317//Toxoplasma gondii chloroplast, complete genome//0.062:354:58//U87145

R-HEM BB1000318//Human DNA sequence from PAC 292H14 on chromosome Xp21. Contains STS and CA repeat polymorphism//4.5e-52:302:81//AL008710

R-HEM BB1000335//Homo sapiens chromosome 5, P1 clone 1041F10 (LBNL H88), complete sequence//1.9e-16:139:84//AC005179

15 R-HEM BB1000336//Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease//0.0062:231:64//AJ003147

R-HEM BB1000337//CIT-HSP-2329010.TF CIT-HSP Homo sapiens genomic clone 2329O10, genomic survey sequence//1.2e-31:192:92//AQ035976

R-HEM BB1000338//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence//1.9e-39:477:71//AC004605

20 R-HEM BB1000339//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 862K6, WORKING DRAFT SEQUENCE//4.1e-54:357:76//AL031681

R-HEM BB1000341//Homo sapiens 12q24 PAC RPC13-424M6 (Roswell Park Cancer Institute Human PAC library) complete sequence//1.8e-19:501:63//AC002350

25 R-HEM BB1000343//Homo sapiens chromosome 16, cosmid clone 367E12 (LANL), complete sequence//3.6e-41:457:72//AC004644

R-HEM BB1000354//Human DNA sequence from PAC 560B9 on chromosome 1q24-1q25. Contains profilin-like pseudogene, 60S ribosomal protein L4 pseudogene RNA binding protein, ESTs, GSS//7.2e-36:325:74//Z98751

R-HEM BB1000369//Homo sapiens chromosome 4 clone B366O24 map 4q25, complete sequence//9.0e-25:179:79//AC004067

30 R-HEM BB10003741//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 75N14, WORKING DRAFT SEQUENCE//8.4e-58:332:79//Z97199

R-HEM BB1000376//Homo sapiens DNA for amyloid precursor protein, complete cds//2.1e-47:309:88//D87675

R-HEM BB1000391//Homo sapiens clone RG269P13, WORKING DRAFT SEQUENCE, 6 unordered pieces//5.7e-46:302:85//AC005080

35 R-HEM BB1000399//Homo sapiens Rad17-like protein (RAD17) mRNA, complete cds//1.0e-107:531:97//AF076838

R-HEM BB1000402//Human DNA sequence from clone 505B13 on chromosome 1p36.2-36.3 Contains CA repeat and GSSs, complete sequence//1.1e-25:441:67//Z98052

40 R-HEM BB1000404//HS_2246_A2_D01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2246 Col=2 Row=G, genomic survey sequence//0.0025:196:63//AQ084251

R-HEM BB1000420//Homo sapiens Chromosome 22q11.2 Cosmid Clone 817g In IGLC Region, complete sequence//1.2e-29:358:72//AC000053

R-HEM BB1000434//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence//2.8e-51:299:89//AC004069

45 R-HEM BB1000438//HS_2239_B2_E08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2239 Col=16 Row=J, genomic survey sequence//1.3e-10:76:100//AQ067700

R-HEM BB1000441//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 424J12, WORKING DRAFT SEQUENCE//4.4e-60:281:90//Z82207

50 R-HEM BB1000449//Homo sapiens clone DJ0898O18, WORKING DRAFT SEQUENCE, 8 unordered pieces//4.8e-11:228:68//AC004920

R-HEM BB1000455//Homo sapiens clone GS051M12, complete sequence//3.1e-14:388:65//AC005007

R-HEM BB1000472//Homo sapiens chromosome 17, clone HCIT48C15, complete sequence//4.9e-34:320:79//AC003104

55 R-HEM BB1000480//Human DNA sequence from Fosmid 65B7 on chromosome 22q11.2-qter. Contains exons 6-12 of the SLC5A1 (SGLT1) gene for solute carrier family 5 member 1 (SGLT1) gene. The sequence is identical to the sequence in GenBank accession number U08384.

R-HEM BB1000490//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1185N5, WORKING DRAFT SEQUENCE.//1.5e-34:281:81//AL034423

R-HEM BB1000491//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//8.5e-37:483:72//Z93023

5 R-HEM BB1000493//Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF127 LIKE gene, and the PPAR for Peroxisome Proliferator Activated Receptor Delta (PPAR-Delta, PPAR-Beta, Nuclear Hormone Receptor 1, NUC1, NUCI, PPARB). Contains three putative CpG islands, ESTs, STSs, GSSs and a ca repeat polymorphism, complete sequence.//7.6e-14:217:71//AL022721

10 R-HEM BB1000510//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 27K12, WORKING DRAFT SEQUENCE.//7.1e-44:221:80//AL033397

R-HEM BB1000518//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//3.5e-51:280:90//AC002477

15 R-HEM BB1000523//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence.//1.7e-53:304:82//AC004079

R-HEM BB1000530//Homo sapiens chromosome 17, clone hCIT.162_E_12, complete sequence.//4.2e-74:428:92//AC006236

R-HEM BB1000550//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//5.6e-13:112:80//U91321

20 R-HEM BB1000554//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 409J21, WORKING DRAFT SEQUENCE.//5.1e-14:239:63//Z83824

R-HEM BB1000556//Homo sapiens envoplakin (EVPL) mRNA, complete cds.//0.031:275:60//U53786

R-HEM BB1000564//Homo sapiens chromosome 5, Bac clone 189 (LBNL H135), complete sequence.//3.1e-17:227:76//AC005914

25 R-HEM BB1000573//Borrelia afzelii (strain NT28) DNA, internal transcribed spacer.//0.078:161:63//D84405

R-HEM BB1000575//Homo sapiens chromosome 17, clone hRPC.859_O_20, complete sequence.//7.2e-52:260:80//AC003695

R-HEM BB1000586//Human DNA sequence from cosmid V210E9, between markers DXS366 and DXS87 on chromosome X.//2.0e-33:305:79//Z70280

30 R-HEM BB1000589//Homo sapiens chromosome 17, clone hRPK.1064_E_11, complete sequence.//1.3e-14:409:65//AC005208

R-HEM BB1000591//Homo sapiens Xp22 bins 45-47 BAC GSHB-665N22 (Genome Systems Human BAC Library) complete sequence.//6.2e-39:493:71//AC005184

35 R-HEM BB1000592//Homo sapiens 12p13.3 PAC RPC15-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.6e-08:254:64//AC005831

R-HEM BB1000598//Homo sapiens chromosome 11 pac pDJ159ol, complete sequence.//3.3e-38:407:76//AC000381

R-HEM BB1000623//CIT-HSP-2374P17.TR CIT-HSP Homo sapiens genomic clone 2374P17, genomic survey sequence.//1.3e-41:212:100//AQ109717

40 R-HEM BB1000630//Human DNA sequence from clone 413H6 on chromosome 6p22.3-24.3. Contains a hamster Androgen-dependent Expressed Protein like protein gene, ESTs and GSSs, complete sequence.//5.2e-31:319:78//AL022724

R-HEM BB1000631//Sequence 28 from patent US 5708157.//6.8e-20:208:80//I80058

45 R-HEM BB1000632//Homo sapiens Cosmid C4, WORKING DRAFT SEQUENCE, 1 ordered pieces.//7.4e-47:457:75//AC004176

R-HEM BB1000637//Human BAC clone RG094H21 from 7q21-q22, complete sequence.//2.9e-45:263:87//AC003085

R-HEM BB1000638//Genomic sequence from Human 6, complete sequence.//9.1e-34:375:73//AC002112

50 R-HEM BB1000643//HS_2242_A2_B07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2242 Col=14 Row=C, genomic survey sequence.//0.010:239:60//AQ065993

R-HEM BB1000649//Homo sapiens RBP56/hTAFII68 gene, exon 7.//8.3e-63:306:100//AB010061

R-HEM BB1000652//Human DNA sequence from PAC 467D16 on chromosome 6p22.3-24.1. Contains the 3' part of the SCA1 (ataxin-1) gene with a poly-glutamine (CAG repeat) polymorphism, the 3' part of the GMPR (GMP reductase, Guanosine 5'-monophosphate oxidoreductase) gene, ESTs and an STS with a polymorphic CA repeat.//3.3e-14:450:64//AL009031

55 R-HEM BB1000665//Arabidopsis thaliana genomic DNA clone

Accession No.

R-HEM BB1000671//Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF127 LIKE gene, and the PPAR for Peroxisome Proliferator Activated Receptor Delta (PPAR-Delta, PPAR-Beta, Nuclear Hormone Receptor 1, NUC1, NUCI, PPARB). Contains three putative CpG islands, ESTs, STSs, GSSs and a ca repeat polymorphism, complete sequence.//7.6e-14:217:71//AL022721

mosome X.//6.8e-58:296:85//Z83313

R-HEM BB1000673//CITBI-E1-2506F20.TR CITBI-E1 Homo sapiens genomic clone 2506F20, genomic survey sequence.//0.98:71:76//AQ264731

R-HEM BB1000684//Human DNA sequence from clone 1158E12 on chromosome Xp11.23-11.4 Contains EST, STS, GSS, CpG island, complete sequence.//2.6e-11:153:77//AL031584

R-nnnnnnnnnnnn//Homo sapiens neuroan1 mRNA, complete cds.//2.0e-50:287:93//AF040723

R-HEM BB1000705//Homo sapiens chromosome 19, cosmid R30538, complete sequence.//3.4e-18:340:65//AC005943

R-HEM BB1000706//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 462C17, WORKING DRAFT SEQUENCE.//4.7e-10:358:64//AL033380

R-HEM BB1000709//RPCI11-79A8.TV RPCI11 Homo sapiens genomic clone R-79A8, genomic survey sequence.//1.4e-40:262:89//AQ282374

R-HEM BB1000725//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MGN6, complete sequence.//0.00018:386:60//AB017066

R-HEM BB1000726//Homo sapiens PAC clone DJ1185I07 from 7q11.23-q21, complete sequence.//1.5e-48:316:88//AC004990

R-HEM BB1000738//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//7.1e-53:382:85//AC004875

R-HEM BB1000749//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//6.5e-51:438:80//AC005069

R-HEM BB1000763//Plasmid Col Ib-P9 (from E.coli K12) colicin Ib promoter region and 5' coding region.//1.0:115:63//K02071

R-HEM BB1000770//Human Rhesus blood group antigen (RHCE) gene, intron 6, partial sequence.//5.6e-24:183:86//U83205

R-HEM BB1000781//Homo sapiens Xp22 PACs RPC11-263P4 and RPC11-164K3 complete sequence.//0.00054:154:67//AC003046

R-HEM BB1000789//RPCI11-2I14.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-2I14, genomic survey sequence.//3.0e-09:299:64//B63628

R-HEM BB1000790//Human Chromosome 16 BAC clone CIT987SK-A-362G6, complete sequence.//4.5e-46:185:85//U95740

R-HEM BB1000794//HS_3253_A1_G06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3253 Col=11 Row=M, genomic survey sequence.//5.7e-13:172:65//AQ216291

R-HEM BB1000807

R-HEM BB1000810//Human BAC clone RG114A06 from 7q31, complete sequence.//1.3e-24:385:71//AC002542

R-HEM BB1000821

R-HEM BB1000822//CITBI-E1-2517E13.TF CITBI-E1 Homo sapiens genomic clone 2517E13, genomic survey sequence.//4.5e-08:278:64//AQ279944

R-HEM BB1000826//Homo sapiens genomic DNA, chromosome 21q11.1, segment 14/28, WORKING DRAFT SEQUENCE.//1.2e-44:521:72//AP000043

R-HEM BB1000827//Homo sapiens clone DJ0981O07, complete sequence.//6.8e-43:319:84//AC006017

R-HEM BB1000831//HS_3247_B2_A09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3247 Col=18 Row=B, genomic survey sequence.//5.5e-74:381:96//AQ223850

R-HEM BB1000835//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//4.2e-17:167:80//AL021368

R-HEM BB1000840//Homo sapiens clone DJ1039L24, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.9e-26:220:73//AC005283

R-HEM BB1000848//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//7.8e-39:356:79//AC004086

R-HEM BB1000852//HS_3075_A2_B07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=14 Row=C, genomic survey sequence.//3.4e-11:151:75//AQ138816

R-HEM BB1000870//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 72E17, WORKING DRAFT SEQUENCE.//1.8e-44:454:75//AL033523

R-HEM BB1000876//Human DNA sequence from clone 72E17, WORKING DRAFT SEQUENCE, 1 unordered piece.//0.0016:221:65//AQ244741

R-HEM BB1000883//Human DNA sequence from clone 72E17, WORKING DRAFT SEQUENCE, 1 unordered piece.//0.62:238:62//

AC005621

R-HEM BB1000887//Synthetic human/adenovirus type 5 recombination junction.//9.9e-24:275:76//M34061

R-HEM BB1000888//CIT-HSP-2282A13.TR CIT-HSP Homo sapiens genomic clone 2282A13, genomic survey sequence.//2.4e-05:310:60//AQ000826

5 R-HEM BB1000890//Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 20 unordered pieces.//6.5e-44:305:84//AC005995

R-HEM BB1000893//Homo sapiens BAC clone RG363E19 from 7q31.1, complete sequence.//3.7e-30:265:80//AC004492

10 R-HEM BB1000908//RPCI11-13P12.TV RPCI-11 Homo sapiens genomic clone RPCI-11-13P12, genomic survey sequence.//0.98:183:61//B76199

R-HEM BB1000910//Homo sapiens Chromosome 22q11.2 Cosmid Clone 50d10 In IGLC Region, complete sequence.//1.7e-28:302:76//AC000024

R-HEM BB1000913//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.//4.1e-34:314:76//AC003037

15 R-HEM BB1000915//Human chromosome 16p11.2-p12 BAC clone CIT987SK-224D6 complete sequence.//6.3e-09:536:59//U95739

R-HEM BB1000917//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 169I5, WORKING DRAFT SEQUENCE.//1.6e-47:234:86//Z93015

R-HEM BB1000927

20 R-HEM BB1000947//CIT-HSP-2287M13.TF CIT-HSP Homo sapiens genomic clone 2287M13, genomic survey sequence.//0.090:115:69//B99228

R-HEM BB1000959//Homo sapiens chromosome 17, clone HRPC905N1, complete sequence.//5.7e-89:544:90//AC003098

25 R-HEM BB1000973//Arabidopsis thaliana chromosome II BAC F2I9 genomic sequence, complete sequence.//0.038:377:58//AC005560

R-HEM BB1000975//Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence.//1.0e-05:342:62//AC006234

R-HEM BB1000981//CIT-HSP-2386J13.TF.1 CIT-HSP Homo sapiens genomic clone 2386J13, genomic survey sequence.//1.1e-18:231:74//AQ239443

30 R-HEM BB1000985//HS_3184_A1_D12_T7 CIT Approved Human Genomic Sperm Library D. Homo sapiens genomic clone Plate=3184 Col=23 Row=G, genomic survey sequence.//6.3e-52:286:95//AQ150008

R-HEM BB1000991

R-HEM BB1000996//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence.//1.4e-42:343:81//AC002368

35 R-HEM BB1001004

R-HEM BB1001008//CITBI-E1-2504L23.TF CITBI-E1 Homo sapiens genomic clone 2504L23, genomic survey sequence.//3.1e-57:317:94//AQ262056

R-HEM BB1001011//HS_3017_B1_G03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3017 Col=5 Row=N, genomic survey sequence.//7.3e-34:237:86//AQ101944

40 R-HEM BB1001014//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 460J8, WORKING DRAFT SEQUENCE.//2.4e-49:417:80//AL031662

R-HEM BB1001020//Homo sapiens Xp22 BAC GS-377014 (Genome Systems Human BAC library) complete sequence.//7.6e-41:303:76//AC002549

R-HEM BB1001024//Homo sapiens (subclone 2_g5 from P1 H16) DNA sequence.//7.4e-48:341:85//L48475

45 R-HEM BB1001037//Homo sapiens 22q11 BAC Clone 489d1 In MDR Region, complete sequence.//2.0e-50:416:82//AC005527

R-HEM BB1001047//Homo sapiens chromosome 19, cosmid R31973, complete sequence.//8.4e-22:288:71//AC004699

R-HEM BB1001051//H.sapiens mRNA for FAN protein.//7.1e-18:114:98//X96586

50 R-HEM BB1001056//Homo sapiens clone DJ0953A04, WORKING DRAFT SEQUENCE, 5 unordered pieces.//6.1e-94:520:93//AC006014

R-HEM BB1001058//Homo sapiens clone UWGC:y17c131 from 6p21, complete sequence.//1.1e-56:242:82//AC004187

55 R-HEM BB1001060//Human Tigger1 transposable element, complete consensus sequence.//4.2e-66:323:81//U49973

R-HEM BB1001063//Human DNA sequence from BAC clone

R-HEM BB1001068//Human DNA sequence from BAC clone

R-HEM BB1001068//Human DNA sequence from BAC clone 100512.9//AF034803

R-HEMBB1001096//Human DNA sequence from PAC 246O8, between markers DXS6791 and DXS8038 on chromosome X contains ESTs.//2.4e-13:225:69//Z76735

R-HEMBB1001102//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.4e-35:295:80//AL022577

R-HEMBB1001105//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 462O23, WORKING DRAFT SEQUENCE.//7.9e-46:380:80//AL031431

R-HEMBB1001114//Homo sapiens DNA sequence from PAC 119E23 on chromosome Xq25-q27.1. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2), 5'UTR. ESTs, STS.//1.1e-38:306:84//Z99570

R-HEMBB1001117//RPCI11-35I8.TK RPCI-11 Homo sapiens genomic clone RPCI-11-35I8, genomic survey sequence.//1.5e-08:67:100//AQ047113

R-HEMBB1001119//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//9.0e-26:481:67//AC003071

R-HEMBB1001126//Human DNA sequence from clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.045:127:69//Z99495

R-HEMBB1001133//Human SS-A/Ro ribonucleoprotein autoantigen 60 kd subunit mRNA, complete cds.//5.0e-23:285:73//M25077

R-HEMBB1001137//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-09, complete sequence.//2.5e-07:334:62//AL010222

R-HEMBB1001142//Human BAC clone RG164L14 from 7q21-q22, complete sequence.//2.5e-46:412:79//AC002564

R-HEMBB1001151//Mus musculus IFN alpha-treated embryonic fibroblast mRNA.//1.8e-11:148:77//J51904

R-HEMBB1001153//RPCI11-10L7.TP RPCI-11 Homo sapiens genomic clone RPCI-11-10L7, genomic survey sequence.//2.3e-34:213:82//B71766

R-HEMBB1001169//Homo sapiens chromosome 17, clone HCIT39G8, complete sequence.//0.040:465:56//AC003070

R-nnnnnnnnnnnn//Sequence 1 from patent US 5618695.//2.8e-15:176:80//I40055

R-HEMBB1001177

R-HEMBB1001182//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-52, complete sequence.//1.9e-05:174:70//AL010226

R-HEMBB1001199

R-HEMBB1001208

R-HEMBB1001209//RPCI11-41E13.TP RPCI-11 Homo sapiens genomic clone RPCI-11-41E13, genomic survey sequence.//1.1e-95:473:97//AQ029098

R-HEMBB1001210//Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence.//6.2e-08:412:61//AC005199

R-HEMBB1001218//RPCI11-13L8.TV RPCI-11 Homo sapiens genomic clone RPCI-11-13L8, genomic survey sequence.//1.0e-46:498:74//B75158

R-HEMBB1001221//RPCI11-62024.TJ RPCI11 Homo sapiens genomic clone R-62024, genomic survey sequence.//3.2e-09:215:68//AQ200950

R-HEMBB1001234

R-HEMBB1001242

R-HEMBB1001249//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.4e-33:361:72//AC005377

R-HEMBB1001253//Homo sapiens chromosome 3, olfactory receptor pseudogene cluster 1, complete sequence, and myosin light chain kinase (MLCK) pseudogene, partial sequence.//3.8e-105:517:98//AF042089

R-HEMBB1001254//Methanococcus jannaschii section 3 of 150 of the complete genome.//0.96:203:61//U67461

R-HEMBB1001267//Human DNA sequence from clone 14O9 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032, complete sequence.//2.8e-39:320:80//Z98046

R-HEMBB1001271//Homo sapiens chromosome 17, clone hRPK.349_A_8, complete sequence.//3.9e-47:494:75//AC005544

R-HEMBB1001282//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 184.I9, WORKING DRAFT SEQUENCE.//0.0011:67:73//A_001407

R-HEMBB1001283

R-HEMBB1001284//Homo sapiens chromosome 17, clone hRPK.349_A_8, complete sequence.//2.0e-

31:301:78//AC005601

R-HEM BB1001294//Homo sapiens BAC clone RG060N22 from 7q21, complete sequence.//0.053:283:60//AC003083

R-HEM BB1001302

5 R-HEM BB1001304//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 27K12, WORKING DRAFT SEQUENCE.//6.3e-15:396:64//AL033397

R-HEM BB1001314//Homo sapiens genomic DNA, 21q region, clone: f30F8SpN6, genomic survey sequence.//3.4e-42:293:86//AG013777

R-HEM BB1001315//Human NFE genomic fragment.//7.5e-30:243:78//M98511

10 R-HEM BB1001317//Homo sapiens chromosome 17, clone hRPC.1028_K_7, complete sequence.//2.3e-39:301:82//AC004585

R-HEM BB1001326//HS_3054_A1_F12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=23 Row=K, genomic survey sequence.//0.90:117:63//AQ106096

15 R-HEM BB1001331//Mus musculus mRNA for hepatoma-derived growth factor, complete cds, strain:BALB/c.//0.037:103:77//D63850

R-HEM BB1001335//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.//9.1e-19:229:77//AC003037

R-HEM BB1001337

R-HEM BB1001339//Homo sapiens FSHD-associated repeat DNA, proximal region.//2.9e-45:551:72//U85056

20 R-HEM BB1001346//Homo sapiens phenylalanine-tRNA synthetase (FARS1) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//2.7e-59:292:99//AF097441

R-HEM BB1001348//Homo sapiens clone DJ0691F11, WORKING DRAFT SEQUENCE, 11 unordered pieces.//9.1e-41:326:82//AC004859

25 R-HEM BB1001356//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 424J12, WORKING DRAFT SEQUENCE.//1.8e-11:213:67//Z82207

R-HEM BB1001364//HS_3050_A2_F05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3050 Col=10 Row=K, genomic survey sequence.//1.8e-21:158:91//AQ133940

R-HEM BB1001366//Homo sapiens chromosome 10 clone CIT987SK-1188I5 map 10p11.2-10p12.1, complete sequence.//4.1e-37:419:73//AC005876

30 R-HEM BB1001367//Human Chromosome 16 BAC clone CIT987SK-A-234F9, complete sequence.//9.5e-15:201:75//U91326

R-HEM BB1001369//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 477J10, WORKING DRAFT SEQUENCE.//1.8e-28:224:83//AL021686

35 R-HEM BB1001380//HS_2267_B1_F11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2267 Col=21 Row=L, genomic survey sequence.//4.0e-14:100:95//AQ084896

R-HEM BB1001384//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, complete cds.//9.6e-55:312:81//AF071314

R-HEM BB1001387//Homo sapiens chromosome 9, P1 clone 8660 (LBNL H105), complete sequence.//1.0:166:63//AC003953

40 R-HEM BB1001394//Homo sapiens chromosome 17, clone hRPK.215_E_13, complete sequence.//1.4e-55:494:76//AC005549

R-HEM BB1001410//Homo sapiens PAC clone DJ1102B04 from 7q11.23-7q21, complete sequence.//0.011:208:63//AC006204

45 R-HEM BB1001424//Homo sapiens, WORKING DRAFT SEQUENCE, 76 unordered pieces.//1.5e-22:325:69//AC002370

R-HEM BB1001426//Homo sapiens 12q24 PAC RPCI3-424M6 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.3e-46:328:84//AC002350

R-HEM BB1001429//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0481P14; HTGS phase 1, WORKING DRAFT SEQUENCE, 7 unordered pieces.//6.6e-105:550:95//AC006160

50 R-HEM BB1001436

R-HEM BB1001443//HS_2228_A1_B05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=9 Row=C, genomic survey sequence.//0.37:173:62//AQ066934

R-HEM BB1001449//Homo sapiens clone DJ1129E22, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.7e-23:339:69//AC005522

55 R-HEM BB1001454//Homo sapiens chromosome 5, P1 clone 1307e8 (LBNL H60) complete sequence.//1.1e-39:299:84//AC005355

R-HEM BB1001455//Homo sapiens chromosome 1, P1 clone 1307e8 (LBNL H60) complete sequence.//1.1e-39:299:84//AC005355

R-HEM BB1001456

R-HEM BB1001463//Homo sapiens PAC clone DJ0777023 from 7p14-p15, complete sequence.//1.2e-50:317:89//AC005154

R-HEM BB1001464//CIT-HSP-2370C10.TF CIT-HSP Homo sapiens genomic clone 2370C10, genomic survey sequence.//0.20:95:71//AQ107941

5 R-HEM BB1001482//Mus musculus clone OST20235, genomic survey sequence.//4.3e-09:192:70//AF046762

R-HEM BB1001500//Human DNA sequence from PAC 465G10 on chromosome X contains Menkes Disease (ATP7A) putative Cu⁺⁺-transporting P-type ATPase exons 2 to 21, PGAM-B, ESTs.//1.9e-21:253:70//Z94801

R-HEM BB1001521//Mus musculus clone OST1209, genomic survey sequence.//7.5e-30:332:75//AF046642

10 R-HEM BB1001527//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces.//9.5e-55:483:76//AC005000

R-HEM BB1001531//Human BAC clone 7E17 from 12q, complete sequence.//1.3e-08:159:71//AC002070

R-HEM BB1001535//Human DNA sequence from cosmid E127C11 on chromosome 22q11.2-qter contains STS.//4.0e-30:286:79//Z74581

15 R-HEM BB1001536//Homo sapiens cosmid clone LUCA16 from 3p21.3, complete sequence.//1.6e-39:342:80//U73169

R-HEM BB1001537//Genomic sequence from Human 9q34, complete sequence.//3.7e-41:361:77//AC000394

R-HEM BB1001555//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-485G10, complete sequence.//0.34:212:61//AC003049

R-HEM BB1001562//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-328A3, complete sequence.//8.0e-40:267:88//AC002301

20 R-HEM BB1001564//Homo sapiens clone DJ0414A15, WORKING DRAFT SEQUENCE, 9 unordered pieces.//5.1e-30:286:76//AC005225

R-HEM BB1001565//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12 unordered pieces.//2.5e-15:194:75//AC004840

25 R-HEM BB1001585//Human DNA sequence from clone 790B6 on chromosome 20p11.22-12.2. Contains STSs and GSSs, complete sequence.//2.6e-33:234:79//AL031677

R-HEM BB1001586//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces.//2.7e-30:371:74//AC005236

R-HEM BB1001588//Homo sapiens Xp22 GS-52411 (Genome Systems Human BAC library), complete sequence.//8.0e-32:323:73//AC003106

30 R-HEM BB1001603//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-59, complete sequence.//0.034:302:59//AL010235

R-HEM BB1001618//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and OpG island.//7.1e-31:503:68//Z93023

35 R-HEM BB1001619//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence.//3.7e-50:539:72//AC002368

R-HEM BB1001630//Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome 6 HindIII fragment ESTs. polymorphic CA repeat, CpG island, CpG island genomic fragments.//1.3e-27:228:82//Z86062

40 R-HEM BB1001635//Homo Sapiens Chromosome X clone bW XD90, complete sequence.//1.5e-23:407:69//AC004075

R-HEM BB1001637//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence.//3.9e-54:519:74//AC002368

R-HEM BB1001641//Human DNA sequence from clone 133H11 on chromosome 6p24. Contains STSs, GSSs and genomic marker D6S410, complete sequence.//1.9e-08:464:60//AL024506

45 R-HEM BB1001653//Homo sapiens chromosome 17, clone HCIT3L16, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.8e-39:318:82//AC002344

R-HEM BB1001665//***ALU WARNING: Human Alu-Sp subfamily consensus sequence.//3.8e-47:283:90//U14572

R-HEM BB1001668

50 R-HEM BB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds.//1.8e-115:573:97//AB014546

R-HEM BB1001684//Sequence 1 from patent US 5700927.//1.9e-40:343:77//I86429

R-HEM BB1001685//Homo sapiens chromosome 17, clone hRPK.721_K_1, complete sequence.//2.6e-43:31:83//AC005411

R-HEM BB1001695

55 R-HEM BB1001704//CIT-HSP-2324C15.TR CIT-HSP Homo sapiens genomic clone 2324C15 genomic survey sequence.//0.0074:259:58//AQ008701

R-HEM BB1001707//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-319E8, complete sequence.//7.7e-32:241:76//AC004020

R-HEM BB1001717//CIT-HSP-2378C19.TF CIT-HSP Homo sapiens genomic clone 2378C19, genomic survey sequence.//4.8e-35:228:89//AQ108992

5 R-HEM BB1001735//Homo sapiens chromosome 5, BAC clone 114k9 (LBNL H94), complete sequence.//1.8e-10:80:90//AC005613

R-HEM BB1001736//CIT-HSP-2369K6.TF CIT-HSP Homo sapiens genomic clone 2369K6, genomic survey sequence.//9.9e-38:242:90//AQ075221

10 R-HEM BB1001747//Homo sapiens cosmids Qc14E2, Qc12H12, Qc11F9, Qc10G9, LA1733 and Qc17B8 from Xq28, complete sequence.//3.3e-60:366:80//U82671

R-HEM BB1001749//Homo sapiens chromosome 17, clone hRPK.259_G_18, complete sequence.//1.4e-60:242:92//AC005829

R-HEM BB1001753//RPC11-59J22.TK RPC11 Homo sapiens genomic clone R-59J22, genomic survey sequence.//6.2e-08:281:64//AQ200046

15 R-HEM BB1001756//Homo sapiens BAC clone RG293F17 from 7p15-p21, complete sequence.//3.1e-18:395:67//AC004130

R-HEM BB1001760//Homo sapiens genomic DNA, chromosome 21q11.1, segment 21/28, WORKING DRAFT SEQUENCE.//9.9e-18:416:64//AP000050

20 R-HEM BB1001762//Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (IAalpha) and major histocompatibility protein class II beta chain (IEbeta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-like (NG10), hypothetical protein (NG8), and butyrophilin-like (NG11) genes, partial cds; NG12 pseudogene, partial sequence; and hypothetical butyrophilin-like protein (NG13) gene, partial cds.//0.21:521:57//AF050157

25 R-HEM BB1001785//Torulopsis glabrata mitochondrial intergenic region ATPase 6 -ATPase 9 genes.//0.00073:189:65//X02170

R-HEM BB1001797//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.0049:322:62//AC005140

R-HEM BB1001802//Human desmin gene, complete cds.//8.1e-95:510:93//M63391

30 R-HEM BB1001812//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 356B8, WORKING DRAFT SEQUENCE.//1.3e-71:368:96//Z98882

R-HEM BB1001816//Homo sapiens chromosome 21 PAC LLNLP704G1150Q13.//8.4e-21:164:76//AJ006996

R-HEM BB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds.//1.7e-104:498:98//AF056209

35 R-HEM BB1001836//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//9.2e-44:388:71//AC005328

R-HEM BB1001839

R-HEM BB1001850//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP10, complete sequence.//0.00093:488:60//AB005241

R-HEM BB1001863//Human poly(ADP-ribose) polymerase gene, 5' end.//1.2e-16:458:65//M60436

40 R-HEM BB1001867//Human DNA sequence from cosmid U25D11, between markers DXS366 and DXS87 on chromosome X.//5.0e-31:399:74//Z68327

R-HEM BB1001868//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN8, complete sequence.//0.26:303:59//AB020754

45 R-HEM BB1001869//Homo sapiens chromosome 17, clone hCIT529I10, complete sequence.//7.0e-37:285:85//AC002553

R-HEM BB1001872//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y44F5, WORKING DRAFT SEQUENCE.//0.093:367:58//AL009027

R-HEM BB1001874

50 R-HEM BB1001875//Lactococcus lactis DPC3147 plasmid pMRC01, complete plasmid sequence.//0.037:406:60//AE001272

R-HEM BB1001880//Homo sapiens chromosome 17, clone hRPK.235_I_10, complete sequence.//1.3e-49:461:77//AC005922

R-HEM BB1001899//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y116A8, WORKING DRAFT SEQUENCE.//0.56:295:60//Z98858

55 R-HEM BB1001905//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y738F9 WORKING DRAFT SEQUENCE.//1.2e-08:181:75//AF001115

R-HEM BB1001906

R-HEM BB1001908//Homo sapiens chromosome 17, clone hRPK.235_I_10, complete sequence.//2.3e-36:274:76//AC001231

R-HEM BB1001910//Homo sapiens chromosome 17, clone HCIT39G8, complete sequence.//3.5e-41:408:76//AC003070

R-HEM BB1001911//Homo sapiens *** SEQUENCING IN PROGRESS *** , WORKING DRAFT SEQUENCE //6.1e-64:310:89//AJ011929

5 R-HEM BB1001915//Mouse mRNA for arylhydrocarbon receptor, complete cds.//2.0e-20:220:78//D38417

R-HEM BB1001921//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1141E15, WORKING DRAFT SEQUENCE //1.9e-47:410:80//AL034422

R-HEM BB1001922//Homo sapiens chromosome 17, clone HCIT421K24, complete sequence.//6.2e-32:378:74//AC004099

10 R-HEM BB1001925//Human Chromosome 11 overlapping pacs pDJ235k10 and pDJ239b22, WORKING DRAFT SEQUENCE, 17 unordered pieces.//8.2e-41:304:84//AC000406

R-HEM BB1001930//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 10/11 //8.3e-12:202:69//AB020867

R-HEM BB1001944//P.falciparum gene for beta subunit RNA polymerase.//0.00090:264:62//X75544

15 R-HEM BB1001945//Swietenia humilis DNA for simple tandem repeat (242bp).//0.056:224:62//AJ000408

R-HEM BB1001947//RPC111-60L13.TJ RPC111 Homo sapiens genomic clone R-60L13, genomic survey sequence.//7.4e-23:146:94//AQ202335

R-HEM BB1001950//Human DNA sequence from clone 415G2 on chromosome 22 Contains synapsin IIIa exon 1, EST and GSS, complete sequence.//0.57:115:68//Z83846

20 R-HEM BB1001952//Homo Sapiens Chromosome X clone bW XD171, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.6e-36:283:84//AC004676

R-HEM BB1001953//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//8.9e-60:334:82//AC005037

R-HEM BB1001957//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.9e-56:518:77//AC005077

25 R-HEM BB1001962//Homo sapiens chromosome 16, BAC clone 462G18 (LANL), complete sequence.//3.2e-19:157:86//AC005736

R-HEM BB1001967//Homo sapiens DNA for amyloid precursor protein, complete cds.//5.7e-68:314:89//D87675

R-HEM BB1001973//Homo sapiens *** SEQUENCING IN PROGRESS *** from PAC E7.1 / cosmid 40M1, WORKING DRAFT SEQUENCE //1.4e-37:484:70//AJ009617

30 R-HEM BB1001983//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 215D11, WORKING DRAFT SEQUENCE.//2.1e-28:286:75//AL034417

R-HEM BB1001988//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1112F19, WORKING DRAFT SEQUENCE //6.9e-29:203:88//AL034420

35 R-HEM BB1001990//Homo sapiens full-length insert cDNA clone ZC33G03 //7.8e-95:456:99//AF086192

R-HEM BB1001996

R-HEM BB1001997//Homo sapiens clone RG050N15, WORKING DRAFT SEQUENCE, 26 unordered pieces.//6.4e-26:162:83//AC005055

R-HEM BB1002002//Human DNA sequence from PAC 2A2 on chromosome X contains ESTs.//8.2e-83:362:93//Z84816

40 R-HEM BB1002005//Homo sapiens chromosome 3p clone RPC15-1034C16, WORKING DRAFT SEQUENCE, 45 unordered pieces.//8.5e-36:291:83//AC005903

R-HEM BB1002009//Homo sapiens clone DJ0828F13, complete sequence.//5.6e-08:307:65//AC004904

R-HEM BB1002015//HS-1039-A1-C10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 821 Col=19 Row=E, genomic survey sequence.//1.9e-05:375:62//B36336

45 R-HEM BB1002042//CIT-HSP-2313E13.TF CIT-HSP Homo sapiens genomic clone 2313E13, genomic survey sequence.//0.34:241:62//AQ028389

R-HEM BB1002043//Homo sapiens chromosome 21, P1 clone LBL#8 (LBNL H8), complete sequence.//7.4e-35:297:82//AC005612

50 R-HEM BB1002044//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//5.8e-96:582:90//AC005740

R-HEM BB1002045//Homo sapiens chromosome 19, cosmid F22676, complete sequence.//4.7e-63:575:77//AC005778

R-HEM BB1002049//Human Chromosome X clone bW XD187, complete sequence.1/1.9e-21:384:64//AC004383

55 R-HEM BB1002050//Homo sapiens chromosome 17, clone hRPK.112 J. 9. complete sequence //2.5e-37:368:76//AC005553

R-HEM BB1002069//Homo sapiens chromosome 19, cosmid R33516, complete sequence.//2.3e-73:449:84//AC004799

R-HEM BB1002092//Homo sapiens chromosome 17, clone hRPK.269_G_24, complete sequence.//3.8e-45:307:87//AC005828

5 R-HEM BB1002094//Homo sapiens chromosome 19, cosmid R30538, complete sequence.//3.1e-47:457:76//AC005943

R-HEM BB1002115//HS_2223_B1_G10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2223 Col=19 Row=N, genomic survey sequence.//3.0e-58:295:98//AQ152279

R-HEM BB1002139//***ALU WARNING: Human Alu-Sq subfamily consensus sequence.//6.6e-49:283:93//U14573

10 R-HEM BB1002142//Homo sapiens clone DJ0813F11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.1e-45:451:76//AC006006

R-HEM BB1002152//Homo sapiens chromosome 10 clone CIT987SK-1079E16 map 10q25, complete sequence.//1.3e-57:359:81//AC005881

R-HEM BB1002189//Human Chromosome 11 pac pDJ392a17, complete sequence.//4.5e-43:420:77//AC000385

15 R-HEM BB1002190//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//8.2e-33:340:64//AC004913

R-HEM BB1002193//Sequence 5 from patent US 5709858.//3.2e-23:154:92//I80846

R-HEM BB1002217//Homo sapiens clone HS19.2 Alu-Ya5 sequence.//2.6e-52:415:81//AF015148

R-HEM BB1002218//, complete sequence.//3.4e-17:178:82//AC005300

20 R-HEM BB1002232//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0052122; HTGS phase 1, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.6e-55:292:88//AC004599

R-HEM BB1002247//Homo sapiens chromosome 17, clone hRPK.259_G_18, complete sequence.//2.9e-13:227:70//AC005829

25 R-HEM BB1002249//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 455J7, WORKING DRAFT SEQUENCE.//1.1e-06:284:64//AL031733

R-HEM BB1002254//Human Chromosome X, WORKING DRAFT SEQUENCE, 6 unordered pieces.//6.3e-104:593:91//AC002415

R-HEM BB1002255//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 292E10, WORKING DRAFT SEQUENCE.//2.1e-40:284:85//Z93930

30 R-HEM BB1002266//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-10, complete sequence.//1.3e-09:371:63//AL010216

R-HEM BB1002280//Homo sapiens PAC clone DJ0545C24 from 7q21-q22, complete sequence.//1.3e-39:247:86//AC004534

R-HEM BB1002300//Human Chromosome 11 Cosmid cSRL30h11, complete sequence.//4.1e-84:549:86//U73642

35 R-HEM BB1002306//Homo sapiens BAC clone RG136N17 from 7p15-p21, complete sequence.//2.5e-10:164:71//AC004129

R-HEM BB1002327//Homo sapiens BAC clone GS539F22 from 7p12-p14, complete sequence.//0.39:365:59//AC005028

R-HEM BB1002329//HS-1049-B1-D05-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 771 Col=9 Row=H, genomic survey sequence.//0.96:180:58//B39313

40 R-HEM BB1002340//Homo sapiens PAC clone DJ0659J06 from 7q33-q35, complete sequence.//7.9e-17:258:73//AC004849

R-HEM BB1002342//Homo sapiens mRNA for putative thioredoxin-like protein.//6.9e-96:479:97//AJ010841

45 R-HEM BB1002358//Human Xp22 BAC CT-285I15 (from CalTech/Research Genetics), PAC RPC11-27C22 (from Roswell Park Cancer Center), and Cosmid U35B5 (from Lawrence Livermore), complete sequence.//2.3e-53:309:83//AC002366

R-HEM BB1002359//Homo sapiens clone NH0486I22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.9e-27:350:74//AC005038

50 R-HEM BB1002364//Homo sapiens Xp22 PAC RPC11-108M6 (Roswell Park Cancer Center PAC library) complete sequence.//8.6e-53:302:79//AC003036

R-HEM BB1002371//Human gene for catalase (EC 1.11.1.6) exon 11 mapping to chromosome 11, band p13.//3.2e-38:199:100//X04094

R-HEM BB1002381//Homo sapiens (JH8) mRNA, partial cds.//3.2e-07:120:78//AF072467

55 R-HEM BB1002383//Human DNA sequence from cosmid U19H10 on chromosome X. Contains ESTs and CA repeat.//0.98:351:58//AL021182

R-HEM BB1002387//HS_1052_B2_G10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=1052 Col=2 Row=N, genomic survey sequence.//2.1e-57:155:87//B4101

R-HEM BB1002414//Homo sapiens chromosome 11 clone hRPK.269_G_24, complete sequence.//3.4e-25:202:87//AC005881

79//AC005730

R-HEM BB1002425//Homo sapiens chromosome 19, cosmid R33516, complete sequence.//3.6e-60:401:87//AC004799

R-HEM BB1002442//Homo sapiens clone UWGC:r9a from 6p21, complete sequence.//3.1e-51:358:81//AC006046

5 R-HEM BB1002453//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 86D1, WORKING DRAFT SEQUENCE.//1.4e-115:557:98//AL034349

R-HEM BB1002457//Human DNA sequence from clone 364I22 on chromosome Xq21.31-22.3. Contains an STS and GSSs, complete sequence.//6.3e-37:338:80//AL031012

10 R-HEM BB1002458//Homo sapiens T-cell receptor alpha delta locus from bases 250472 to 501670 (section 2 of 5) of the Complete Nucleotide Sequence.//9.7e-09:314:64//AE000659

R-HEM BB1002477//Arabidopsis thaliana DNA chromosome 4, BAC clone T12H17 (ESSAll project).//0.42:110:74//AL021635

R-HEM BB1002489//Salvelinus fontinalis microsatellite sequence SFO-12.//6.6e-06:167:71//U50302

15 R-HEM BB1002492//RPCI11-74F21.TK RPCI11 Homo sapiens genomic clone R-74F21, genomic survey sequence.//3.1e-14:410:63//AQ238960

R-HEM BB1002495//HS_3220_A2_F07_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3220 Col=14 Row=K, genomic survey sequence.//1.3e-24:137:100//AQ180762

R-HEM BB1002502//Homo sapiens chromosome 17, clone hRPK.346_K_10, complete sequence.//9.6e-81:538:86//AC006120

20 R-HEM BB1002509//Human DNA sequence from clone 581F12 on chromosome Xq21. Contains Eukaryotic Translation Initiation Factor EIF3 P35 Subunit and 60S Ribosomal protein L22 pseudogenes. Contains ESTs, complete sequence.//0.0061:482:57//AL031313

R-HEM BB1002510//HS_2179_A1_F03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2179 Col=5 Row=K, genomic survey sequence.//6.9e-35:423:72//AQ298309

25 R-HEM BB1002520//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 27K12, WORKING DRAFT SEQUENCE.//2.0e-62:201:85//AL033397

R-HEM BB1002522//Homo sapiens chromosome 5, Pac clone 61c2 (LBNL H139), complete sequence.//0.99:323:58//AC004225

R-HEM BB1002531

30 R-HEM BB1002534//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 2/15, WORKING DRAFT SEQUENCE.//1.0e-61:380:79//AP000009

R-HEM BB1002545//RPCI11-2F3.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-2F3, genomic survey sequence.//3.5e-12:414:63//B63283

R-HEM BB1002550

35 R-HEM BB1002556//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0481P14; HTGS phase 1, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.6e-62:299:85//AC006160

R-HEM BB1002579//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1141E15, WORKING DRAFT SEQUENCE.//1.7e-42:286:88//AL034422

R-HEM BB1002582//Homo sapiens clone DJ1119N05, complete sequence.//3.0e-14:426:60//AC004968

40 R-HEM BB1002590//Homo sapiens clone RG132J19, complete sequence.//1.1e-30:392:74//AC005163

R-HEM BB1002596//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 508I15, WORKING DRAFT SEQUENCE.//8.5e-44:335:83//AL021707

R-HEM BB1002600//Homo sapiens 12p13.3 PAC RPCI5-1063M23 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.0e-105:470:96//AC005865

45 R-HEM BB1002601//Homo sapiens chromosome 17, clone HRPC837J1, complete sequence.//1.3e-44:445:77//AC004223

R-HEM BB1002603//Homo sapiens clone UWGC:y23c049 from 6p21, complete sequence.//7.0e-40:321:82//AC006162

50 R-HEM BB1002607//CIT-HSP-2347D7.TF CIT-HSP Homo sapiens genomic clone 2347D7, genomic survey sequence.//1.1e-44:234:98//AQ060197

R-HEM BB1002610//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//7.0e-22:455:65//U91321

R-HEM BB1002613//Homo sapiens 12p13.3 BAC RPCI11-476M19 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//3.0e-72:302:85//AC005908

55 R-HEM BB1002614//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//3.8e-44:445:77//AC004223

R-HEM BB1002615//Homo sapiens chromosome 4, BAC clone C0481P14; HTGS phase 1, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.6e-62:299:85//AC006160

R-HEMBB1002623//Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete sequence//2.4e-41:326:83//AC004953

R-HEMBB1002635//Homo sapiens chromosome 12p13.3 clone RPC111-189M20, WORKING DRAFT SEQUENCE, 39 unordered pieces//2.6e-42:360:80//AC005910

5 R-HEMBB1002664//Homo sapiens chromosome 21q22.3 PAC 171F15, complete sequence//9.1e-51:335:87//AF042090

R-HEMBB1002677//Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein (cg2), and CG7 (cg7) genes, complete cds//0.0011:399:59//AF030694

10 R-HEMBB1002683//Homo sapiens chromosome 21q22.3 PAC 171F15, complete sequence//4.1e-55:515:76//AF042090

R-HEMBB1002684//Human BAC clone RG066D11 from 7q22, complete sequence//1.7e-18:504:62//AC002430

R-HEMBB1002686//Homo sapiens full-length insert cDNA clone ZC65D06//7.0e-85:413:99//AF086217

R-HEMBB1002692//Homo sapiens 12p13.3 BAC RPC111-319E16 (Roswell Park Cancer Institute Human BAC Library) complete sequence//9.8e-69:505:82//AC006206

15 R-HEMBB1002697//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces//0.26:390:58//AC004153

R-HEMBB1002699//Human NFE genomic fragment//8.0e-32:226:79//M98511

R-HEMBB1002702//CIT-HSP-344K23.TVC CIT-HSP Homo sapiens genomic clone 344K23, genomic survey sequence//8.6e-43:351:8011859764

20 R-HEMBB1002705//Plasmodium yoelii rhoptry protein, complete cds//0.0064:454:59//L27838

R-HEMBB1002712//Human DNA sequence from clone 505B13 on chromosome 1p36.2-36.3 Contains CA repeat and GSSs, complete sequence//9.6e-09:187:67//Z98052

R-MAMMA1000009//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces//4.1e-21:201:80//AC005037

25 R-MAMMA1000019//Homo sapiens chromosome 21q22.2 PAC clone P169K17, complete sequence//4.2e-48:306:82//AF015720

R-MAMMA1000020//Human DNA sequence from clone 551E13 on chromosome Xp11.2-11.3 Contains farnesyl pyrophosphate synthetase pseudogene, VT4 protein pseudogene, EST, GSS, complete sequence//1.4e-41:306:86//AL022163

30 R-MAMMA1000025//Human DNA sequence from clone 512B11 on chromosome 6p24-25. Contains the Desmoplakin I (DPI) gene, ESTs, STSs and GSSs, complete sequence//6.1e-36:281:83//AL031058

R-MAMMA1000043//Homo sapiens Chromosome 22q11.2 Cosmid Clone 8c In DGCR Region, complete sequence//1.3e-67:321:88//AC000090

35 R-MAMMA1000045//Homo sapiens chromosome 4 clone B220G8 map 4q21, complete sequence//6.7e-86:559:86//AC004054

R-MAMMA1000055//Branta canadensis CA dinucleotide repeat locus Bcamicr1//0.79:63:77//AF025889

R-MAMMA1000057//Homo sapiens DNA sequence from cosmid ICK0721Q on chromosome 6. Contains a 60S Ribosomal Protein L35A LIKE pseudogene, a gene coding for a 60S Ribosomal Protein L12 LIKE protein in an

40 intron of the HSET gene coding for a Kinesin related protein, the PHF1 (PHF2) gene coding for alternative splice products PHD finger proteins 1 and 2, the gene coding for five different alternatively spliced mRNAs coding for a protein similar to CYTA (CYCY) and identical to a polypeptide coded for by a known patented cDNA, and the first two exons of the gene coding for the human homolog of the rat synaptic ras GTPase-activating protein p135 SynGAP. Contains three predicted CpG islands, ESTs and an STS, complete sequence//1.6e-53:397:83//AL021366

45 R-MAMMA1000069//Homo sapiens clone RG052H06, WORKING DRAFT SEQUENCE, 11 unordered pieces//2.0e-37:295:83//AC005057

R-MAMMA1000084//Homo sapiens chromosome Xp22-135-136 clone GSHB-56711, WORKING DRAFT SEQUENCE, 35 unordered pieces//7.1e-45:296:88//AC005867

50 R-MAMMA1000085

R-MAMMA1000092//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 774G10, WORKING DRAFT SEQUENCE//8.2e-34:539:69//AL034410

R-MAMMA1000103//Homo sapiens chromosome 17, clone hCIT.91_J_4, complete sequence//3.4e-39:297:85//AC003976

55 R-MAMMA1000117//Homo sapiens p47-phox (NCF1) pseudogene, clone P38, exon 5//2.6e-07:162:67//U69641

R-MAMMA1000129//Homo sapiens clone D1076B01, WORKING DRAFT SEQUENCE, 11 unordered pieces//1.1e-37:295:83//AC005057

R-MAMMA1000130//Homo sapiens clone D1076B01, WORKING DRAFT SEQUENCE, 11 unordered pieces//1.1e-37:295:83//AC005057

R-MAMMA1000134//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//9.7e-18:171:80//AC005328

R-MAMMA1000139//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.2e-49:366:75//AC005000

5 R-MAMMA1000143//Homo sapiens *** SEQUENCING IN PROGRESS *** from PAC D9.2, WORKING DRAFT SEQUENCE.//3.9e-56:318:89//AJ009615

R-MAMMA1000155//Human DNA sequence from clone 323M22 on chromosome 22q13.1-13.2. Contains the 5' part of the human ortholog of chicken P52 and mouse H74, and a novel gene coding for a protein similar to KIAA0173 and worm Tubulin Tyrosine Ligase. Contains ESTs, STSs, GSSs, genomic marker D22S418 and putative CpG islands, complete sequence.//2.1e-68:562:78//AL022476

10 R-MAMMA1000163//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//5.3e-06:408:58//AC005089

R-MAMMA1000171//CIT-HSP-2335L20.TR CIT-HSP Homo sapiens genomic clone 2335L20, genomic survey sequence.//1.5e-42:173:89//AQ037381

15 R-MAMMA1000173

R-MAMMA1000175//H.sapiens CpG island DNA genomic MseI fragment, clone 186c5, reverse read cpg186c5.r1b.//0.072:90:72//Z57594

R-MAMMA1000183//Homo sapiens Xp22 BAC GSHB-184P14 (Genome Systems Human BAC library) complete sequence.//1.5e-44:445:75//AC004552

20 R-MAMMA1000198//Homo sapiens clone c102D0968, complete sequence.//1.9e-23:135:85//AF038667

R-MAMMA1000221//HS_3242_B2_H02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3242 Col=4 Row=P, genomic survey sequence.//0.031:167:67//AQ220385

R-MAMMA1000227//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1071N3, WORKING DRAFT SEQUENCE.//4.5e-36:487:71//AL031728

25 R-MAMMA1000241//Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Choroideraemia protein, Tapetochoroidal Dystrophy (TCD) protein). Contains ESTs and an STS, complete sequence.//6.2e-07:445:59//AL022401

R-MAMMA1000251//Homo sapiens chromosome 19, cosmid F23465, complete sequence.//1.6e-25:390:69//AC005266

30 R-MAMMA1000254//Homo sapiens DNA sequence from BAC 1216H12 on chromosome 22q12. Contains a pseudogene with similarity to part of mouse Ninein and the KIAA0609 gene for a protein similar to C. elegans K09C8.4. Contains ESTs, GSSs and a gggt repeat polymorphism, complete sequence.//1.1e-37:327:80//AL008715

R-MAMMA1000257//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1125A11, WORKING DRAFT SEQUENCE.//1.3e-22:281:74//AL034549

35 R-MAMMA1000264//*** SEQUENCING IN PROGRESS *** EPM1/APECED region of chromosome 21, clones A68E8, B127P21, B173L3, B23N8, C1242C9, C579E2, A70B6, B159G9, B175D10, B52C10, C124G1 Note: Sequencing in this region has been discontinued by the Stanford Human Genome Center, WORKING DRAFT SEQUENCE, 50 unordered pieces.//1.7e-29:337:67//AC003656

40 R-MAMMA1000266//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 681N20, WORKING DRAFT SEQUENCE.//7.7e-37:339:80//AL031670

R-MAMMA1000270//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//1.2e-40:283:86//AF001549

45 R-MAMMA1000277//CIT-HSP-516K6.TP CIT-HSP Homo sapiens genomic clone 516K6, genomic survey sequence.//3.0e-29:265:80//B49900

R-MAMMA1000278//Sequence 25 from patent US 5708157 //2.6e-39:282:82//I80056

R-MAMMA1000279//Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence.//1.6e-52:295:84//AC004494

50 R-MAMMA1000284//CITBI-E1-2522B20.TF CITBI-E1 Homo sapiens genomic clone 2522B20, genomic survey sequence.//1.8e-11:288:61//AQ280722

R-MAMMA1000287

R-MAMMA1000302//Homo sapiens chromosome 17, clone hRPK.112_J_9, complete sequence.//4.1e-16:169:77//AC005553

55 R-MAMMA1000307//RPCI11-89L1.TV RPCI11 Homo sapiens genomic clone R-89L1, genomic survey sequence.//1.3e-86:429:97//AQ284795

R-MAMMA1000309//Homo sapiens chromosome 17, cosmid clone 390H2 (LANL), complete sequence.//1.6e-52:295:84//AC004494

R-MAMMA1000311//Homo sapiens chromosome 17, cosmid clone 390H2 (LANL), complete sequence.//1.6e-52:295:84//AC004494

R-MAMMA1000312//Homo sapiens chromosome 17, cosmid clone 390H2 (LANL), complete sequence.//1.6e-52:295:84//AC004494

R-MAMMA1000313//Homo sapiens chromosome 17, cosmid clone 390H2 (LANL), complete sequence.//1.6e-52:295:84//AC004494

R-MAMMA1000314//Homo sapiens chromosome 17, cosmid clone 390H2 (LANL), complete sequence.//1.6e-52:295:84//AC004494

R-MAMMA1000315//Homo sapiens chromosome 17, cosmid clone 390H2 (LANL), complete sequence.//1.6e-52:295:84//AC004494

R-MAMMA1000316//Homo sapiens chromosome 17, cosmid clone 390H2 (LANL), complete sequence.//1.6e-52:295:84//AC004494

R-MAMMA1000317//Homo sapiens chromosome 17, cosmid clone 390H2 (LANL), complete sequence.//1.6e-52:295:84//AC004494

R-MAMMA1000318//Homo sapiens chromosome 17, cosmid clone 390H2 (LANL), complete sequence.//1.6e-52:295:84//AC004494

DRAFT SEQUENCE.//1.3e-43:318:83//Z82207

R-MAMMA1000522//Human DNA sequence from clone 739H11 on chromosome 1p33-34.2 Contains KIAA0237 gene, EST, STS, GSS, complete sequence.//4.4e-13:202:73//AL031289

R-MAMMA1000559//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 169I5, WORKING

DRAFT SEQUENCE.//2.2e-30:245:83//Z93015

R-MAMMA1000565//Homo sapiens chromosome 10 clone LA10NC01_183_B_7 map 10q24, WORKING DRAFT SEQUENCE, 1 ordered pieces.//3.6e-39:281:80//U82205

R-MAMMA1000567//Rattus norvegicus nonmuscle caldesmon mRNA, complete cds.//9.2e-19:216:76//U18419

R-MAMMA1000576

R-MAMMA1000583//Homo sapiens chromosome 17, clone hRPK.112_H_10, complete sequence.//5.4e-53:297:85//AC005666

R-MAMMA1000585//Homo sapiens clone DJ1015P16, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.2e-35:450:71//AC006018

R-MAMMA1000594//Homo sapiens *** SEQUENCING IN PROGRESS *** from cosmid 5L5, WORKING DRAFT SEQUENCE.//4.3e-26:293:75//AJ009613

R-MAMMA1000597//CIT-HSP-2341F4.TF CIT-HSP Homo sapiens genomic clone 2341F4, genomic survey sequence.//0.83:110:70//AQ057131

R-MAMMA1000605//Homo sapiens clone DJ1090E20, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.6e-50:290:86//AC004956

R-MAMMA1000612//CIT-HSP-2334J18.TF CIT-HSP Homo sapiens genomic clone 2334J18, genomic survey sequence.//0.76:132:65//AQ038364

R-MAMMA1000616//Ibalia leucospoides mitochondrion 16S rRNA gene, partial sequence.//6.8e-06:431:59//U06970

R-MAMMA1000621//Human NBR2 mRNA, complete cds.//5.3e-27:258:80//U88573

R-MAMMA1000623

R-MAMMA1000625//Homo sapiens chromosome 19, cosmid R31665, complete sequence.//3.3e-07:325:63//AC005498

R-MAMMA1000643//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 39B17, WORKING DRAFT SEQUENCE.//1.4e-06:236:68//AL023656

R-MAMMA1000664//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0326F06; HTGS phase 1, WORKING DRAFT SEQUENCE, 16 unordered pieces.//1.4e-40:338:81//AC004555

R-MAMMA1000669//Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG island, complete sequence.//1.2e-46:327:86//AL021578

R-MAMMA1000670

R-MAMMA1000672//Human DNA sequence from clone 478D8 on chromosome 6p24. Contains STSs and GSSs, complete sequence.//2.2e-29:328:76//AL031785

R-MAMMA1000684//Mus musculus frizzled-1 mRNA, complete cds.//0.21:247:63//AF054623

R-MAMMA1000696//Human Chromosome X clone bWDX173, WORKING DRAFT SEQUENCE, 2 ordered pieces.//2.7e-46:464:71//AC004387

R-MAMMA1000707//Homo sapiens clone RG219E16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.4e-09:244:66//AC005075

R-MAMMA1000713//Homo sapiens clone DJ0425I02, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.7e-51:439:74//AC005478

R-MAMMA1000714//Homo sapiens BAC clone RG152H24 from 7p15-p21, complete sequence.//2.8e-29:288:75//AC004694

R-MAMMA1000718//Human Xp22 BAC CT-285I15 (from CalTech/Research Genetics), PAC RPCI1-27C22 (from Roswell Park Cancer Center), and Cosmid U35B5 (from Lawrence Livermore), complete sequence.//3.0e-37:231:91//AC002366

R-MAMMA1000720//Homo sapiens chromosome 19, cosmid R33632, complete sequence.//1.4e-35:299:81//AC005781

R-MAMMA1000723//Human DNA sequence from clone 551E13 on chromosome Xp11.2-11.3 Contains farnesyl pyrophosphate synthetase pseudogene, VT4 protein pseudogene, EST, GSS, complete sequence.//3.9e-59:409:79//AL022163

R-MAMMA1000731//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//9.4e-29:560:66//AC005077

R-MAMMA1000732//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//9.4e-29:560:66//AC005077

R-MAMMA1000733//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 732E4, WORKING DRAFT SEQUENCE.//4.1e-29:377:71//AL008722

R-MAMMA1000734//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 191J18, WORKING DRAFT SEQUENCE.//2.0e-108:420:99//AL024507

R-MAMMA1000738//Human V beta T-cell receptor (TCRBV) gene locus.//6.6e-41:347:82//U03115

R-MAMMA1000744//T27O8-T7 TAMU Arabidopsis thaliana genomic clone T27O8, genomic survey sequence.//0.095:367:60//B20150

R-MAMMA1000746//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0135005; HTGS phase 1, WORKING DRAFT SEQUENCE, 23 unordered pieces.//7.4e-95:569:87//AC004661

R-MAMMA1000752//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//1.3e-48:295:84//AC003071

R-MAMMA1000760//Human DNA sequence from clone B79B4 on chromosome 22 Contains CA repeat and GSS, complete sequence.//5.7e-45:347:82//Z82178

R-MAMMA1000761//Homo sapiens cosmid clone LUCA16 from 3p21.3, complete sequence.//1.1e-32:292:80//U73169

R-MAMMA1000775//Homo sapiens chromosome 17, clone hRPK.22_N_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//2.5e-50:467:79//AC005412

R-MAMMA1000776//Human BAC clone GS552A01 from 7q21-q22, complete sequence.//1.0e-63:429:79//AC002454

R-MAMMA1000778//Human DNA sequence from 4PTEL, Huntington's Disease Region, chromosome 4p16.3.//3.5e-25:234:81//Z95704

R-MAMMA1000782//Human DNA sequence from clone 459L4 on chromosome 6p22.3-24.1 Contains EST, STS, GSS, complete sequence.//0.0021:119:74//AL031120

R-MAMMA1000798//Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3.//6.3e-08:269:64//AJ229042

R-MAMMA1000802//Homo sapiens chromosome 19, cosmid R33729, complete sequence.//1.1e-36:261:80//AC005339

R-MAMMA1000831//CIT-HSP-2387J3.TF.1 CIT-HSP Homo sapiens genomic clone 2387J3, genomic survey sequence.//0.68:156:65//AQ240807

R-MAMMA1000839//Homo sapiens chromosome 17, clone hRPK.726_O_12, WORKING DRAFT SEQUENCE, 6 unordered pieces.//4.6e-50:335:86//AC005517

R-MAMMA1000841//Human Chromosome 16 BAC clone CIT987SK-A-972D3, complete sequence.//1.3e-40:322:77//U91323

R-MAMMA1000842//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 341D10, WORKING DRAFT SEQUENCE.//4.1e-44:471:74//Z97985

R-MAMMA1000843//Homo sapiens clone 82F9, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.85:394:60//AC004815

R-MAMMA1000845//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P1, WORKING DRAFT SEQUENCE.//0.54:303:63//AL031744

R-MAMMA1000851//Homo sapiens chromosome X, MeCP2 locus, complete sequence.//1.7e-10:115:83//AF030876

R-MAMMA1000855//Homo sapiens PAC clone 278C19 from 12q, complete sequence.//5.0e-44:352:83//AC004263

R-MAMMA1000856//Homo sapiens chromosome 19, cosmid F24200, complete sequence.//1.8e-10:149:74//AC00461

R-MAMMA1000862//Hepatitis C virus genomic RNA, 3' nontranslated region, partial sequence. clone #16.//8.1e-05:205:66//AF009075

R-MAMMA1000863//Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12, U115B9 (Lawrence Livermore human cosmid library) complete sequence.//2.9e-49:421:80//AC002364

R-MAMMA1000865//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-328A3, complete sequence.//9.1e-41:302:83//AC002301

R-MAMMA1000867//Human BRCA1, Rho7 and vat1 genes, complete cds, and ipf35 gene, partial cds.//1.9e-17:500:61//L78833

R-MAMMA1000875//Homo sapiens chromosome 16, cosmid clone RT99 (LANL), complete sequenced.//1.2e-17:211:74//AC004653

R-MAMMA1000876//Homo sapiens clone RT99

complete sequence.//1.2e-17:211:74//AC004653

R-MAMMA1000877//Homo sapiens DNA sequence from clone RT99B3 on chromosome Xp22.17-Xp22.22. Contains

ESTs STS and CpG island//3.2e-34:354:75//Z93023

R-MAMMA1000880//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-575C2, complete sequence//1.4e-41:411:74//AC002425

R-MAMMA1000883

5 R-MAMMA1000897

R-MAMMA1000905//Homo sapiens chromosome 5, P1 clone 274A11 (LBNL H66), complete sequence//1.3e-73:304:91//AC004506

R-MAMMA1000906//Human DNA from chromosome 19-specific cosmid F14150, genomic sequence, complete sequence//8.4e-23:194:83//AC003110

10 R-MAMMA1000908//Human Chromosome 15q26.1 PAC clone pDJ416i6, complete sequence//1.5e-09:170:71//AC003024

R-MAMMA1000914//Homo sapiens PAC clone DJ0740L10 from 7p13-p14, complete sequence//8.3e-13:323:67//AC005247

15 R-MAMMA1000921//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE//6.8e-28:333:72//AL034379

R-MAMMA1000931//HS_3227_B1_B03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3227 Col=5 Row=D, genomic survey sequence//1.4e-55:443:79//AQ191777

R-MAMMA1000940//Homo sapiens clone RG013F03, WORKING DRAFT SEQUENCE, 6 unordered pieces//2.0e-43:340:84//AC005046

20 R-MAMMA1000941//Homo sapiens chromosome 17, clone 297N7, complete sequence//1.8e-53:330:84//AC002347

R-MAMMA1000942//Human Chromosome X clone bWXD187, complete sequence//1.2e-39:391:74//AC004383

R-MAMMA1000943//Human PAC clone DJ327A19 from Xq25-q26, complete sequence//4.6e-75:566:81//AC002477

25 R-MAMMA1000956//Plasmodium falciparum MAL3P7, complete sequence//0.013:285:59//AL034559

R-MAMMA1000957//Homo sapiens clone RG339C12, WORKING DRAFT SEQUENCE, 10 unordered pieces//5.2e-45:288:90//AC005096

R-MAMMA1000962//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered pieces//2.9e-108:561:96//AC006001

30 R-MAMMA1000968//Homo sapiens PAC clone 278C19 from 12q, complete sequence//3.9e-41:287:87//AC004263

R-MAMMA1000975//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence//9.4e-65:542:79//Z95152

35 R-MAMMA1000979//Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1..333303//3.2e-34:296:80//AJ011930

R-MAMMA1000987//Homo sapiens CC chemokine gene cluster, complete sequence//1.7e-40:255:87//AF088219

40 R-MAMMA1000998//Homo sapiens PAC clone DJ1152D16 from Xq23, complete sequence//2.5e-39:315:73//AC005190

R-MAMMA1001003//Homo sapiens chromosome 10 clone CIT-HSP-1338F24 map 10p11.2-10p12.1, complete sequence//2.4e-52:296:84//AC006101

R-MAMMA1001008//Homo sapiens *** SEQUENCING IN PROGRESS *** WORKING DRAFT SEQUENCE//7.9e-88:432:98//AJ011929

45 R-MAMMA1001021//Homo sapiens PAC clone DJ0859M06 from 7q11, complete sequence//3.8e-39:286:87//AC004910

R-MAMMA1001024//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces//2.0e-31:274:80//AC004913

R-MAMMA1001030//Homo sapiens full-length insert cDNA clone ZD96C01//3.2e-99:469:99//AF088074

50 R-MAMMA1001035//RPCI-1-46G8Sp6 RPCI-1 Homo sapiens genomic clone RPCI-1-46G8Sp6, genomic survey sequence//3.5e-49:270:90//AQ275285

R-MAMMA1001038//Homo sapiens chromosome 3, olfactory receptor pseudogene cluster 1, complete sequence, and myosin light chain kinase (MLCK) pseudogene, partial sequence//1.1e-41:285:87//AF042089

R-nnnnnnnnnnnnn

55 R-MAMMA1001050//Homo sapiens genomic DNA, 237 kb segment from 6p21.3 region including HI A genes WORKING DRAFT SEQUENCE//1.3e-55:334:21//Z94392

R-MAMMA1001051//Homo sapiens genomic DNA, 237 kb segment from 6p21.3 region including HI A genes WORKING DRAFT SEQUENCE//1.3e-55:334:21//Z94392

R-MAMMA1001067//CIT-HSP-2371K20.TF CIT-HSP Homo sapiens genomic clone 2371K20, genomic survey sequence./7.2e-65:946:95//AQ111326

R-MAMMA1001073

R-MAMMA1001074//Homo sapiens BAC clone NH0400O10 from Y, complete sequence.//8.6e-33:457:69//AC006040

R-MAMMA1001075//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence //0.15:325:62//AC004605

R-MAMMA1001078//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence//1.6e-45:344:84//AC005609

R-MAMMA1001082//Human genomic DNA sequence from clone 308O1 on chromosome Xp11.3-11.4. Contains EST, CA repeat, STS, GSS, CpG island.//8.5e-15:413:64//Z93403

R-MAMMA1001091//Sequence 7 from patent US 5468610 //0.0027:159:64//115499

R-MAMMA1001092//Homo sapiens chromosome 17, clone hRPK.372_K_20, complete sequence//2.0e-51:267:82//AC005951

R-MAMMA1001105//Homo sapiens DNA sequence from PAC 119E23 on chromosome Xq25-q27.1. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2),5'UTR. ESTs, STS.//6.9e-22:178:85/Z99570

R-MAMMA1001110//Homo sapiens chromosome 17, clone HRPC1169K15, complete sequence//3.0e-19:141:81//AC003963

R-MAMMA1001126//Human DNA from overlapping chromosome 7 PAC and P1 clones containing the XRCC2 gene, genomic sequence, complete sequence//2.2e-46:462:75//AC003109

R-MAMMA1001133//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 120G22, WORKING DRAFT SEQUENCE.//1.8e-68:455:86//AL031847

R-MAMMA1001139//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y738F9, WORKING DRAFT SEQUENCE.//7.1e-09:i00:84//AL022345

R-MAMMA1001143//Papio hamadryas lipoprotein lipase (LPL) gene, intron 7//1.9e-49:362:85//U73684
R-MAMMA1001145//Homo sapiens chromosome 17, clone hRPK.235_I_10, complete sequence//9.5e-49:512:
74//AC005922

R-MAMMA1001154//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-88D1 ~complete genomic sequence, complete sequence //1.5e-29;305:76//AC002289

R-MAMMA1001161//Human DNA sequence from clone 681J21 on chromosome 1q23.2-24.3 Contains CpG island, complete sequence//1.1e-64:339:90//AL031286

R-MAMMA1001162//Human DNA from cosmid DNA MMDB (f10080) and MMDC (f13544) from chromosome 19q13.3 (obtained by automated sequence analysis)//3.4e-09:243:64//M89651

R-MAMMA1001181//Human Chromosome X clone bWXD173, WORKING DRAFT SEQUENCE, 2 ordered pieces./3.7e-29;351:74//AC004387

R-MAMMA1001186//Homo sapiens chromosome 19, cosmid R28778, complete sequence.//2.2e-25:415:68//AC006125

R-MAMMA1001191//Homo sapiens T-cell receptor alpha delta locus from bases 1000498 to 1071650 (section 5 of 5) of the Complete Nucleotide Sequence//0.99:243:61//AE000662

R-MAMMA1001198//Mus musculus eps15R mRNA, complete cds.//8.0e-57:223:86//U29156

R-MAMMA1001202//Mus musculus clone OST13722, genomic survey sequence.//1.0e-30:220:85//AF046748

R-MAMMA1001203//Homo sapiens chromosome 17, clone hRPK.22_N_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//8.9e-61:567:78//AC005412

R-MAMMA1001206//Homo sapiens chromosome 5, P1 clone 854b11 (LBNL H44), complete sequence//4.6e-08:442:61//AC004763

R-MAMMA1001215//Homo sapiens chromosome 19, CIT-HSP BAC 470n8, complete sequence.//1.3e-117:564:97//AC005393

R-MAMMA1001220//HS-1023-A1-G10-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 802 Col=19 Row=M. genomic survey sequence.//6.0e-16:276:68//B33708

R-MAMMA1001222//F17E12TFB IGF Arabidopsis thaliana genomic clone F17E12, genomic survey sequence.
0.041:277:61//B97762

R-MAMMA1001243

R-MAMMA1001244//HS-1058-A2-G01-MF.abi CIT Human Genomic Sperm Library C Homo-sapiens genomic clone Plate=CT 780 Col=2 Row=M. genomic survey sequence.//3.5e-05:104.74//B43862

R-MAMMA1001249//H.sapiens DNA for matrix attachment region.//0.0013:95:75//Z54221

B MAMMA1001256/H. mar. BAC. 1. GS:BBF18

MMV

[illegible]

R-MAMMA1001268//Human DNA sequence from PAC 225D2 on chromosome Xq21. Contains ESTs, CA repeat.//1.1e-47:352:85//Z95124

R-MAMMA1001271

R-MAMMA1001274//H.sapiens DNA for trapped exon (ID HMC07C06), genomic survey sequence.//3.1e-40:232:93//X88457

R-MAMMA1001280//Homo sapiens full-length insert cDNA clone YW26C09.//1.9e-112:574:95//AF087976

R-MAMMA1001292//Human DNA sequence from clone 1170K4 on chromosome 22q12.2-13.1. Contains three novel genes, one of which codes for a Trypsin family protein with class A LDL receptor domains, and the IL2RB gene for Interleukin 2 Receptor, Beta (IL-2 Receptor, CD122 antigen). Contains a putative CpG island, ESTs, and GSSs, complete sequence.//2.9e-114:582:96//AL022314

R-MAMMA1001296//Human DNA sequence from PAC 487J7 on chromosome 6q21-22.1. Contains an unknown gene coding for three alternative mRNAs. Contains ESTs, STSs, a BAC end-sequence (GSS) and a CA repeat polymorphism.//1.9e-64:268:88//AL008730

R-MAMMA1001298//Homo sapiens chromosome 17, clone hRPK.849_N_15, complete sequence.//1.5e-38:306:83//AC005703

R-MAMMA1001305//Human DNA sequence from PAC 127B20 on chromosome 22q11.2-qter, contains gene for GTPase-activating protein similar to rhoGAP protein, ribosomal protein L6 pseudogene, ESTs and CA repeat.//1.5e-37:306:82//Z83838

R-MAMMA1001322//Homo sapiens DNA sequence from PAC 434O14 on chromosome 1q32.3-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IIRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//2.4e-15:260:71//AL022398

R-MAMMA1001324//Homo sapiens chromosome 19, cosmid F23269, complete sequence.//4.0e-06:90:83//AC005614

R-MAMMA1001330//Human BAC clone RG066D11 from 7q22, complete sequence.//1.4e-45:439:74//AC002430

R-MAMMA1001341//Human DNA sequence from PAC 211D12 on chromosome 20q12-13.2. Contains Krs-2, K+ channel protein, stress responsive.//1.3e-24:137:81//Z93016

R-MAMMA1001343//Human Chromosome 16 BAC clone CIT987SK-A-17E1, complete sequence.//5.4e-51:197:89//AC002041

R-MAMMA1001346//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-233A8, complete sequence.//0.99:182:64//AC004685

R-MAMMA1001383//Homo sapiens clone 82F9, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.9e-42:303:86//AC004815

R-MAMMA1001388//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 508I15, WORKING DRAFT SEQUENCE.//1.5e-44:324:83//AL021707

R-MAMMA1001397//Homo sapiens genomic DNA, chromosome 21q11.1, segment 15/28, WORKING DRAFT SEQUENCE.//2.0e-39:254:89//AP000044

R-MAMMA1001408//Homo sapiens chromosome 12q24.1, WORKING DRAFT SEQUENCE, 33 unordered pieces.//9.4e-36:251:88//AC005805

R-MAMMA1001411//T15F1-T7.1 TAMU Arabidopsis thaliana genomic clone T15F1, genomic survey sequence.//1.0:98:71//AQ248928

R-MAMMA1001419//Homo sapiens translation initiation factor 4e mRNA, complete cds.//4.8e-18:117:96//AF038957

R-MAMMA1001420//Homo sapiens chromosome 5, P1 clone 1041F10 (LBNL H88), complete sequence.//2.8e-09:377:63//AC005179

R-MAMMA1001435//S.pombe chromosome I cosmid c26H5.//1.0:356:59//Z99126

R-MAMMA1001442//Homo sapiens chromosome 4 clone B150J4 map 4q25, complete sequence.//3.4e-17:259:72//AC004047

R-MAMMA1001446//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//2.9e-17:231:71//AC004491

R-MAMMA1001452//Human DNA sequence from clone 452M16 on chromosome Xq21.1-21.33 Contains capping protein alpha subunit isoform 1 pseudogene, STS, GSS, and CA repeat, complete sequence.//6.1e-50:558:73//AL024493

R-MAMMA1001465//cSRL-2F3-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-2F3, genomic survey sequence.//3.0e-23:141:96//B04295

R-MAMMA1001476//Mus musculus coding known mRNA, complete sequence.//1.0:100:100//Z99126

R-MAMMA1001476//Mus musculus coding known mRNA, complete sequence.//1.0:100:100//Z99126

R-MAMMA1001476//Mus musculus coding known mRNA, complete sequence.//1.0:100:100//Z99126

R-MAMMA1001501

R-MAMMA1001502//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 356B7, WORKING DRAFT SEQUENCE.//4.3e-19:349:64//AL031714

R-MAMMA1001510

5 R-MAMMA1001522//Homo sapiens chromosome 5, BAC clone 24h24 (LBNL H194), complete sequence.//1.5e-09:136:75//AC005352

R-MAMMA1001547//Human Chromosome X, complete sequence.//3.5e-40:300:84//AC002418

R-MAMMA1001551//Human DNA sequence from PAC 42616 on chromosome 1p34.1-1p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatase-1, ESTs, and a CA repeat.//1.1e-57:282:89//AL020997

10 R-MAMMA1001575

R-MAMMA1001576//Human gamma-tubulin mRNA, complete cds.//7.6e-60:530:78//M61764

R-MAMMA1001590//Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds.//1.3e-29:161:86//U78027

15 R-MAMMA1001600//Homo sapiens 12q24 PAC RPC11-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//2.1e-18:390:66//AC004216

R-MAMMA1001604//Human DNA sequence from clone 1042K10 on chromosome 22q13.1-13.2. Contains the ADSL gene for Adenylosuccinate lyase (EC 4.3.2.2, Adenylosuccinase, ASL) and 4 novel genes (one with probable rabGAP domains and Src homology domain 3). Contains ESTs, STSs, GSSs and a putative CpG island, complete sequence.//1.0:227:62//AL022238

20 R-MAMMA1001606//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 228H13, WORKING DRAFT SEQUENCE.//1.3e-17:219:69//AL031985

R-MAMMA1001620//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018D12, WORKING DRAFT SEQUENCE.//2.1e-51:298:84//AL031650

25 R-MAMMA1001627//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 229A8, WORKING DRAFT SEQUENCE.//7.8e-45:328:85//Z86090

R-MAMMA1001630//, complete sequence.//2.5e-08:170:72//AC005399

R-MAMMA1001633//Homo sapiens chromosome 10 clone CIT987SK-1057L21 map 10q25, complete sequence.//2.2e-21:241:70//AC005386

30 R-MAMMA1001635//Homo sapiens DNA sequence from PAC 230G1 on chromosome Xp11.3. Contains EST, STS and GSS, complete sequence.//1.1e-32:346:74//Z84466

R-MAMMA1001649

R-MAMMA1001663//Homo sapiens clone 162B15, complete sequence.//9.4e-68:267:89//AC004811

R-MAMMA1001670//Human DNA sequence from PAC 75N13 on chromosome Xq21.1. Contains ZNF6 like gene, ESTs, STSs and CpG islands.//1.7e-49:322:88//Z82216

35 R-MAMMA1001671//Homo sapiens chromosome 19, cosmid F23269, complete sequence.//2.4e-114:575:96//AC005614

R-MAMMA1001679//CIT-HSP-2335N4.TF CIT-HSP Homo sapiens genomic clone 2335N4, genomic survey sequence.//2.4e-82:400:99//AQ037393

40 R-MAMMA1001683//Homo sapiens Chromosome 7 BAC Clone 239c10, WORKING DRAFT SEQUENCE, 9 unordered pieces.//5.7e-47:533:72//AC004166

R-MAMMA1001686//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//6.6e-12:194:72//AC005261

R-MAMMA1001692//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y738F9, WORKING DRAFT SEQUENCE.//9.6e-44:414:77//AL022345

45 R-MAMMA1001711//Homo sapiens clone BAC 9H13 chromosome 8 map 8q21, complete sequence.//3.1e-31:436:70//AF110324

R-MAMMA1001715//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 73E16, WORKING DRAFT SEQUENCE.//8.8e-76:524:84//Z95330

R-MAMMA1001730

50 R-MAMMA1001735//Cricetulus griseus (chinese hamster) mRNA for beta tubulin (clone B9T), partial.//2.7e-13:382:63//X60786

R-MAMMA1001740//Homo sapiens genomic DNA, chromosome 21q11.1, segment 21/28, WORKING DRAFT SEQUENCE.//3.9e-47:318:87//AP000050

R-MAMMA1001743//Homo sapiens clone DJ0981O07, complete sequence.//4.0e-108:566:95//AC006017

55 R-MAMMA1001744

R-MAMMA1001745

R-MAMMA1001746

R-MAMMA1001747

R-MAMMA1001748

R-MAMMA1001749

R-MAMMA1001750

R-MAMMA1001751

R-MAMMA1001752

R-MAMMA1001753

R-MAMMA1001754

R-MAMMA1001755//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 73E16, WORKING DRAFT SEQUENCE.//8.8e-76:524:84//Z95330

AC005625

R-MAMMA1001754//Bos taurus vacuolar proton pump subunit SFD alpha isoform (SFD) mRNA, complete cds.//4.7e-34:320:77//AF041338

R-MAMMA1001757//Homo sapiens chromosome 17, clone hRPC.4_G_17, complete sequence.//4.7e-10:244:67//AC003688

R-MAMMA1001760//RPCI11-38L16.TV RPCI-11 Homo sapiens genomic clone RPCI-11-38L16, genomic survey sequence.//1.3e-10:236:64//AQ029432

R-MAMMA1001764//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.74:361:60//AC005140

R-MAMMA1001768//Homo sapiens chromosome 17, clone hRPK.147_L_13, complete sequence.//1.6e-42:416:76//AC005332

R-MAMMA1001769//Homo sapiens chromosome 17, clone hRPC.1073_F_15, complete sequence.//1.4e-13:129:83//AC004686

R-MAMMA1001771//M.musculus mRNA for semaphorin B.//1.1e-34:530:69//X85991

R-MAMMA1001783//Homo sapiens Chromosome 2 BAC Clone 376a1, WORKING DRAFT SEQUENCE, 17 unordered pieces.//1.1e-42:282:85//AC000360

R-MAMMA1001785//Human chromosome 16p13.11 BAC clone CIT987SK-98H8 complete sequence.//3.0e-49:282:86//U91319

R-MAMMA1001788

R-MAMMA1001790//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//9.8e-43:530:71//AC004913

R-MAMMA1001806//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-319E8, complete sequence.//1.8e-43:324:79//AC004020

R-MAMMA1001812//Plasmodium falciparum chromosome 2, section 69 of 73 of the complete sequence.//0.65:183:63//AE001432

R-MAMMA1001815//Homo sapiens clone GS223D04, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.1e-10:417:62//AC005018

R-MAMMA1001817//Homo sapiens Xp22-83 BAC GSHB-324M7 (Genome Systems Human BAC Library) complete sequence.//2.6e-40:313:84//AC005859

R-MAMMA1001818

R-MAMMA1001820//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//2.2e-45:340:82//AC004086

R-MAMMA1001824//Homo sapiens clone DJ1107K15, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.9e-53:291:85//AC004966

R-MAMMA1001836//HS_3164_B1_A02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3164 Col=3 Row=B, genomic survey sequence.//6.5e-08:79:89//AQ185484

R-MAMMA1001837//Homo sapiens chromosome 19, overlapping cosmids F18547, F11133, R27945, R28830 and R32804, complete sequence.//8.4e-55:309:85//AC003682

R-MAMMA1001848//Homo sapiens PAC clone DJ0296G17 from Xq23, complete sequence.//1.6e-16:125:90//AC006144

R-MAMMA1001851//Genomic sequence from Human 9q34, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.4e-50:516:74//AC002099

R-MAMMA1001854//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-575C2, complete sequence.//1.7e-38:308:82//AC002425

R-MAMMA1001858//Human Xq13 3' end of PAC 92E23 containing the X inactivation transcript (XIST) gene, complete sequence.//6.5e-50:283:86//U80460

R-MAMMA1001864//Human Chromosome 15q26.1 PAC clone pDJ398g19, WORKING DRAFT SEQUENCE, 21 unordered pieces.//3.4e-36:224:86//AC005143

R-nnnnnnnnnnnnn//Plasmodium falciparum chromosome 2, section 54 of 73 of the complete sequence.//1.4e-11:495:63//AE001417

R-MAMMA1001874//Human chromosome 1 BAC 308G1 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.2e-42:446:76//AC003117

R-MAMMA1001878//Human DNA sequence from PAC 431A14 on chromosome 6p21. Contains CYCLOPHILIN (PEPTIDYLPROLYL ISOMERASE) like and CIP1 (WAF1, CDKNA1, CDKN1, MDA-6, SDI1, PIC1, CAP20) genes. Contains probable GTPase and receptor genes and ESTs. STSs and CpG islands.//6.9e-44:391:78//Z85996

MAMMA1001880 Homo sapiens

1001880 Homo sapiens

MAMMA1001890 Homo sapiens chromosome 10 DNA sequence.//1.6e-38:308:82//Z85996

quence, complete sequence.//1.7e-43:283:86//AC002303

R-MAMMA1001907//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 385E7, WORKING DRAFT SEQUENCE.//1.4e-48:420:79//AL031720

R-nnnnnnnnnnn//Saccharomyces cerevisiae chromosome IV cosmid 9481.//2.9e-14:505:60//U28373

R-MAMMA1001931//Homo sapiens NACP/alpha-synuclein gene, allele A0, intron 4, partial sequence.//0.51:162:63//AF041008

R-MAMMA1001956//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50O24, WORKING DRAFT SEQUENCE.//1.4e-51:422:79//AL034380

R-MAMMA1001963//Homo sapiens clone HS19.3 Alu-Ya5 sequence.//1.9e-31:163:91//AF015149

R-MAMMA1001969//Human DNA from chromosome 19 cosmid F19410, genomic sequence, complete sequence.//8.7e-10:186:76//AC002128

R-MAMMA1001970//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//1.0e-62:298:86//AC003071

R-MAMMA1001992//Human Chromosome 15q26.1 PAC clone pDJ460g16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.8e-44:525:72//AC004581

R-MAMMA1002009//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 109G6, WORKING DRAFT SEQUENCE.//1.4e-43:282:79//AL023879

R-MAMMA1002011

R-MAMMA1002032//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 469D22, WORKING DRAFT SEQUENCE.//1.1e-39:310:84//AL031284

R-MAMMA1002033//Homo sapiens chromosome 5, Pac clone 162o17 (LBNL H147), complete sequence.//2.5e-17:170:81//AC003954

R-MAMMA1002041//Homo sapiens PAC clone DJ0728D04, complete sequence.//8.7e-79:296:85//AC004865

R-MAMMA1002042//Human chromosome 16 BAC clone CIT987SK-A-962B4, complete sequence.//8.8e-46:386:80//U91318

R-MAMMA1002047//Human chromosome 16 BAC clone CIT987SK-A-962B4, complete sequence.//1.9e-32:326:75//U91318

R-MAMMA1002056//Homo sapiens chromosome 17, clone hRPK.506_H_21, complete sequence.//6.6e-48:367:82//AC005962

R-MAMMA1002058//Homo sapiens clone RG038K21, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.25:139:69//AC005052

R-MAMMA1002068//Homo Sapiens Chromosome X clone bWXD171, WORKING DRAFT SEQUENCE, 1 ordered pieces.//2.2e-45:406:78//AC004676

R-MAMMA1002078//Homo sapiens chromosome 17, clone hRPK.401_O_9, complete sequence.//2.3e-22:357:64//AC005291

R-MAMMA1002082//Homo sapiens PAC clone 278C19 from 12q, complete sequence.//2.5e-38:304:82//AC004263

R-MAMMA1002084//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1174N9, WORKING DRAFT SEQUENCE.//8.9e-41:319:83//AL031602

R-MAMMA1002093//CIT-HSP-2060J9.TF CIT-HSP Homo sapiens genomic clone 2060J9, genomic survey sequence.//9.7e-17:129:88//B69983

R-MAMMA1002108

R-MAMMA1002118//Human DNA sequence from cosmid E116C6, on chromosome 22 Contains ESTs, complete sequence.//0.94:168:64//Z73495

R-MAMMA1002125//Homo sapiens chromosome 17, clone hRPK.63_A_1, complete sequence.//4.8e-40:313:83//AC005670

R-MAMMA1002132//Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete sequence.//2.0e-70:461:83//AC004953

R-MAMMA1002140//Human DNA sequence from PAC 465G10 on chromosome X contains Menkes Disease (ATP7A) putative Cu⁺⁺-transporting P-type ATPase exons 2 to 21, PGAM-B, ESTs.//1.1e-32:477:73//Z94801

R-MAMMA1002143//Homo sapiens platelet-activating factor acetylhydrolase gene, promoter region and exon 1.//6.6e-06:130:73//AF027357

R-MAMMA1002145//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 126A5, WORKING DRAFT SEQUENCE.//6.0e-19:242:73//AL031447

R-MAMMA1002153//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0281M17-ITGS phase 1, WORKING DRAFT SEQUENCE.//1.1e-43:283:86//AC002303

R-MAMMA1002154//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1174N9, WORKING DRAFT SEQUENCE.//8.9e-41:319:83//AL031602

R-MAMMA1002156//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter, complete sequence.//5.1e-37:305:82//AC004997

R-MAMMA1002158//Human DNA sequence from clone 1049G16 on chromosome 20q12-13.2 Contains gene similar to GLUCOSAMINE-6-SULFATASE, a nuclear receptor coactivator gene, ESTs, STSs, GSSs, complete sequence.//8.1e-34:296:81//AL034418

5 R-MAMMA1002170//Human DNA sequence from clone 1163J1 on chromosome 22q13.2-13.33. Contains the 3' part of a gene for the ortholog of mouse transmembrane receptor Celsr1, a novel gene for a protein similar to C. elegans B0035.16 and bacterial tRNA (5-Methylaminomethyl-2-thiouridylate)-Methyltransferases, and the 3' part of a novel gene for a protein similar to mouse B99. Contains ESTs, GSSs and putative CpG islands, complete sequence.//7.9e-39:332:82//AL031588

10 R-MAMMA1002174//Homo sapiens chromosome 10 clone CIT987SK-1109P11, complete sequence.//4.4e-12:189:72//AC005871

R-MAMMA1002198//Homo sapiens clone DJ0800G07, complete sequence.//1.1e-48:338:81//AC004890

15 R-MAMMA1002209//Homo sapiens chromosome 17, clone hRPK.156_L_14, complete sequence.//1.2e-23:269:74//AC005821

R-MAMMA1002215//Homo sapiens clone GS250N06, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.2e-12:243:68//AC005158

R-MAMMA1002219//Homo sapiens 12p13.3 RPC14-773N5 (Roswell Park Cancer Institute Human PAC library) complete sequence.//3.3e-45:295:88//AC004802

20 R-MAMMA1002230//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE.//7.3e-41:385:78//AL034379

R-MAMMA1002236//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds.//7.3e-45:363:79//U38253

25 R-MAMMA1002243//Homo sapiens chromosome 17, clone hRPK.112_H_10, complete sequence.//2.8e-119:582:98//AC005666

R-MAMMA1002250//Homo sapiens chromosome 16, P1 clone 109-9G (LANL), complete sequence.//4.7e-42:319:84//AC005600

R-MAMMA1002267//Homo sapiens chromosome 17, clone hRPK.346_K_10, complete sequence.//1.5e-33:571:67//AC006120

30 R-MAMMA1002268//Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds.//2.3e-35:462:70//AF068749

R-MAMMA1002269//345I17.TV CIT978SKA1 Homo sapiens genomic clone A-345I17, genomic survey sequence.//4.7e-05:153:69//B15590

R-MAMMA1002282//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 112K5, WORKING DRAFT SEQUENCE.//8.5e-37:467:71//Z85987

35 R-MAMMA1002292//Hordeum vulgare lipoxxygenase 2 (LoxC) mRNA, complete cds.//0.074:178:61//L37358

R-MAMMA1002293//Homo sapiens chromosome 16, cosmid clone RT167 (LANL), complete sequence.//5.8e-26:355:71//AC005568

R-MAMMA1002294//Homo sapiens chromosome 17, clone hRPC.1110_E_20, complete sequence.//1.2e-35:281:82//AC004231

40 R-MAMMA1002297//Human DNA sequence from cosmid L174G8, Huntington's Disease Region, chromosome 4p16.3.//6.7e-48:381:80//Z69375

R-MAMMA1002298//Homo sapiens BAC clone RG208H19 from 7q11.23, complete sequence.//.8e-17:296:70//AC005074

45 R-MAMMA1002299//HS_3116_A2_F07_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3116 Col=14 Row=K, genomic survey sequence.//4.1e-60:354:91//AQ140526

R-MAMMA1002308

R-MAMMA1002310//Human DNA sequence from cosmid B10B1 on chromosome 22 Contains ESTs, CA repeat and STS, complete sequence.//9.9e-35:283:83//Z73979

50 R-MAMMA1002311//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//1.3e-86:503:90//AC006210

R-MAMMA1002312//H.sapiens gene encoding La autoantigen.//1.3e-23:382:67//X97869

R-MAMMA1002317//Human DNA sequence from clone 48G12 on chromosome Xq27.1-27.3. Contains STSs and GSSs, complete sequence.//1.3e-59:323:87//AL031054

55 R-MAMMA1002319//Homo sapiens chromosome 19, fosmid 39347, complete sequence.//2.2e-106:522:98//AC005756

R-MAMMA1002320//Homo sapiens chromosome 19, fosmid 39347, complete sequence.//2.2e-106:522:98//AC005756

R-MAMMA1002321//Homo sapiens chromosome 19, fosmid 39347, complete sequence.//2.2e-106:522:98//AC005756

R-MAMMA1002329//M.musculus mRNA for semaphorin B.//2.0e-12:210:73//X85991
 R-MAMMA1002332//Homo sapiens PAC clone DJ1139101 from Xq23, complete sequence.//3.4e-46:393:71//AC004973
 R-MAMMA1002333//HS_3245_A1_B04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3245 Col=7 Row=C, genomic survey sequence.//3.1e-21:146:92//AQ205759
 5 R-MAMMA1002339//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//9.7e-39:310:79//AF001549
 R-MAMMA1002347//Homo sapiens 12q24.1 PAC RPCI3-305I20 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.2e-46:443:76//AC006088
 10 R-MAMMA1002351//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1059H15, WORKING DRAFT SEQUENCE.//1.1e-90:553:89//AL022100
 R-MAMMA1002352//Homo sapiens mRNA for leukemia associated gene 2.//8.8e-81:388:92//Y15228
 R-MAMMA1002353//Homo sapiens 12q24 BAC RPCI11-162P23 (Roswell Park Cancer Institute Human BAC library) complete sequence.//5.5e-35:302:80//AC002996
 15 R-MAMMA1002355//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 222E13, WORKING DRAFT SEQUENCE.//5.4e-52:361:76//Z93241
 R-MAMMA1002356//Homo sapiens chromosome 17, clone hRPC.842_A_23, complete sequence.//8.3e-28:187:91//AC004662
 R-MAMMA1002359//Human DNA sequence from cosmid L118D5, Huntington's Disease Region, chromosome 4p16.3 contains CpG islands.//6.3e-47:297:85//268869
 20 R-MAMMA1002360//HS_2163_B2_C08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2163 Col=16 Row=F, genomic survey sequence.//1.5e-20:374:66//AQ125213
 R-MAMMA1002361//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 349A12, WORKING DRAFT SEQUENCE.//2.2e-35:264:85//AL033520
 25 R-MAMMA1002362//H.sapiens PEX gene.//1.8e-40:243:86//Y10196
 R-MAMMA1002380//RPCI11-73J4.TJ RPCI11 Homo sapiens genomic clone R-73J4, genomic survey sequence.//1.7e-38:295:77//AQ268168
 R-MAMMA1002384//Homo sapiens 12q13.1 PAC RPCI1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.5e-37:311:81//AC004801
 30 R-MAMMA1002385
 R-MAMMA1002392//Human BAC clone RG066D11 from 7q22, complete sequence.//2.0e-37:365:77//AC002430
 R-MAMMA1002411//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 64K7, WORKING DRAFT SEQUENCE.//9.4e-22:496:65//AL031668
 35 R-MAMMA1002413//Homo sapient 12q24.2 PAC RPCI1-157K6 (Roswell Park Cancer Institute Human PAC library) complete sequence.//2.3e-15:153:77//AC005146
 R-MAMMA1002417//Human DNA sequence from PAC 426I6 on chromosome 1p34.1-1p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatase-1, ESTs, and a CA repeat.//1.8e-23:508:62//AL020997
 R-MAMMA1002427//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//2.5e-37:288:84//U91321
 40 R-MAMMA1002428//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1185N5, WORKING DRAFT SEQUENCE.//6.0e-05:130:75//AL034423
 R-MAMMA1002434//Homo sapiens DNA sequence from PAC 380E11 on chromosome 6p22.3-p24. Contains HB15 gene, ESTs, CA repeat, STS and GSS.//4.8e-18:205:78//AL022396
 R-MAMMA1002446//CIT-HSP-2021L14.TR CIT-HSP Homo sapiens genomic clone 2021L14, genomic survey sequence.//4.6e-41:387:72//B65379
 45 R-MAMMA1002454//Homo sapiens chromosome 19, cosmid F23259, complete sequence.//1.2e-67:491:82//AC005512
 R-MAMMA1002461//Homo sapiens PAC clone 166H1 from 12q, complete sequence.//1.4e-28:188:85//AC003982
 R-MAMMA1002470//Saccharomyces cerevisiae chromosome VIII cosmid 9205.//6.3e-09:280:61//U10556
 50 R-MAMMA1002475//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.//1.5e-25:310:74//Z83822
 R-MAMMA1002480//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.2e-98:533:93//AC005077
 R-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds.//2.7e-114:560:97//AF055460
 55 R-MAMMA1002494//Human DNA sequence from cosmid L174G8, Huntington's Disease Region, chromosome 4p16.3 contains CpG islands.//6.3e-47:297:85//268869

R-MAMMA1002494//Human DNA sequence from cosmid L174G8, Huntington's Disease Region, chromosome 4p16.3 contains CpG islands.//6.3e-47:297:85//268869

R-MAMMA1002494//Human DNA sequence from cosmid L174G8, Huntington's Disease Region, chromosome 4p16.3 contains CpG islands.//6.3e-47:297:85//268869

DRAFT SEQUENCE, 5 unordered pieces.//0.012:460:60//AC005139

R-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds.//1.2e-101:529:95//AF065214

R-MAMMA1002545//Homo sapiens ribosomal protein s4 Y isoform gene, complete cds.//6.6e-50:471:77//AF041427

R-MAMMA1002554//Homo sapiens chromosome 4 clone B227H22 map 4q25, complete sequence.//5.7e-38:279:84//AC004056

R-MAMMA1002556//Homo sapiens chromosome 10 clone CIT-HSP-1255F20 map 10p11.2-10p12.1, complete sequence.//9.6e-13:237:67//AC005878

R-MAMMA1002566//CITBI-E1-2509P21.TR CITBI-E1 Homo sapiens genomic clone 2509P21, genomic survey sequence.//9.7e-14:216:73//AQ261427

R-MAMMA1002571//CITBI-E1-2516L21.TF CITBI-E1 Homo sapiens genomic clone 2516L21, genomic survey sequence.//4.6e-25:142:99//AQ279542

R-MAMMA1002573//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 811H13, WORKING DRAFT SEQUENCE.//1.1e-30:250:82//AL023805

R-MAMMA1002585//Rabbit angiotensin-converting enzyme (ACE) gene, 5' end.//1.0:196:61//M58580

R-MAMMA1002590//H.sapiens CpG island DNA genomic MseI fragment, clone 8d5, forward read cpg8d5.f1g.//1.0:114:64//Z63758

R-MAMMA1002597//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1103G7, WORKING DRAFT SEQUENCE.//9.0e-96:459:98//AL034548

R-MAMMA1002598//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 120G22, WORKING DRAFT SEQUENCE.//0.79:362:58//AL031847

R-MAMMA1002603//Homo sapiens chromosome 17, clone hRPK.214_C_8, complete sequence.//1.3e-46:333:80//AC005803

R-MAMMA1002612//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 269M15, WORKING DRAFT SEQUENCE.//7.4e-41:283:86//AL021395

R-MAMMA1002617//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 591N18, WORKING DRAFT SEQUENCE.//1.7e-20:308:71//AL031594

R-MAMMA1002618//Homo sapiens clone RG122E10, complete sequence.//1.2e-31:230:76//AC005067

R-MAMMA1002619//Homo sapiens chromosome 21 PAC RPCIP704E14135Q2.//9.0e-113:551:98//AJ010598

R-MAMMA1002622//Homo sapiens chromosome 4 clone B207D4 map 4q25, complete sequence.//2.8e-43:324:83//AC004050

R-MAMMA1002623//Homo sapiens chromosome 17, clone hRPC.1171_I_10, complete sequence.//2.7e-80:344:84//AC004687

R-MAMMA1002625//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1056L3, WORKING DRAFT SEQUENCE.//2.6e-34:391:72//AL031727

R-MAMMA1002629//Human DNA from overlapping chromosome 19-specific cosmid R32543,, and F15613 containing ZNF gene family member, genomic sequence, complete sequence.//5.5e-58:346:81//AC003006

R-MAMMA1002636//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.1e-52:285:92//AC004895

R-MAMMA1002637//Mus musculus kinesin light chain 2 (Klc2) mRNA, complete cds.//2.1e-13:359:64//AF055666

R-MAMMA1002646//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 394I7, WORKING DRAFT SEQUENCE.//2.5e-24:285:68//AL023585

R-MAMMA1002650//Human IGF-II gene exon 2 for insulin-like growth factor II located on chromosome 11.//0.64:237:61//X03424

R-MAMMA1002655//Homo sapiens mini satellite cebI repeat region.//0.18:152:65//AF048727

R-MAMMA1002662//Homo sapiens clone DJ0739M23, complete sequence.//2.5e-46:370:82//AC004870

R-MAMMA1002665//Human DNA sequence from PAC 435C23 on chromosome X. Contains ESTs.//7.4e-55:298:92//Z92844

R-MAMMA1002671//RPCI11-45M10.TK RPCI11 Homo sapiens genomic clone R-45M10, genomic survey sequence.//0.99:151:66//AQ194411

R-MAMMA1002673//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and GSSs, complete sequence.//3.1e-38:410:76//AL022162

R-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds.//1.4e-107:544:96//D86987

R-MAMMA1002685//Homo sapiens clone B227H22 map 4q25, complete sequence.//5.7e-38:279:84//AC004056

R-MAMMA1002686//Homo sapiens clone B227H22 map 4q25, complete sequence.//5.7e-38:279:84//AC004056

R-MAMMA1002698//Homo sapiens XP22.102.104 BAC GSHB-590015 (Genome Systems Human BAC library)

complete sequence//1.1e-38:299:83//AC004673

R-MAMMA1002699//Mus musculus intersectin-EH binding protein lbp1 mRNA, partial cds.//3.3e-05:61:93//AF057285

R-MAMMA1002701//Homo sapiens gene for AF-6, complete cds.//3.5e-39:317:81//AB011399

R-MAMMA1002708//Homo sapiens 12p13.3 PAC RPCI5-977L1 (Roswell Park Cancer Institute Human PAC library) complete sequence//0.26:365:62//AC005293

R-MAMMA1002711//Homo sapiens chromosome 21 PAC LLNLP704F18108Q13//2.5e-31:304:77//AJ006995

R-MAMMA1002721//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 473B4, WORKING DRAFT SEQUENCE.//2.3e-40:279:87//Z83826

R-MAMMA1002727//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.45:183:64//AC004710

R-MAMMA1002728//Human Chromosome 11 Overlapping Cosmids cSRL72g7 and cSRL140b8, complete sequence.//1.1e-42:410:74//AC002037

R-MAMMA1002744//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence.//1.6e-19:473:63//U96629

R-MAMMA1002746//Homo sapiens chromosome 17, clone hRPK.136_H_19, complete sequence.//2.2e-108:544:97//AC005856

R-MAMMA1002748//Homo sapiens 3p22 Contig 7 PAC RPCI4-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//5.9e-106:551:95//AC006055

R-MAMMA1002754//Homo sapiens clone GS259H13, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.7e-34:305:79//AC005020

R-MAMMA1002758//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//0.00014:130:74//U95626

R-MAMMA1002764//Homo sapiens chromosome 19, cosmid H33632, complete sequence.//8.7e-10:118:81//AC005781

R-MAMMA1002765//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//1.2e-31:290:78//AC006128

R-MAMMA1002769//Human DNA sequence from PAC 36J3, between markers DXS1192 and DXS102 on chromosome X.//0.94:260:62//Z82975

R-MAMMA1002780//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 620E11, WORKING DRAFT SEQUENCE.//2.6e-21:529:62//AL031667

R-MAMMA1002782//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 199H16, WORKING DRAFT SEQUENCE.//2.8e-30:234:72//AL022320

R-MAMMA1002796//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 237J2, WORKING DRAFT SEQUENCE.//1.0:155:66//AL021394

R-MAMMA1002807//Human DNA sequence from BAC 941F9 on chromosome 22q11.2-qter. Contains ESTs, STSs and 3' part of FIBULIN-1 D PRECURSOR like gene, part of a Brain Protein E46 like gene and a CpG island, complete sequence.//5.0e-42:443:75//Z95331

R-MAMMA1002820//345M16.TVB CIT978SKA1 Homo sapiens genomic clone A-345M16, genomic survey sequence.//1.3e-14:95:87//B17487

R-MAMMA1002830//Human PAC clone DJ515N1 from 22q11.2-q22, complete sequence.//4.1 e-20:223:74//AC002073

R-MAMMA1002833//Homo sapiens Xp22 bins 3-5 PAC RPCI4-617A9 (Roswell Park Cancer Institute Human PAC Library) containing Arylsulfatase D and E genes, complete sequence.//1.8e-37:295:84//AC005295

R-MAMMA1002835

R-MAMMA1002838//Human gene hY3 encoding a cytoplasmic Ro RNA.//4.4e-14:108:92//V00585

R-MAMMA1002842//CIT-HSP-2017022.TRB CIT-HSP Homo sapiens genomic clone 2017022, genomic survey sequence.//5.2e-43:168:85//B67141

R-MAMMA1002843//Homo sapiens clone GS051M12, complete sequence.//8.7e-44:525:71//AC005007

R-MAMMA1002844

R-MAMMA1002858//H.sapiens ERF-1 mRNA 3' end.//2.8e-99:361:91//X79067

R-MAMMA1002868//Homo sapiens clone DJ0852O24, WORKING DRAFT SEQUENCE, 2 unordered pieces.//9.6e-39:288:81//AC004906

R-MAMMA1002871//Homo sapiens BAC clone NH0539B24 from 7p15.1-p14, complete sequence.//0.0022:490:57//AC006044

R-MAMMA1002881//Homo sapiens chromosome 11, cosmid H33632, complete sequence.//8.7e-10:118:81//AC005781

R-MAMMA1002882//Homo sapiens chromosome 11, cosmid F20900, complete sequence.//1.2e-31:290:78//AC006128

R-MAMMA1002883//Homo sapiens chromosome 11, cosmid F20900, complete sequence.//1.2e-31:290:78//AC006128

cds for thymopoietin beta.//5.1e-41:264:87//U18271

R-MAMMA1002886//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS. CpG island, complete sequence.//4.7e-32:216:90//AL022069

R-MAMMA1002887

R-MAMMA1002890

3.4e-49:376:81//AG006257

R-MAMMA1002892//Homo sapiens PAC clone DJ0765G07 from 7q11, complete sequence.//6.0e-60:344:79//AC004881

R-MAMMA1002895//RPCI11-90K13.TV RPCI11 Homo sapiens genomic clone R-90K13, genomic survey sequence.//2.1e-34:300:77//AQ283502

R-MAMMA1002908//Human Chromosome X, complete sequence.//4.2e-39:297:85//AC004070

R-MAMMA1002909//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0442P12; HTGS phase 1, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.4e-23:344:74//AC005798

R-MAMMA1002930//Homo sapiens PAC clone DJ1048B16 from 7q34-q36, complete sequence.//5.2e-39:261:88//AC006019

R-MAMMA1002938//C.pasteurianum gap gene.//1.0:343:59//X72219

R-MAMMA1002941//Homo sapiens chromosome 17, clone hRPK.346_K_10, complete sequence.//6.3e-88:556:87//AC006120

R-MAMMA1002947

0.48:156:69//AC005469

R-MAMMA1002964//Human DNA sequence from PAC 426I6 on chromosome 1p34.1-1p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatase-1, ESTs, and a CA repeat.//1.2e-39:473:73//AL020997

R-MAMMA1002970//Homo sapiens chromosome 5, P1 clone 793c5 (LBNL H57), complete sequence.//4.7e-47:420:77//AC005200

R-MAMMA1002972//alpha 1 syntrophin [human, mRNA Partial, 1771 nt].//0.97:305:62//S81737

R-MAMMA1002973//Human DNA sequence from cosmid V210E9, between markers DXS366 and DXS87 on chromosome X.//2.6e-35:256:85//Z70280

R-MAMMA1002982 1.0e-27:110:85//AG005524

R-MAMMA1002987//Homo sapiens PAC clone DJ1086D14, complete sequence.//1.4e-28:527:66//AC004460

R-MAMMA1003003//Homo sapiens chromosome 10 clone CRI-JC2059 map 10q24.1-10q24.2, WORKING DRAFT SEQUENCE, 1 ordered pieces.//7.9e-48:418:78//AC006109

R-MAMMA1003004//, complete sequence.//2.0e-12:442:61//AC005406

R-MAMMA1003007//Homo sapiens chromosome 10 clone CRI-JC2059 map 10q24.1-10q24.2, WORKING DRAFT SEQUENCE, 1 ordered pieces.//1.7e-48:293:91//AC006109

R-MAMMA1003011//A-306G8.TP CIT978SK Homo sapiens genomic clone A-306G8, genomic survey sequence.//0.45:168:64//B18092

R-MAMMA1003015//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//2.9e-44:399:77//AC005740

R-MAMMA1003019//RPCI11-9J9.TV RPCI-11 Homo sapiens genomic clone RPCI-11-9J9, genomic survey sequence.//2.7e-14:294:68//B71583

R-MAMMA1003026//HS_2166_B2_C12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2166 Col=24 Row=F, genomic survey sequence.//0.021:189:64//AQ125639

R-MAMMA1003031//Homo sapiens chromosome 5, BAC clone 319C17 (LBNL H159), complete sequence.//1.8e-98:525:95//AC005214

R-MAMMA1003035//Homo sapiens 12q13.1 Cosmid C174F5 (Lawrence Livermore LL12NC01 or LL12NC02 human cosmid libraries) complete sequence.//6.7e-06:297:63//AC004550

R-MAMMA1003039//RPCI11-56J17.TJ RPCI11 Homo sapiens genomic clone R-56J17, genomic survey sequence.//0.21:375:59//AQ081889

R-MAMMA1003040//Human DNA sequence from cosmid L108f12, Huntington's Disease Region, chromosome 4p16.3.//2.7e-29:298:67//Z49235

R-MAMMA1003044//Homo sapiens chromosome 19, cosmid R30676, complete sequence.//2.9e-14:113:91//AC004560

R-MAMMA1003047

R-MAMMA1003049

R-MAMMA1003055//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 377F16, WORKING DRAFT SEQUENCE //2.3e-45:317:86//Z93783

10536

R-MAMMA1003057//M.domesticus MD6 mRNA//6.2e-42:326:82//X54352
 R-MAMMA1003066//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 473B4, WORKING
 DRAFT SEQUENCE.//3.1e-49:299:87//Z83826
 R-MAMMA1003089//Homo sapiens BAC clone RG298G08 from 7p15-p21, complete sequence.//2.7e-30:520:67//
 5 AC005084
 R-MAMMA1003099//RPCI11-8N9.TP RPCI-11 Homo sapiens genomic clone RPCI-11-8N9, genomic survey se-
 quence.//4.2e-44:338:82//B71494
 R-MAMMA1003104//Mus musculus rostral cerebellar malformation protein (rcm) mRNA, complete cds.//3.4e-48:
 423:79//J72634
 10 R-MAMMA1003113//Homo sapiens chromosome 12p13.3 clone RPCI11-433J6, WORKING DRAFT SEQUENCE,
 100 unordered pieces.//4.8e-114:567:97//AC006087
 R-MAMMA1003127//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 250D10, WORKING
 DRAFT SEQUENCE.//1.4e-34:283:83//Z99716
 R-MAMMA1003135//P.knowlesi Mbn-cutting sites in lambda KBS50.//0.010:243:62//M38776
 15 R-MAMMA1003140//Homo sapiens chromosome 17, clone HCIT87G17, complete sequence.//6.7e-34:288:81//
 AC003663
 R-MAMMA1003146//Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, com-
 plete cds.//4.8e-08:438:59//M97514
 R-nnnnnnnnnnnn//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 598F2, WORKING
 20 DRAFT SEQUENCE.//1.7e-63:149:94//AL021579
 R-MAMMA1003166//HS_3128_A1_B01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3128 Col=1 Row=C, genomic survey sequence.//3.0e-17:261:70//AQ140766
 R-NT2RM2002580//Homo sapiens clone 24781 mRNA sequence.//2.6e-111:593:94//AF070640
 R-NT2RM4000024
 25 R-NT2RM4000027//Homo sapiens PAC clone DJ1194E14 from 7p21, complete sequence.//0.026:476:56//
 AC004993
 R-NT2RM4000030//Mus musculus musculus sex determining protein (Sry) gene, complete cds.//0.00044:378:59//
 U70653
 R-NT2RM4000046//M.mulatta MHC DR beta 6 gene encoding major histocompatibility complex.//0.27:130:64//
 30 Z26239
 R-NT2RM4000061
 R-NT2RM4000085//Homo sapiens clone 24700 unknown mRNA, partial cds.//7.2e-112:550:97//AF070639
 R-NT2RM4000086//RPCI11-6J23.TV RPCI-11 Homo sapiens genomic clone RPCI-11-6J23, genomic survey se-
 quence.//7.2e-18:277:71//B49463
 35 R-NT2RM4000104//F.rubripes GSS sequence, clone 063K10aG5, genomic survey sequence.//3.6e-08:287:61//
 Z88817
 R-NT2RM4000139//Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence.//9.4e-08:
 336:65//AC005199
 R-NT2RM4000155
 40 R-NT2RM4000156//Homo sapiens chromosome 17, clone hRPK.136_H_19, complete sequence.//3.4e-23:335:
 72//AC005856
 R-nnnnnnnnnnnn//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//1.6e-87:551:87//
 D12646
 R-NT2RM4000169//Human ribosomal protein L37a mRNA sequence.//5.9e-14:122:88//L22154
 45 R-NT2RM4000191
 R-NT2RM4000197//HS_3241_A2_H05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3241 Col=10 Row=O, genomic survey sequence.//2.8e-86:430:97//AQ206812
 R-NT2RM4000199//Mus musculus Yp BAC GSMB-368G7 (Genome Systems Mouse BAC Library) complete se-
 quence.//0.0047:193:63//AC006056
 50 R-NT2RM4000200
 R-NT2RM4000202//Homo sapiens chromosome 16, cosmid clone 378E2 (LANL), complete sequence.//2.1e-40:
 334:76//AC004035
 R-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds.//5.2e-102:546:94//AB018255
 R-NT2RM4000215
 55 R-nnnnnnnnnnnn//Homo sapiens chromosome 10 clone CIT987SK-1144G6 map 10q25.1, complete sequence.//
 2.1e-55:303:86//AC005283
 R-NT2RM4000233//Homo sapiens chromosome 10 clone CIT987SK-1144G6 map 10q25.1, complete sequence.//
 2.1e-55:303:86//AC005283
 R-NT2RM4000244//Homo sapiens chromosome 10 clone CIT987SK-1144G6 map 10q25.1, complete sequence.//
 2.1e-55:303:86//AC005283

49:322:88//AC006116

R-NT2RM4000251//Homo sapiens Chromosome 22q11.2 BAC Clone 72f8 In DGCR Region, complete sequence.//0.97:184:66//AC000085

R-NT2RM4000265//Human PAC clone DJ073F11 from Xq23, complete sequence.//6.2e-66:552:78//AC000055

5 R-NT2RM4000290//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 39417, WORKING DRAFT SEQUENCE.//1.4e-05:229:65//AL023585

R-NT2RM4000324

R-NT2RM4000327//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 75N14, WORKING DRAFT SEQUENCE.//3.3e-42:443:75//Z97199

10 R-NT2RM4000344//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE, 12 unordered pieces.//6.4e-64:433:84//AC004826

R-NT2RM4000349//Human mRNA for KIAA0005 gene, complete cds.//7.7e-11:210:69//D13630

R-NT2RM4000354//Caenorhabditis elegans cosmid T14A8.//0.084:257:60//U50066

R-NT2RM4000356

15 R-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cds.//8.7e-112:577:95//AB014542

R-NT2RM4000368

1.6e-48:348:85//AG006257

R-NT2RM4000386//Rat mRNA for growth potentiating factor, complete cds.//4.4e-35:141:87//D42148

20 R-NT2RM4000395//RPCI11-8N9.TP RPCI-11 Homo sapiens genomic clone RPCI-11-8N9, genomic survey sequence.//1.4e-25:207:75//871494

R-NT2RM4000414//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 228H13, WORKING DRAFT SEQUENCE.//7.1e-17:492:64//AL031985

R-NT2RM4000421//RPCI11-66B1.TK RPCI11 Homo sapiens genomic clone R-66B1, genomic survey sequence.//1.8e-40:311:82//AQ241167

25 R-NT2RM4000425//Homo sapiens chromosome Xp22-135-136 clone GSHB-56711, WORKING DRAFT SEQUENCE, 35 unordered pieces.//2.5e-47:316:87//AC005867

R-NT2RM4000433//Mus musculus retinoic acid-responsive protein (Stra6) mRNA, complete cds.//1.6e-17:133:78//AF062476

R-NT2RM4000457

30 R-NT2RM4000471//Homo sapiens mRNA for putative tRNA splicing protein, partial.//4.6e-113:559:96//AJ010952

R-NT2RM4000486//Homo sapiens mRNA, complete cds, clone:RES4-22C.//0.00015:170:67//AB000461

R-NT2RM4000496

R-NT2RM4000511//Rat troponin T cardiac isoform gene, complete cds.//0.21:290:58//M80829

35 R-NT2RM4000514//CIT-HSP-2169K4.TR CIT-HSP Homo sapiens genomic clone 2169K4, genomic survey sequence.//1.5e-20:150:89//B95717

R-nnnnnnnnnnnn//HS-1024-B2-G01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 803 Col=2 Row=N, genomic survey sequence.//6.3e-10:74:98//B34556

R-NT2RM4000520//Caenorhabditis elegans cosmid F36H12.//0.15:406:61//AF078790

R-NT2RM4000531

40 R-NT2RM4000532//Plasmodium falciparum chromosome 2, section 28 of 73 of the complete sequence.//1.0:119:66//AE001391

R-NT2RM4000534//paramecium species 4.51er mt dna dimer: replication init. region, clone 2.//9.8e-05:326:60//K00909

R-NT2RM4000585//HS_3252_A2_G08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=16 Row=M, genomic survey sequence.//1.9e-69:376:93//AQ219890

45 R-NT2RM4000590//CIT-HSP-539O24.TV CIT-HSP Homo sapiens genomic clone 539O24, genomic survey sequence.//1.7e-38:226:93//B50657

R-NT2RM4000595//Human Chromosome X clone bWXD342, complete sequence.//1.0:239:61//AC004072

R-NT2RM4000603//RPCI11-49P13.TK RPCI11 Homo sapiens genomic clone R-49P13, genomic survey sequence.//0.77:139:64//AQ051950

50 R-nnnnnnnnnnnnn

R-NT2RM4000616//HS_3107_A2_B03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3107 Col=6 Row=C, genomic survey sequence.//1.3e-54:272:99//AQ210034

R-NT2RM4000674

55 R-NT2RM4000689//Mus musculus pericentrin mRNA, complete cds.//3.5e-70:551:80//U05823

R-NT2RM4000698

R-NT2RM4000717//Plasmodium falciparum MAL3P8, complete sequence//0.050:387:58//AL034560
R-NT2RM4000733//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE//1.0e-107:566:95//AL034379
R-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds//1.1e-103:536:95//AB018303
R-NT2RM4000741//CIT-HSP-2294N4.TR CIT-HSP Homo sapiens genomic clone 2294N4, genomic survey sequence//5.2e-41:244:93//AQ006361
R-NT2RM4000751//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 537K23, WORKING DRAFT SEQUENCE//2.7e-28:416:67//AL034405
R-NT2RM4000764//Human HepG2 3' region Mbol cDNA, clone hmd3g01m3//2.1e-33:199:96//D17217
R-NT2RM4000778//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library) complete sequence//0.00060:241:62//AC002980
R-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds//2.9e-104:546:94//AB007920
R-NT2RM4000787//Homo sapiens, clone hRPK.3_A_1, complete sequence//5.3e-32:321:77//AC006198
R-NT2RM4000790//Homo sapiens chromosome 19, cosmid R27216, complete sequence//1.9e-111:552:97//AC005306
R-NT2RM4000795//Homo sapiens Chromosome 17p13 Cosmid Clone cos39, complete sequence//0.74:364:57//U58675
R-NT2RM4000796//Homo sapiens full-length insert cDNA clone ZD62D10//2.7e-105:510:98//AF086348
R-NT2RM4000798//Human polymorphic epithelial mucin core protein mRNA, 3' end//7.7e-27:158:96//M21868
R-NT2RM4000813
R-NT2RM4000820//, complete sequence//2.0e-104:432:97//AC005406
R-NT2RM4000833//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX122, complete sequence//2.0e-07:166:68//AB012248
R-NT2RM4000846//Rabies virus matrix (M) protein mRNA, complete cds//0.073:70:84//M22013
R-NT2RM4000852//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces//1.0:237:62//AC004709
R-NT2RM4000855
R-ntntntntntntntntntntnt//HS_3189_B2_B08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3189 Col=16 Row=D, genomic survey sequence//2.1e-06:114:73//AQ300597
R-NT2RM4000895//Pan troglodytes HS19.8-similar locus and Y Alu element, genomic survey sequence//3.8e-46:207:91//AF077058
R-NT2RM4000950//Human BAC clone RG341D10 from 7p15-p21, complete sequence//1.0:336:60//AC002530
R-NT2RM4000971//Human Xq28 cosmids U126G1, U142F2, U69B6, U145C10, U169A5, U84H1, U24D12, U80A7, U153E6, L35485, and R7-163A8 containing iduronate 2-sulfatase gene and pseudogene, complete sequence//7.1e-09:259:64//AF011889
R-NT2RM4000979
R-NT2RM4000996//HS_3164_A1_E02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3164 Col=3 Row=I, genomic survey sequence//2.0e-82:443:94//AQ141622
R-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds//1.2e-112:545:97//AB018272
R-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds//7.9e-113:556:97//AB014539
R-NT2RM4001032//Homo sapiens Surf-5 and Surf-6 genes//1.2e-10:120:82//AJ224639
R-NT2RM4001047//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 163G9, WORKING DRAFT SEQUENCE//1.0:158:67//AL008733
R-NT2RM4001054//CIT-HSP-2292N8.TR CIT-HSP Homo sapiens genomic clone 2292N8, genomic survey sequence//5.8e-19:118:97//AQ004096
R-ntntntntntntntntntntnt//Mouse DNA with homology to EBV IR3 repeat, segment 1, clone Mu2//1.0e-05:271:64//M10296
R-NT2RM4001092//CITBI-E1-2524J20.TR CITBI-E1 Homo sapiens genomic clone 2524J20, genomic survey sequence//1.0:186:63//AQ277294
R-NT2RM4001116
R-NT2RM4001140//Homo sapiens PAC clone DJ0964C11 from 7p14-p15, complete sequence//3.6e-79:468:90//AC004593
R-NT2RM4001151//HS_2270_B1_E05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2270 Col=9 Row=J, genomic survey sequence//5.5e-62:312:98//AQ163739
R-NT2RM4001155//Homo sapiens chromosome 12p13.3 clone RPC14-816N1, WORKING DRAFT SEQUENCE 31 unordered pieces//1.4e-107:536:97//AC005841

R-NT2RM4001187//X.laevis xUBFbeta2 mRNA for upstream binding factor 1.//0.019:177:63//X57201

R-NT2RM4001191//HS_3002_A1_F05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3002 Col=9 Row=K, genomic survey sequence.//3.9e-33:230:75//AQ088791

R-NT2RM4001200//Homo sapiens full-length insert cDNA clone YL35H03.//7.5e-69:335:99//AF085857

5 R-NT2RM4001203

R-NT2RM4001204

R-NT2RM4001217

R-NT2RM4001256

R-NT2RM4001258

10 R-NT2RM4001309

R-NT2RM4001313//Homo sapiens 12q24.1 PAC RPC11-71H24 (Roswell Park Cancer Institute Human PAC library) complete sequence.//0.00055:183:63//AC004551

R-NT2RM4001316//Homo sapiens chromosome 17, clone hCIT.117_K_16, complete sequence.//4.5e-21:212:79//AC004757

15 R-NT2RM4001320//CIT-HSP-2303E22.TR CIT-HSP Homo sapiens genomic clone 2303E22, genomic survey sequence.//3.8e-30:86:89//AQ021084

R-NT2RM4001340

0.0027:493:60//AC005133

R-NT2RM4001344

20 R-NT2RM4001347//CITBI-E1-2506I20.TR CITBI-E1 Homo sapiens genomic clone 2506I20, genomic survey sequence.//6.5e-16:1.01:99//AQ262797

R-NT2RM4001371//CITBI-E1-2503G21.TR CITBI-E1 Homo sapiens genomic clone 2503G21, genomic survey sequence.//0.063:140:65//AQ265776

R-NT2RM4001382//HS_3044_A1_F02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3044 Col=3 Row=K, genomic survey sequence.//0.96:103:66//AQ098668

25 R-NT2RM4001384//R.norvegicus mRNA for dendrin.//8.5e-07:120:75//Y09000

R-NT2RM4001410//Bovine cytochrome P450-scc mRNA fragment.//2.3e-15:199:75//M25920

R-NT2RM4001411//Rattus norvegicus FcεRI gamma-chain interacting protein SH2-B (SH2-B) mRNA, complete cds.//1.7e-55:235:83//U57391

30 R-NT2RM4001412

R-NT2RM4001414//Homo sapiens Xp22 Cosmids U98B4 and U24F2 (Lawrence Livermore human cosmid library) complete sequence.//1.7e-80:489:89//U69730

R-NT2RM4001437//RPC111-56D2.TJ RPC111 Homo sapiens genomic clone R-56D2, genomic survey sequence.//3.8e-43:250:93//AQ081969

35 R-NT2RM4001444//Homo sapiens Xp22-171-173 BAC GSHB-312I4 (Genome Systems Human BAC Library) complete sequence.//0.0034:224:63//AC005926

R-NT2RM4001454//Homo Sapiens Chromosome X clone bWXD90, complete sequence.//2.4e-33:360:68//AC004075

R-NT2RM4001455//HS_3229_B1_E04_MR CIT Approved-Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3229 Col=7 Row=J, genomic survey sequence.//1.0:183:61//AQ191289

40 R-NT2RM4001483//Homo sapiens clone DJ0826E18, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.2e-51:451:79//AC005282

R-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds.//2.2e-102:547:93//AB014585

R-NT2RM4001519//HS_2208_A1_F07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2208 Col=13 Row=K, genomic survey sequence.//0.25:214:63//AQ091836

45 R-NT2RM4001522//H.sapiens gene for Cu/Zn-superoxide dismutase.//3.6e-13:246:70//Z29336

R-NT2RM4001557//Plasmodium falciparum MAL3P4, complete sequence.//0.055:320:58//AL008970

R-NT2RM4001565//Homo sapiens chromosome 12p13.3 clone RPC111-189M20, WORKING DRAFT SEQUENCE, 39 unordered pieces.//3.9e-26:329:72//AC005910

50 R-NT2RM4001566//Human trophinin mRNA, complete cds.//6.3e-38:296:86//U04811

R-NT2RM4001569//Human DNA sequence from clone 461P17 on chromosome 20q12-13.2. Contains four novel (pseudo)genes for proteins with Kunitz/Bovine pancreatic trypsin inhibitor and/or WAP-type (Whey Acidic Protein) 'four-disulfide core' domains, COX6C (Cytochrome C Oxidase Polypeptide VIC, EC 1.9.3.1) and RPL5 (60S Ribosomal Protein L5) pseudogenes, a pseudogene similar to part of the HSPD1 (HSP60, Mitochondrial Matrix Protein P1 precursor, Heat Shock Protein 60, GROEL protein, HUCHA60) gene, and the Major Epididymis-specific protein F4 precursor (HF4, Epididymis Secretory protein F4, WAP-type (Whey Acidic Protein) 'four-disulfide core' domain).

55

R-NT2RM4001582//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//5.4e-60:558:77//AF071317

R-nnnnnnnnnnnn//M.musculus mRNA of enhancer-trap-locus 1.//4.8e-86:565:85//X69942

R-NT2RM4001594//Human interleukin-13 (IL-13) precursor gene, complete cds.//0.083:283:61//U31120

5 R-NT2RM4001597//HS_2059_A1_G11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2059 Col=21 Row=M, genomic survey sequence.//4.4e-09:105:83//AQ245136

R-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds.//6.7e-111:565:95//AB018334

R-NT2RM4001611//Homarus americanus ryanodine receptor (RyR) mRNA, partial cds.//1.0:364:61//AF051936

10 R-NT2RM4001629//RPC111-54G14.TJ RPC111 Homo sapiens genomic clone R-54G14, genomic survey sequence.//0.0018:347:61//AQ083173

R-NT2RM4001650

R-NT2RM4001662//Homo sapiens DNA sequence from PAC 159A15 on chromosome Xp11.21-p11.23. Contains inter-alpha-trypsin inhibitor heavy chain H3 precursor-like protein.//0.75:212:62//AL022575

R-NT2RM4001666//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-233A8, complete sequence.//2.6e-26:461:65//AC004685

15 R-NT2RM4001682//Human DNA sequence from clone 30M3 on chromosome 6p22.1-22.3. Contains three novel genes, one similar to C. elegans Y63D3A.4 and one similar to (predicted) plant, worm, yeast and archaea bacterial genes, and the first exon of the KIAA0319 gene. Contains ESTs, GSSs and putative CpG islands, complete sequence.//1.5e-107:544:96//AL031775

20 R-NT2RM4001710//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 126A5, WORKING DRAFT SEQUENCE.//1.8e-110:580:95//AL031447

R-NT2RM4001714//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//3.1e-10:543:59//AC004153

R-nnnnnnnnnnnn//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs, complete sequence.//8.7e-111:577:94//AL034430

25 R-NT2RM4001731//Ovis aries dinucleotide repeat polymorphism at MAF92 locus.//0.017:93:73//M80527

R-NT2RM4001741//Mouse mRNA for talin.//2.4e-34:273:83//X56123

R-NT2RM4001746//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 316G12, WORKING DRAFT SEQUENCE.//1.7e-112:567:96//AL031709

30 R-NT2RM4001754//Homo sapiens PAC clone 248O15 from 13q12-q13, complete sequence.//1.4e-64:475:83//AC002483

R-NT2RM4001758//R.norvegicus mRNA for serine/threonine kinase MARK1.//1.9e-18:202:78//Z83868

R-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds.//2.0e-22:236:80//AB018270

R-NT2RM4001783//Homo sapiens clone DJ0981O07, complete sequence.//4.4e-106:551:95//AC006017

35 R-NT2RM4001810//T28D3TF TAMU Arabidopsis thaliana genomic clone T28D3, genomic survey sequence.//0.76:279:60//B27099

R-NT2RM4001813

R-NT2RM4001823

R-NT2RM4001828//HS_3073_A2_E01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3073 Col=2 Row=I, genomic survey sequence.//1.6e-46:255:96//AQ121030

40 R-NT2RM4001836//Sus scrofa microsatellite S0398 sequence.//9.4e-06:141:69//U78024

R-NT2RM4001841//Salmo salar microsatellite Ssa65 DNA.//1.5e-06:175:65//AF019184

R-NT2RM4001842//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//5.0e-07:332:61//AC005077

45 R-NT2RM4001856//Mus musculus clone OST16642, genomic survey sequence.//4.8e-30:235:85//AF046633

R-nnnnnnnnnnnn//Hs_3244_B1_F10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3244 Col=19 Row=L, genomic survey sequence.//3.0e-40:263:89//AQ252798

R-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC.//5.0e-119:592:97//Y17711

R-NT2RM4001876//Megastigmus wachtlit dinucleotide microsatellite, clone

50 MWA47CT.//0.13:134:64//AJ001069

R-NT2RM4001880

R-NT2RM4001905//HS_2016_B1_H11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2016 Col=21 Row=P, genomic survey sequence.//0.0066:264:59//AQ226877

R-NT2RM4001922//HS_2228_B2_B07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=14 Row=D, genomic survey sequence.//2.5e-35:205:96//AQ065498

55 R-NT2RM4001930//Homo sapiens chromosome 17 clone hRPC 34 M 21 complete sequence.//1.0e-107:544:96//AL031775

98//AC005207

R-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds.//6.2e-109:556:95//AF098162

R-NT2RM4001953//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 473B4, WORKING DRAFT SEQUENCE.//1.3e-08:175:70//Z83826

5 R-NT2RM4001965//CIT-HSP-385N14.TR CIT-HSP Homo sapiens genomic clone 385N14, genomic survey sequence.//5.7e-69:532:81//B55044

R-nnnnnnnnnnnn//R.norvegicus mRNA for IP63 protein.//1.9e-61:352:83//X99330

R-NT2RM4001979//Homo sapiens full-length insert cDNA clone ZD29F04.//1.1e-98:465:100//AF086241

R-NT2RM4001984//Borrelia burgdorferi (section 47 of 70) of the complete genome.//0.14:461:60//AE001161

10 R-NT2RM4001987

R-NT2RM4002013

R-NT2RM4002018

R-NT2RM4002034//Homo sapiens chromosome 5, BAC clone 24p24 (LBNL H195), complete sequence.//3.6e-42:277:89//AC005353

15 R-NT2RM4002044//Homo sapiens PAC clone DJ1102B04 from 7q11.23-7q21, complete sequence.//0.83:476:57//AC006204

R-NT2RM4002054

R-NT2RM4002062//Human microsomal epoxide hydrolase gene, exons 5 and 6.//0.11:136:67//U06659

20 R-NT2RM4002063//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//2.9e-99:503:96//U82267

R-nnnnnnnnnnnn//Homo sapiens CAGH45 mRNA, complete cds.//9.6e-41:554:68//U80742

R-NT2RM4002067//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 329A5, WORKING DRAFT SEQUENCE.//7.7e-64:476:81//Z97832

R-NT2RM4002073//Mus musculus fatty acid transport protein 3 mRNA, partial cds.//1.1e-33:238:85//AF072758

25 R-NT2RM4002075//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.0031:403:57//AC005504

R-NT2RM4002093//Human Chromosome 11 pac pDJ227b23, WORKING DRAFT SEQUENCE, 19 unordered pieces.//9.4e-07:322:62//AC000383

30 R-nnnnnnnnnnnn//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//5.6e-44:432:74//D12646

R-NT2RM4002128//Human HepG2 partial cDNA, clone hmd2e12m5.//2.0e-26:186:90//D17000

R-NT2RM4002140

R-NT2RM4002145//Homo sapiens full-length insert cDNA clone ZD38E12.//1.4e-15:193:76//AF086247

R-NT2RM4002146//Human ABL gene, intron 1b, partial sequence.//0.66:170:63//U07562

35 R-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, partial cds.//4.5e-110:560:96//AF084535

R-NT2RM4002174//Homo sapiens chromosome 17, clone hRPK.74_E_22, complete sequence.//8.0e-43:302:85//AC005696

R-NT2RM4002189

R-NT2RM4002194//Human Cosmid g5129g129 from 7q31.3, complete sequence.//0.29:382:60//AC003960

40 R-NT2RM4002205//Spiroplasma virus (SpV1-R8A2 B) complete genome.//3.5e-05:432:56//X51344

R-NT2RM4002213

R-NT2RM4002226//Homo sapiens chromosome 17, clone HCIT187M2, complete sequence.//0.94:198:61//AC004448

R-NT2RM4002251

45 R-NT2RM4002256//Homo sapiens PAC clone DJ0570D02 from 7p13-p14, complete sequence.//2.3e-58:299:85//AC004837

R-NT2RM4002266//H.sapiens CpG island DNA genomic MseI fragment, clone 179f11, forward read cpg179f11.ft1a.//0.72:97:69//Z57487

50 R-NT2RM4002278//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//7.5e-49:405:84//AC005069

R-NT2RM4002281//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 702J19, WORKING DRAFT SEQUENCE.//1.7e-13:168:77//AL033531

R-NT2RM4002287

55 R-NT2RM4002294//Homo Sapiens Chromosome X clone bWXD171, WORKING DRAFT SEQUENCE, 1 ordered pieces.//0.98:208:65//AC004676

R-NT2RM4002301//Homo sapiens chromosome 17, clone hRPK.74_E_22, complete sequence.//8.0e-43:302:85//AC005696

R-NT2RM4002302//Human DNA sequence from clone hRPK.74_E_22, complete sequence.//8.0e-43:302:85//AC005696

R-NT2RM4002303//Human DNA sequence from clone hRPK.74_E_22, complete sequence.//8.0e-43:302:85//AC005696

gene similar to GPISG20 and other exonucleases). Contains ESTs, STSs, GSSs, genomic markers D6S1691 and D6S299 and a ca repeat polymorphism, complete sequence.//1.9e-35:265:84//AL032822

R-nnnnnnnnnnnn//Human mRNA for KIAA0319 gene, complete cds.//2.4e-42:569:68//AB002317

R-NT2RM4002344//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.013:391:59//AC004709

R-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds.//8.6e-121:593:97//AB014549

R-NT2RM4002374//Human DNA sequence from cosmid U131B10, between markers DXS366 and DXS87 on chromosome X contains XK membrane transport protein, ESTs and STS.//3.8e-44:258:86//Z73417

R-NT2RM4002383//Human Chromosome 15q26.1 PAC clone pDJ10k5 containing human DNA polymerase gamma (polg) gene, complete sequence.//0.00084:345:60//AC005316

R-NT2RM4002390

R-NT2RM4002409//RPCI11-45M10.TK RPCI11 Homo sapiens genomic clone R-45M10, genomic survey sequence.//0.99:151:66//AQ194411

R-NT2RM4002438

R-NT2RM4002446//Human DNA sequence from clone 360A4 on chromosome 16. Contains ESTs, complete sequence.//2.8e-103:533:95//AL031008

R-NT2RM4002452

R-NT2RM4002457//Homo sapiens chromosome 16, cosmid clone 321D4 (LANL), complete sequence.//0.99:171:64//AC004034

R-NT2RM4002460//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//0.96:94:71//Z92545

R-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds.//2.9e-102:508:97//AF083255

R-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds.//7.0e-31:172:98//AB014591

R-NT2RM4002493//CIT-HSP-2296C24.TF CIT-HSP Homo sapiens genomic clone 2296C24, genomic survey sequence.//0.46:182:62//AQ006882

R-NT2RM4002499//Human v-fos transformation effector protein (Fte-1), mRNA complete cds.//7.3e-24:134:99//M84711

R-NT2RM4002504//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence.//3.9e-11:334:63//AC002368

R-nnnnnnnnnnnn

R-NT2RM4002532//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 341D10, WORKING DRAFT SEQUENCE.//3.4e-17:171:79//Z97985

R-NT2RM4002534

R-NT2RM4002567//Homo sapiens chromosome 7 clone UWGC:g1564a040 from 7p14-15, complete sequence.//2.2e-26:181:76//AC005271

R-NT2RM4002571

R-NT2RM4002593//CIT-HSP-2303L15.TF CIT-HSP Homo sapiens genomic clone 2303L15, genomic survey sequence.//0.034:73:82//AQ015579

R-NT2RM4002623//Homo sapiens clone UWGC:g1564a209 from 7p14-15, complete sequence.//0.0014:670:55//AC005862

R-NT2RP2000001//Plasmodium falciparum chromosome 2, section 59 of 73 of the complete sequence.//0.00087:251:59//AE001422

R-NT2RP2000006//Human DNA sequence from PAC 155D22 on chromosome 6q27. Contains EST, STSs and a GSS.//2.7e-37:259:86//Z97205

R-NT2RP2000008//RPCI11-41G16.TP RPCI-11 Homo sapiens genomic clone RPCI-11-41G16, genomic survey sequence.//4.1e-25:365:70//AQ029090

R-NT2RP2000027//Homo sapiens chromosome 17, clone HCIT305D20, complete sequence.//6.0e-05:307:62//AC004098

R-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds.//8.4e-41:223:96//AB018290

R-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//5.8e-63:325:96//AF061749

R-NT2RP2000054//Human tyrosinase gene, 5'-flanking region (containing enhancer element responsible for pigment cell-specific transcription).//0.88:210:60//D26163

R-NT2RP2000056//Homo sapiens mRNA for KIAA0747 protein, partial cds.//8.4e-41:223:96//AB018290

R-NT2RP2000057//Homo sapiens mRNA for KIAA0747 protein, partial cds.//8.4e-41:223:96//AB018290

R-NT2RP2000067//Homo sapiens mRNA for growth-potentiating factor, complete cds.//0.0014:670:55//AC005862

R-NT2RP2000070//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//3.1e-76:381:98//AC005754

R-NT2RP2000076//Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence.//2.3e-06:380:60//AE001372

5 R-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds.//3.5e-77:379:97+++F050079

R-NT2RP2000079//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1125A11, WORKING DRAFT SEQUENCE.//6.5e-32:314:78//AL034549

R-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds.//5.6e-74:378:96//AB018338

10 R-NT2RP2000091//Homo sapiens clone RG015P03, complete sequence.//9.3e-21:226:76//AC005048

R-NT2RP2000097//Human DNA sequence from cosmid U209G1 on chromosome X.//9.2e-40:278:81//Z68873

R-NT2RP2000098//Human BAC clone RG333F24 from 7q11.2-q21, complete sequence.//0.34:132:65//AC004015

R-NT2RP2000108//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//3.1e-09:259:67//AC003973

15 R-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds.//1.8e-74:386:95//AB018356

R-NT2RP2000120//CITBI-E1-2503M8.TR CITBI-E1 Homo sapiens genomic clone 2503M8, genomic survey sequence.//5.1e-05:87:77//AQ263909

R-nnnnnnnnnnnnn

20 R-nnnnnnnnnnnnn//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.//4.9e-11:153:69//AC004827

R-NT2RP2000147

R-NT2RP2000153//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//0.0058:261:57//U95626

25 R-NT2RP2000157//Homo sapiens Chr.14 PAC RPC14-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.5e-119:603:96//AC005924

R-NT2RP2000161//CIT-HSP-2045P7.TR CIT-HSP Homo sapiens genomic clone 2045P7, genomic survey sequence.//0.89:173:63//B79728

R-NT2RP2000175

R-NT2RP2000183

30 R-NT2RP2000195//Homo sapiens chromosome 17, clone hRPK.60_A_24, complete sequence.//4.3e-39:306:83//AC005325

R-NT2RP2000205//Human DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

35 R-NT2RP2000224//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence.//7.3e-55:306:94//AC004382

R-NT2RP2000232

R-NT2RP2000233//Mus musculus tumor metastasis associated gene product (MAG) mRNA, complete cds.//7.6e-13:144:75//U88401

40 R-NT2RP2000239//Homo sapiens chromosome 4 clone B353C18 map 4q25, complete sequence.//9.6e-63:410:86//AC004066

R-NT2RP2000248//Caenorhabditis elegans cosmid T01C8.//1.0:282:58//U58726

R-NT2RP2000257//Homo sapiens PAC clone DJ0808G16 from 7q11.23-q21, complete sequence.//2.5e-11:163:72//AC004894

45 R-NT2RP2000258//Arabidopsis thaliana chromosome II BAC T31E10 genomic sequence, complete sequence.//0.58:442:58//AC004077

R-NT2RP2000270//Homo sapiens DNA sequence from PAC 97D16 on chromosome 6p21.3-22.2. Contains an unknown pseudogene, a 60S Ribosomal protein L24 (L30) LIKE pseudogene and histone genes H2BFC (H2B/c), H4FFP (H4/f pseudogene), H2AFC (H2A/c), H3F1K (H3.1/k) and a tRNA-Val pseudogene and tRNA-Thr gene. Contains ESTs, STSs, GSSs and genomic marker D6S464, complete sequence.//1.1e-39:292:84//AL009179

50 R-NT2RP2000274//CIT-HSP-237901.TR CIT-HSP Homo sapiens genomic clone 237901, genomic survey sequence.//6.9e-10:121:81//AQ109409

R-NT2RP2000288

R-NT2RP2000289

R-NT2RP2000297//Homo sapiens full-length insert cDNA clone ZB81C03.//7.7e-109:519:99//AF086165

55 R-NT2RP2000298

R-NT2RP2000316//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000317//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000318//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000319//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000320//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000321//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000322//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000323//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000324//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000325//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000326//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000327//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000328//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000329//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000330//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000331//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000332//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000333//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000334//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000335//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000336//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000337//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000338//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000339//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000340//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000341//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000342//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000343//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000344//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000345//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000346//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000347//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000348//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000349//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000350//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000351//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000352//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000353//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000354//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000355//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000356//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000357//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000358//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000359//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000360//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000361//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000362//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000363//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000364//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000365//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000366//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000367//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000368//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000369//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000370//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000371//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000372//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000373//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000374//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000375//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000376//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000377//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000378//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000379//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000380//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000381//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000382//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000383//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000384//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000385//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000386//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000387//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000388//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000389//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000390//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000391//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000392//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000393//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000394//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000395//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000396//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000397//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000398//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000399//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

R-NT2RP2000400//Homo sapiens DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155

pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence //4.3e-113:580:96//AL022398

R-NT2RP2000329//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces //7.4e-47:367:77//AC006039

R-NT2RP2000337//Anopheles quadrimaculatus NADH dehydrogenase subunits (1-4, 4L, 5-6); cytochrome oxidase subunits (1-3); adenosine triphosphatase subunits (6,8); cytochrome b; transfer RNA; ribosomal RNA (large and small subunits) //4.9e-08:494:58//L04272

R-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds //3.4e-46:262:94//U83981

R-NT2RP2000369//Homo sapiens chromosome 17, clone HCIT169H9, WORKING DRAFT SEQUENCE, 6 unordered pieces //3.0e-07:334:61//AC002993

R-NT2RP2000414//Mouse DNA sequence *** SEQUENCING IN PROGRESS *** from clone BAC394, WORKING DRAFT SEQUENCE //7.0e-08:98:83//AJ004828

R-NT2RP2000420//Homo sapiens chromosome 17, clone hRPK.640_I_15, complete sequence //0.99:150:62//AC005324

R-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds //4.6e-19:142:90//AF102265

R-NT2RP2000438//RPC111-62I13.TK RPC111 Homo sapiens genomic clone R-62I13, genomic survey sequence //3.1e-06:103:79//AQ199572

R-NT2RP2000448//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence //2.0e-22:276:73//AC004691

R-NT2RP2000459//CIT-HSP-2013N9.TR CIT-HSP Homo sapiens genomic clone 2013N9, genomic survey sequence //5.5e-27:205:87//853940

R-NT2RP2000498//Homo sapiens Chromosome 11q23 PAC clone pDJ149k2 containing PLZF gene encoding kruppel-like zinc finger protein, complete sequence //6.0e-12:119:84//AC001234

R-NT2RP2000503//Human CYP11B2 gene for steroid 18-hydroxylase (P-450 C18), 5'-flanking region and exon 1 //0.48:201:64//D10170

R-NT2RP2000510//Bactrocera dorsalis strain Tahiti mitochondrial D-loop region, complete sequence //3.6e-07:472:59//AF033929

R-nnnnnnnnnnnnnnn

R-NT2RP2000523//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 150C2, WORKING DRAFT SEQUENCE //2.3e-61:317:97//AL022318

R-NT2RP2000603//Homo sapiens mRNA for MCM3 import factor, complete cds //6.6e-29:167:97//AB005543

R-NT2RP2000617

R-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds //2.5e-64:335:96//AB014514

R-NT2RP2000644//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat //1.8e-28:383:70//Z92545

R-NT2RP2000656//Homo sapiens DNA sequence from PAC 874C20 on chromosome 6p22.1-22.3. Contains a Zinc Finger Protein ZFP47 LIKE gene, a Zinc Finger Protein pseudogene and a Zinc Finger Protein SRE-ZBP pseudogene. Contains ESTs, STSs and GSSs, complete sequence //0.0093:110:70//AL021997

R-NT2RP2000658//Bacillus thuringiensis chitinase (chi) gene, complete cds //0.73:301:60//U89796

R-NT2RP2000668

R-NT2RP2000678//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 8/15, WORKING DRAFT SEQUENCE //2.8e-11:256:66//AP000015

R-NT2RP2000710//Genomic sequence from Human 17, WORKING DRAFT SEQUENCE, 9 unordered pieces //0.036:176:69//AC002346

R-NT2RP2000715//Homo sapiens PAC clone DJ1066K24 from 7p15, complete sequence //2.7e-110:555:96//AC004540

R-NT2RP2000731//Human DNA sequence from clone 497J21 on chromosome 6q26-27. Contains a KOC (KH-domain containing transcript overexpressed in cancer) pseudogene, genomic marker D6S193, ESTs, STSs and GSSs, and a ca repeat polymorphism, complete sequence //2.6e-18:319:68//AL023775

R-NT2RP2000758//CIT-HSP-507A14.TP CIT-HSP Homo sapiens genomic clone 507A14, genomic survey sequence //1.0:189:60//B50590

R-NT2RP2000764

R-NT2RP2000809//Human DNA sequence from clone H435BHE from 12p11.1 complete sequence //1.1e-11:117:107//AC004040

R-NT2RP2000812//CIT-HSP-2281C3.TP CIT-HSP Homo sapiens genomic clone 2281C3 genomic survey sequence //1.0:189:60//B50590

quence.//9.5e-32:176:97//B99575

R-nnnnnnnnnnnn//paramecium species 5,87 mt dna dimer: replication init. region//0.0077:418:57//K00916

R-NT2RP2000816//F.rubripes GSS sequence, clone 011H02aA6, genomic survey sequence.//0.61:52:73//AL011013

5 R-NT2RP2000819

R-NT2RP2000841//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 43408, WORKING DRAFT SEQUENCE.//0.00012:181:70//AL033504

R-NT2RP2000842//Mus musculus (C57BL/10 X C3H)F2 clone 4.9 novel mRNA from reninexpressing kidney tumor cell line, partial sequence.//3.7e-27:388:72//U13370

10 R-NT2RP2000845//Homo sapiens chromosome 17, clone hRPK.849_N_15, complete sequence.//0.0022:200:68//AC005703

R-NT2RP2000863

R-NT2RP2000880//Homo sapiens mRNA for putative GTP-binding protein, partial.//2.3e-43:279:89//AJ006412

15 R-NT2RP2000892//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 7/10.//0.0028:221:62//AB020875

R-NT2RP2000931//Homo sapiens mRNA for KIAA0723 protein, complete cds.//2.2e-55:290:96//AB018266

R-NT2RP2000938//Homo sapiens full-length insert cDNA clone ZD55G12.//2.1e-37:215:93//AF086336

R-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds.//3.0e-96:494:96//AB018298

R-NT2RP2000965

20 R-NT2RP2000970//Homo sapiens DNA sequence from BAC 747E2 on chromosome 22q12.1. Contains ESTs, STSs and GSSs and genomic marker D22S56, complete sequence.//4.5e-87:440:97//AL021393

R-NT2RP2000985//Homo sapiens chromosome 17, clone hRPK.597_M_12, complete sequence.//5.4e-93:484:95//AC005277

25 R-NT2RP2000987//Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence.//2.1e-06:318:62//AE001372

R-NT2RP2001036//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 41018, WORKING DRAFT SEQUENCE.//2.0e-24:273:73//AL031732

R-NT2RP2001044//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//3.3e-07:365:65//AC005140

30 R-NT2RP2001065//Caenorhabditis elegans cosmid F10G7.//9.2e-06:273:59//U40029

R-NT2RP2001070//CITBI-E1-2503F4.TF CITBI-E1 Homo sapiens genomic clone 2503F4, genomic survey sequence.//0.13:97:72//AQ265973

R-NT2RP2001094//Mycoplasma mycoides mycoides SC immunodominant protein P72 (p72) gene, complete cds, mannitol-1-phosphate dehydrogenase (mt1D) gene, partial cds and insertion sequence IS1296, complete sequence.//0.018:373:57//U61140

35 R-NT2RP2001119

R-NT2RP2001127//Homo sapiens HRIHFB2060 mRNA, partial cds.//4.5e-55:304:94//AB015348

40 R-NT2RP2001137//Homo sapiens DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 PLC-II, PLC-148), the KIAA0395 gene for a probable Zinc Finger Homeobox protein and a 60S Ribosomal Protein L23 LIKE pseudogene. Contains a predicted CpG island, ESTs, STSs and GSSs, complete sequence.//0.69:129:65//AL022394

R-NT2RP2001149//Sequence 5 from Patent US 4798885.//8.5e-28:322:77//I01838

R-NT2RP2001168

45 R-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds.//4.8e-95:490:96//AB 007949

R-NT2RP2001174//CIT-HSP-2170B18.TR CIT-HSP Homo sapiens genomic clone 2170B18, genomic survey sequence.//1.3e-33:204:93//B89680

R-NT2RP2001196//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-65, complete sequence.//1.7e-06:413:61//AL010134

50 R-NT2RP2001218//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS, GSS, complete sequence.//8.5e-15:278:68//AL022153

R-NT2RP2001226//Human DNA sequence from clone 1170D6 on chromosome Xq22.3-23. Contains a pseudogene similar to U-SNRNP associated Cyclophilin (USA-CYP, EC 5.2.1.8), ESTs, an STS and a GSS, complete sequence.//0.0020:462:57//AL030995

55 R-NT2RP2001233//CIT-HSP-2356P23.TR CIT-HSP Homo sapiens genomic clone 2356P23, genomic survey sequence.//1.3e-33:204:93//B89680

R-NT2RP2001233//CIT-HSP-2356P23.TR CIT-HSP

R-NT2RP2001233//CIT-HSP-2356P23.TR CIT-HSP

R-NT2RP2001233//CIT-HSP-2356P23.TR CIT-HSP

R-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds.//4.6e-111:544:97//AB018353
 R-NT2RP2001277//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y59A8,
 WORKING DRAFT SEQUENCE.//0.0058:327:59//Z98870
 R-NT2RP2001290//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING
 DRAFT SEQUENCE, 3 unordered pieces.//0.96:187:65//AC004709
 R-NT2RP2001295//Homo sapiens BAC clone NH0491B03 from 7p21-p15, complete sequence.//0.59:218:62//
 AC006041
 R-NT2RP2001312//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 349A12, WORKING
 DRAFT SEQUENCE.//0.12:117:64//AL033520
 R-NT2RP2001327//Caenorhabditis elegans cosmid R04D3, complete sequence.//0.31:119:66//Z70212
 R-NT2RP2001328//HS_2213_A1_D07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=2213 Col=13 Row=G, genomic survey sequence.//1.7e-22:200:83//AQ136874
 R-NT2RP2001347//Plasmodium falciparum MAL3P8, complete sequence.//0.81:509:56//AL034560
 R-NT2RP2001378//H.sapiens DNA sequence.//0.94:147:63//Z22404
 R-NT2RP2001381//Homo sapiens cyclin E2 mRNA, complete cds.//3.2e-09:75:97//AF091433
 R-NT2RP2001392//Myxococcus xanthus ATP-dependent protease (bsgA) gene, complete cds.//0.079:178:62//
 L19301
 R-NT2RP2001394//Human DNA sequence from PAC 389A20 on chromosome X contains ESTs STS, CpG islands
 and polymorphic CA repeat.//3.4e-60:351:90//Z93242
 R-NT2RP2001397//Hamster mRNA for cyclinB2, complete cds.//5.4e-55:320:83//D17294
 R-NT2RP2001420//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1108D11, WORKING
 DRAFT SEQUENCE.//1.0e-44:246:85//AL034419
 R-NT2RP2001423//Human DNA sequence from clone 726F20 on chromosome 1p36.11-36.23. Contains ESTs
 and a GSS, complete sequence.//3.7e-05:417:61//AL031273 R-NT2RP2001427//Human Chromosome 11 Cosmid
 cSRL34e5, complete sequence.//0.94:287:59//U73643
 R-NT2RP2001436//Mus musculus clone OST1784, genomic survey sequence.//5.2e-31:299:77//AF046702
 R-NT2RP2001440//Rattus norvegicus mRNA for 14-3-3 protein gamma-subtype, complete cds.//7.8e-75:548:83//
 D17447
 R-NT2RP2001445//Homo sapiens 12q13.1 PAC RPC11-228P16 (Roswell Park Cancer Institute Human PAC Li-
 brary) complete sequence.//1.0e-06:452:59//AC004801
 R-NT2RP2001449//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//
 5.1e-08:218:67//AC004846
 R-NT2RP2001450
 R-NT2RP2001467//Human BAC clone RG343P13 from 7q31, complete sequence.//3.8e-31:254:83//AC002465
 R-NT2RP2001506//C.barati p-47, ntnt, bonT genes.//1.2e-06:415:60//Y12091
 R-NT2RP2001511//Plasmodium falciparum MAL3P7, complete sequence.//0.11:155:63//AL034559
 R-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1.//2.1e-104:545:95//Y14494
 R-NT2RP2001526//Homo sapiens chromosome 17, clone hCIT.175_E_5, complete sequence.//7.0e-16:283:68//
 AC004596
 R-NT2RP2001536//Human DNA from chromosome 14-specific cosmid containing XRCC3 DNA repair gene, ge-
 nomic sequence, complete sequence.//7.7e-16:108:96//AF037222
 R-NT2RP2001560//CIT978SK-A-56H4.TP CIT978SK Homo sapiens genomic clone A-56H4, genomic survey se-
 quence.//0.052:112:66//B73597
 R-NT2RP2001569//CIT-HSP-2335F8.TF CIT-HSP Homo sapiens genomic clone 2335F8, genomic survey se-
 quence.//6.0e-78:383:98//AQ042029
 R-NT2RP2001576//Homo sapiens sulfonyleurea receptor (SUR2) gene, exon 37.//0.33:135:66//AF061322
 R-NT2RP2001581//Homo sapiens (clone MFD220) PCR primer.//2.7e-07:240:63//L15407
 R-NT2RP2001597//HS_3016_B2_F06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3016 Col=12 Row=L, genomic survey sequence.//5.3e-45:310:87//AQ118854
 R-NT2RP2001601//Homo sapiens chromosome 17, clone hRPK.855_D_21, complete sequence.//0.015:445:58//
 AC006079
 R-NT2RP2001613//Mus musculus orphan nuclear hormone receptor (CAR) gene, complete sequence.//3.5e-16:
 413:63//AF009326
 R-NT2RP2001628//Phytomonas serpens kinetoplast maxicircle ribosomal protein S12 (G6) edited mRNA, com-
 plete cds.//0.11:190:63//AF034626
 R-NT2RP2001677//Homo sapiens chromosome 17, clone hRPK.855_D_21, complete sequence.//0.015:445:58//
 AC006079

AC004472

R-NT2RP2001678//Human BAC clone RG222A16 from 7q31, complete sequence.//0.95:107:66//AC002385

R-NT2RP2001699//Mus musculus erythroid ankyrin and two alternatively spliced erythroid ankyrins (Ank1) gene, putative exon 41 and partial cds.//8.8e-05:211:63//U76758

5 R-NT2RP2001720//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence.//4.7e-68:352:97//AC004079

R-NT2RP2001721//HS-1052-B1-G06-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 774 Col=11 Row=N, genomic survey sequence.//7.7e-05:346:59//B40914

10 R-NT2RP2001740//HS_3213_A2_D02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=4 Row=G, genomic survey sequence.//1.1e-16:162:82//AQ175104

R-NT2RP2001748//Human gene for L-histidine decarboxylase, complete cds.//2.0e-33:312:77//D16583

R-NT2RP2001762//Homo sapiens chromosome 1, BAC CIT-HSP-292g8 (BC262482), complete sequence.//2.3e-100:435:97//AC004783

15 R-NT2RP2001813//Human leukocyte common antigen T200 (CD45, LCA) gene, exon 9.//0.031:261:60//M23468
R-NT2RP2001861

R-NT2RP2001869//Sequence 5 from patent US 5595900.//4.2e-21:194:77//I34189

R-NT2RP2001876

20 R-NT2RP2001883//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//5.0e-111:485:97//AL031864

R-NT2RP2001900

R-NT2RP2001907//Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds.//5.4e-42:382:77//U07563

25 R-NT2RP2001926//HS_3180_B2_F02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3180 Col=4 Row=L, genomic survey sequence.//2.8e-25:138:80//AQ185415

R-NT2RP2001936//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.0:320:60//AC005504

R-NT2RP2001943//Dictyostelium discoideum PkgA (pkgA) gene, partial cds.//1.4e-08:378:59//AF020280

R-NT2RP2001946//Homo sapiens clone NH0140K04, complete sequence.//3.6e-85:409:100//AC005033

30 R-NT2RP2001947//Human mRNA for KIAA0390 gene, complete cds.//0.85:140:64//AB002388

R-NT2RP2001969

R-NT2RP2001976//CIT-HSP-2281C3.TR CIT-HSP Homo sapiens genomic clone 2281C3, genomic survey sequence.//2.0e-60:307:98//B99575

35 R-NT2RP2001985//Arabidopsis thaliana DNA chromosome 4, BAC clone F1N20 (ESSAll project).//0.031:282:61//AL022140

R-NT2RP2002025

R-NT2RP2002032//CITBI-E1-2502C19.TF CITBI-E1 Homo sapiens genomic clone 2502C19, genomic survey sequence.//1.2e-52:285:95//AQ264715

R-NT2RP2002033//Human (lambda) DNA for immunoglobulin light chain.//1.1e-08:389:61//D88270

40 R-NT2RP2002041//Homo sapiens 12p13.3 BAC RPC11-319E16 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//1.1e-49:264:97//AC006206

R-NT2RP2002046//Human BAC clone GS119P05 from 7q21, complete sequence.//0.0023:429:61//AC004011

R-NT2RP2002047//P.falciparum PK1 gene.//0.00015:239:62//X83707

45 R-NT2RP2002058//HS_2183_A1_G01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=1 Row=M, genomic survey sequence.//1.2e-21:185:84//AQ022560

R-NT2RP2002066//G.gallus microsatellite DNA (LEI0222 (=T15ivD04)).//0.18:102:70//Z83792

R-NT2RP2002070//P.falciparum major merozoite surface antigen (PMMSA) mRNA, complete cds, isolate FC27.//0.95:192:61//M19143

50 R-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence.//3.8e-25:182:86//AF052183

R-NT2RP2002079//Human DNA sequence from clone 431P23 on chromosome 6q27. Contains the first coding exon of the MLLT4 gene for myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (AF-6, Afadin, MLLT-4, ALL-1 fusion partner), and a Serine Palmitoyltransferase 2 (EC 2.3.1.50, Long Chain Base Biosynthesis protein 2, LCB-2, SPT-2) pseudogene. Contains ESTs, STs, GSSs, and a putative CpG island, complete sequence.//1.7e-10:97:90//AL009178

55 R-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein.//4.6e-59:376:89//AJ007509

R-NT2RP2002105

R-NT2RP2002124//Homo sapiens genomic clone 2124, genomic survey sequence.//0.88:147:64//AQ26577

R-NT2RP2002137//Homo sapiens Xp22-175-176 BAC GSHB-484O17 (Genome Systems Human BAC Library) complete sequence//0.0065:294:61//AC005913

R-NT2RP2002154

R-NT2RP2002172//RPC111-90C20.TJ RPC111 Homo sapiens genomic clone R-90C20, genomic survey sequence//0.049:160:65//AQ282591

R-NT2RP2002185//CIT-HSP-2341115.TF CIT-HSP Homo sapiens genomic clone 2341115, genomic survey sequence//6.0e-36:230:90//AQ053355

R-NT2RP2002192//HS_2222_B1_F08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2222 Col=15 Row=L, genomic survey sequence//1.9e-15:249:71//AQ178491

R-NT2RP2002193//Rattus norvegicus potassium channel regulatory protein KChAP mRNA, complete cds//4.7e-35:438:73//AF032872

R-NT2RP2002208//Hansenula wingei mitochondrial DNA, complete sequence//0.00057:468:57//D31785

R-NT2RP2002219//HS_2058_A1_C09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=17 Row=E, genomic survey sequence//3.4e-55:512:77//AQ234380

R-NT2RP2002231//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-31, complete sequence//1.5e-06:398:61//Z98557

R-nnnnnnnnnnnn//Sequence 11 from patent US 5624818//3.3e-91:553:87//I41141

R-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds//3.0e14:132:84//AF005418

R-NT2RP2002259//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 118J21, WORKING DRAFT SEQUENCE//1.6e-96:548:91//AL033527

R-NT2RP2002270//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence//5.1e-06:391:60//AC004605

R-NT2RP2002292//Genomic sequence from Human 13, complete sequence//0.91:159:64//AC001226

R-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds//1.3e-101:527:94//AF069532

R-NT2RP2002316//Plasmodium falciparum chromosome 2, section 45 of 73 of the complete sequence//0.00052:389:59//AE001408

R-NT2RP2002325//Homo sapiens peroxisomal biogenesis factor (PEX11a) mRNA, complete cds//2.3e-112:567:95//AF093668

R-NT2RP2002333//Rat POU domain factor (Brn-5) mRNA//1.5e-22:323:73//L23204

R-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds//3.7e-102:600:89//AF038958

R-NT2RP2002394//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces//0.039:399:59//AC005308

R-NT2RP2002408//HS_2212_A1_E09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2212 Col=17 Row=I, genomic survey sequence//9.6e-35:231:88//AQ184632

R-NT2RP2002426//Human DNA sequence from clone 101G11 on chromosome 22q12. Contains an ACO2 (Mitochondrial Aconitate Hydratase (Aconitase, Citrate Hydro-Lyase, EC 4.2.1.3)) pseudogene, ESTs, STSs, GSSs and a putative CpG island, complete sequence//2.8e-39:308:82//AL021877

R-NT2RP2002439//Leishmania tarentolae mitochondrial electron transport chain component mRNA//0.022:102:71//M74225

R-NT2RP2002457//Homo sapiens DNA sequence from PAC 142L7 on chromosome 6q21. Contains a Laminin Alpha 4 (LAMA4) LIKE gene coding for two alternatively spliced transcripts, a Tubulin Beta LIKE pseudogene, a Connective tissue growth factor (NOV, GIG) LIKE gene, A predicted CpG island, ESTs, STSs and genomic marker D6S416, complete sequence//0.00099:354:59//Z99289

R-NT2RP2002464//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 6/15, WORKING DRAFT SEQUENCE//0.0015:219:67//AP000013

R-NT2RP2002475

R-nnnnnnnnnnnn//Homo sapiens mRNA for ABC transporter 7 protein, complete cds//3.1e-113:605:92//AB005289

R-NT2RP2002498//Human DNA sequence from PAC 162H14 on chromosome 22. Contains 3' part of a FIBULIN 1 like gene and ESTs, complete sequence//0.32:210:64//Z98047

R-NT2RP2002503//Homo sapiens, clone hRPK.15_A_1, complete sequence//4.0e-86:429:98//AC006213

R-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds//2.7e-105:583:91//AB018334

R-NT2RP2002520//Saccharomyces cerevisiae mitochondrial tRNA-Tyr tRNA-Asn. & amp; tRNA-Met genes //1.1e-58:14:223:32

R-NT2RP2002537//Human DNA sequence from PAC 162H14 on chromosome 22. Contains 3' part of a FIBULIN 1 like gene and ESTs, complete sequence//0.32:210:64//Z98047

R-NT2RP2002537//Human DNA sequence from PAC 162H14 on chromosome 22. Contains 3' part of a FIBULIN 1 like gene and ESTs, complete sequence//0.32:210:64//Z98047

R-NT2RP2002986//Human DNA sequence from clone 1147O16 on chromosome Xp21.1-21.3. Contains 13 exons of the DMD muscular dystrophy gene. Contains an STS and GSSs, complete sequence//0.31:219:62//AL031542
 R-NT2RP2002987//Homo sapiens chromosome 18, clone hRPK.24_A_23, complete sequence//1.3e-51:283:88//AC005968

5 R-NT2RP2002993//Human DNA sequence from PAC 106B9 on chromosome Xq21://4.3e-11:430:63//AL021307
 R-NT2RP2003000//Saccharomyces cerevisiae mitochondrion transfer RNA- Leu, Gln, Lys, Arg, Gly, Asp, Ser2, Arg2, Ala, Ile, Tyr, Asn genes//0.00088:347:62//L36887

R-NT2RP2003034//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 2/10//3.5e-33:271:82//AB020870

10 R-NT2RP2003073

R-NT2RP2003099//Homo sapiens PAC clone DJ0886O08 from 7q32-q35, complete sequence//1.5e-45:548:69//AC004914

R-NT2RP2003108

R-NT2RP2003117//Homo sapiens clone DJ1137M13, complete sequence//2.0e-51:323:88//AC005378

15 R-NT2RP2003121//HS_2238_A1_E08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2238 Col=15 Row=I, genomic survey sequence//0.00055:324:61//AQ293058

R-NT2RP2003125

R-NT2RP2003129

R-NT2RP2003137//Human BAC clone RG084D04 from 7q31, complete sequence//1.1e-46:521:74//AC003084

20 R-NT2RP2003161//Homo sapiens chromosome 10 clone CIT-HSP-1287C20, complete sequence//1.0:368:59//AC005879

R-NT2RP2003164//Dictyostelium discoideum actin 4 gene, 3' UTR//1.0:120:64//M25581

R-NT2RP2003165//Homo sapiens chromosome 17, clone hRPK.1018_N_14, complete sequence//2.2e-71:467:86//AC005823

25 R-NT2RP2003177

R-NT2RP2003194//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 996D20, WORKING DRAFT SEQUENCE//1.1e-95:585:88//AL031597

R-NT2RP2003206//P.falciparum interspersed repeat antigen (FIRA) gene//0.039:338:60//M17877

R-NT2RP2003230//Plasmodium falciparum MAL3P6, complete sequence//1.9e-11:542:60//Z98551

30 R-NT2RP2003237//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDH9, complete sequence//1.0:311:60//AB016888

R-NT2RP2003243//CIT-HSP-2368D12.TR CIT-HSP Homo sapiens genomic clone 2368D12, genomic survey sequence//0.39:112:66//AQ077738

35 R-NT2RP2003265//Muridae sp. (mouse-rat, neuroblastoma-glioma hybrid cell line NGD5) mRNA, complete cds//1.3e-38:273:83//L38481

R-NT2RP2003272//Homo sapiens clone UWGC:y17c131 from 6p21, complete sequence//4.4e-15:181:66//AC004187

R-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds//4.2e-110:565:95//AB014525

40 R-NT2RP2003280//Homo sapiens 12p13.3 PAC RPCI5-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence//3.2e-12:221:70//AC005831

R-NT2RP2003286//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence//0.86:379:60//AC005261

R-NT2RP2003293//Homo sapiens clone RG252P22, WORKING DRAFT SEQUENCE, 3 unordered pieces//1.0e-39:418:74//AC005079

45 R-NT2RP2003295//HS_2053_B1_A10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2053 Col=19 Row=B, genomic survey sequence//0.0016:346:61//AQ235251

R-NT2RP2003297//Arabidopsis thaliana chromosome II BAC F4P9 genomic sequence, complete sequence//0.74:397:56//AC002332

R-NT2RP2003308//Homo sapiens PAC clone DJ1098B01 from 7q11.23-q21, complete sequence//0.99:447:60//AC004960

50 R-NT2RP2003329//C.reinhardtii psbB 5' flanking region//0.79:161:59//X59731

R-NT2RP2003339//RPCI11-57H15.TK RPCI11 Homo sapiens genomic clone R-57H15, genomic survey sequence//0.13:184:64//AQ116039

55 R-NT2RP2003347//RPCI11-15B19.TV RPCI-11 Homo sapiens genomic clone RPCI-11-15B19, genomic survey sequence//6.4e-31:218:89//B76357

R-NT2RP2003351//Homo sapiens clone

R-NT2RP2003351

R-NT2RP2003351//HS_2238_A1_E08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2238 Col=15 Row=I, genomic survey sequence//0.00055:324:61//AQ293058

nomic clone Plate=2255 Col=8 Row=D, genomic survey sequence.//1.6e-38:247:90//AQ068937
 R-NT2RP2003393//RPC111-44K6.TJ RPC111 Homo sapiens genomic clone R-44K6, genomic survey sequence.//
 3.9e-31:290:79//AQ020481
 R-NT2RP2003394//Yeast mitochondrial oxi3 gene exon 1 for cytochrome c oxidase subunit I.//5.1e-14:579:61//
 5 X14910
 R-NT2RP2003401//Caprine arthritis-encephalitis virus tat protein (tat) and envelope glycoprotein (env) gene, par-
 tial cds.//0.32:174:66//U81429
 R-NT2RP2003433//Ascidian mRNA for HRSec61, complete cds.//1.5e-10:193:69//D25536
 R-NT2RP2003445//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING
 10 DRAFT SEQUENCE.//4.4e-99:585:89//AL023808
 R-NT2RP2003446
 R-NT2RP2003456//Plasmodium falciparum MAL3P7, complete sequence.//0.98:399:57//AL034559
 R-NT2RP2003480//Homo sapiens full-length insert cDNA clone ZE09A11.//4.7e-111:540:98//AF086540
 R-NT2RP2003499
 15 R-NT2RP2003506
 R-NT2RP2003511
 R-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds.//4.1e-107:566:93//D87460
 R-NT2RP2003517//Human c-sis/platelet-derived growth factor 2 (SIS/PDGF2) mRNA, complete cds.//1.5e-60:
 518:79//M12783
 20 R-NT2RP2003522//HS_2182_A1_D05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=2182 Col=9 Row=G, genomic survey sequence.//0.053:251:60//AQ024304
 R-NT2RP2003533//Homo sapiens chromosome 12p13.3 clone RPC14-816N1, WORKING DRAFT SEQUENCE,
 31 unordered pieces.//1.5e-37:328:80//AC005841
 R-NT2RP2003543//HS_3028_A2_C12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 25 nomic clone Plate=3028 Col=24 Row=E, genomic survey sequence.//2.0e-39:203:100//AQ094957
 R-NT2RP2003559//Homo sapiens full-length insert cDNA clone ZD65E09.//2.3e-59:325:95//AF088055
 R-NT2RP2003564
 R-NT2RP2003581
 R-NT2RP2003596//HS_2163_B1_D11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 30 nomic clone Plate=2163 Col=21 Row=H, genomic survey sequence.//0.0011:212:67//AQ125143
 R-NT2RP2003604//Homo sapiens alpha-catenin-like protein mRNA, complete cds.//5.4e-102:501:97//U97067
 R-NT2RP2003629//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING
 DRAFT SEQUENCE, 9 unordered pieces.//0.0012:363:61//AC005507
 R-NT2RP2003643//Mus musculus mRNA for CMP-N-acetylneuraminic acid synthetase.//5.1e-37:561:68//
 35 AJ006215
 R-NT2RP2003668//Human DNA sequence from PAC 24608, between markers DXS6791 and DXS8038 on chro-
 mosome X contains ESTs.//0.0053:395:58//Z76735
 R-NT2RP2003687//Human BAC clone RG222A16 from 7q31, complete sequence.//8.0e-10:205:67//AC002385
 R-NT2RP2003691//HS_3252_A2_A11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 40 nomic clone Plate=3252 Col=22 Row=A, genomic survey sequence.//5.3e-05:332:60//AQ219783
 R-NT2RP2003702//CIT-HSP-2333P5.TF CIT-HSP Homo sapiens genomic clone 2333P5, genomic survey se-
 quence.//3.9e-43:431:75//AQ035000
 R-NT2RP2003704
 R-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds.//2.6e-45:265:93//AB011097
 45 R-NT2RP2003713//Human DNA sequence from PAC 411B6 on chromosome X *.//0.64:169:67//Z84470
 R-NT2RP2003714//Human DNA sequence from 4PTL, Huntington's Disease Region, chromosome 4p16.3.//
 4.6e-11:152:73//295704
 R-ntntntntntntntntntntnt/H.sapiens mRNA for PIBF1 protein, complete.//0.94:443:59//Y09631
 R-NT2RP2003737//Homo sapiens clone DJ1022114, WORKING DRAFT SEQUENCE, 14 unordered pieces.//
 50 2.2e-109:547:96//AC004951
 R-NT2RP2003751//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-427H10, complete sequence.//4.1e-
 109:545:97//AC004626
 R-NT2RP2003760//B. taurus mRNA for gamma-COP.//6.3e-28:400:69//X70019
 R-NT2RP2003764//Mouse preprosomatostatin gene.//0.90:285:62//X51468
 55 R-NT2RP2003769//Schizosaccharomyces pombe gene for protein involved in sexual development complete
 R-NT2RP2003770//Homo sapiens genomic clone 11022114, WORKING DRAFT SEQUENCE, 14 unordered pieces.//
 R-NT2RP2003771

R-NT2RP2003781//HS_3109_B1_B04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3109 Col=7 Row=D, genomic survey sequence.//1.3e-60:346:92//AQ186749

R-NT2RP2003793

R-NT2RP2003840

R-NT2RP2003857//HS_2205_A2_H12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2205 Col=24 Row=O, genomic survey sequence.//8.1e-22:127:99//AQ151299

R-NT2RP2003859//RPCI11-37G8.TV RPCI-11 Homo sapiens genomic clone RPCI-11-37G8, genomic survey sequence.//8.3e-60:320:95//AQ029850

R-NT2RP2003871//HS_3210_A1_C08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3210 Col=15 Row=E, genomic survey sequence//8.6e-09:322:61//AQ175028

R-NT2RP2003885//RPCI11-7M10.TP RPCI-11 Homo sapiens genomic clone RPCI-11-7M10, genomic survey sequence.//4.7e-67:380:92//B72214

R-NT2RP2003912//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 32B1, WORKING
DRAFT SEQUENCE.//1.2e-33:379:75//AL023693

R-NT2RP2003952

R-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds.//2.3e-114:568:97//ABQ14458

R-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds.//1.1e-107:540:97//AB007916

R-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds.//7.7e-114:568:96//AB018347

R-NT2RP2003984

R-NT2RP2003986//Human Chromosome 11 pac pDJ197h17, WORKING DRAFT SEQUENCE, 11 unordered piec-
es//6.6e-99:551:92//AC0003 82

R-NT2RP2003988

R-NT2RP2004014

R-NT2RP2004041//Homo sapiens chromosome 19, cosmid F17127, complete sequence.//4.9e-114:568:97//AC004780

R-NT2RP2004042//nbxb0020F03r CUGI Rice BAC Library *Oryza sativa* genomic clone nbxb0020F03r, genomic survey sequence//0.11:195:64//AQ258389

R-nnnnnnnnnnnnn//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 134019, WORKING
DRAFT SEQUENCE.//7.6e-110:564:95//AL034555

R-NT2RP2004081//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE. 5 unordered pieces.//0.012:503:57//AC005308

R-NT2RP2004098//H.sapiens CpG island DNA genomic Mse1 fragment, clone 133h3, reverse read
cpg133h3.rt1a.//7.9e-25:140:100//Z64530

R-NT2RP2004124

R-NT2RP2004142//CIT-HSP-2316F21.TR CIT-HSP Homo sapiens genomic clone 2316F21, genomic survey sequence.//2.8e-83:409:98//AQ034964

R-NT2RP2004152//HS_3065_A2_D04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3065 Col=8 Row=G, genomic survey sequence.//2.5e-62:304:100//AQ137776

R-NT2RP2004165//*Anthocidaris crassispina* mRNA for dynein beta-heavy chain, complete cds.//3.4e-20:343:65//D01021

R-NT2RP2004170//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone B33108;
HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces//2.5e-89:587:86//AC004064

R-NT2RP2004172//Dictyostelium discoideum LTR-retrotransposon Skipper, partial genomic sequence, 3' end//
0.24:440:60//AF017047

R-NT2RP2004187//RPC

quence.//3.1e-05:175:66//AQ198120
R-NT2RP2004194

R-NT2RP2004196

R-NT2RP2004207//Homo sapiens BAC clone GS421I03 from Xq25-q26, complete sequence.//0.19:175:64//

AC005023

R-NT2RP2004226//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING DRAFT SEQUENCE.//6.1e-17:445:64//AL023808

R-NT2RP2004232//M.musculus (Balb/c) mRNA for serine/threonine protein kinase.//3.2e-25:326:71//Z34524

[illegible]

R-NT2RP2004242

R-NT2RP2004245//Homo sapiens DNA sequence from PAC 455H14 on chromosome Xq21.3-22.3. Contains genomic marker DXS1203 with a CA repeat polymorphism, STSs and GSSs, complete sequence.//5.1e-08:236:65//AL023280

5 R-NT2RP2004270//Lycopersicon esculentum ldh2 gene.//0.98:259:61//Y10603

R-NT2RP2004300//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1068F16, WORKING DRAFT SEQUENCE.//5.0e-14:396:65//AL023913

R-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete cds.//1.5e-108:544:96//AF000416

R-NT2RP2004321//Caenorhabditis elegans cosmid F47B8, complete sequence.//0.0078:333:61//Z77662

10 R-NT2RP2004339//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete sequence.//1.4e-75:306:86//AC005229

R-NT2RP2004347//RPC11-90N11.TJ RPC11 Homo sapiens genomic clone R-90N11, genomic survey sequence.//2.9e-87:494:92//AQ284548

15 R-NT2RP2004364//Human DNA sequence from clone 422F24 on chromosome 6q24.1-25.2. Contains a novel gene similar to C. elegans C02C2.5. Contains ESTs, STSs and GSSs, complete sequence.//4.2e-10:161:76//AL031010

R-NT2RP2004365//Plasmodium falciparum chromosome 2, section 70 of 73 of the complete sequence.//3.6e-08:483:57//AE001433

20 R-NT2RP2004366//F.rubripes GSS sequence, clone 013B16aF3, genomic survey sequence.//2.1e-05:128:67//AL000528

R-NT2RP2004373//Homo sapiens 12q24.2 BAC RPC11-407A16 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.81:205:62//AC006065

R-NT2RP2004389//HS_2183_B2_H04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=8 Row=P, genomic survey sequence.//3.9e-06:82:84//AQ063969

25 R-NT2RP2004392//Ceratovacuna sp. mitochondrial cytochrome oxidase I (3' end), cytochrome oxidase II (complete cds) and transfer RNA-Leu gene.//2.7e-06:495:58//L39993

R-NT2RP2004396//Homo sapiens BAC clone RG135C18 from 7q21, complete sequence.//6.4e-111:572:96//AC005164

30 R-NT2RP2004399//Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence, complete sequence.//0.13:253:64//AC006085

R-NT2RP2004400//HS_3238_A2_H11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=22 Row=O, genomic survey sequence.//5.1e-23:162:89//AQ211412

R-NT2RP2004412//Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds.//2.6e-09:458:60//M97514

35 R-NT2RP2004425//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs, complete sequence.//0.99:481:56//AL022718

40 R-NT2RP2004476//Rattus norvegicus activity and neurotransmitter-induced early gene 6 (ania-6) mRNA, 3'UTR.//5.3e-99:600:90//AF030091

R-NT2RP2004490//Homo sapiens chromosome 16, P1 clone 94-10H (LANL), complete sequence.//3.9e-115:575:97//AC005591

R-NT2RP2004512//Plasmodium falciparum MAL3P3, complete sequence.//0.00034:517:58//Z98547

R-NT2RP2004523//Homo sapiens clone DJ0800G07, complete sequence.//1.8e-115:571:97//AC004890

45 R-NT2RP2004538//Homo sapiens BAC clone RG318C11 from 7p14-p15, complete sequence.//1.7e-47:322:87//AC005091

R-NT2RP2004551//Homo sapiens Xp22 bins 45-47 BAC GSHB-665N22 (Genome Systems Human BAC Library) complete sequence.//0.035:511:58//AC005184

50 R-NT2RP2004568//T7C20-Sp6 TAMU Arabidopsis thaliana genomic clone T7C20, genomic survey sequence.//0.70:446:54//B08766

R-NT2RP2004580//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 136B1, WORKING DRAFT SEQUENCE.//2.2e-53:397:74//AL031768

R-NT2RP2004587//CIT-HSP-2376P22.TF CIT-HSP Homo sapiens genomic clone 2376P22, genomic survey sequence.//0.0079:223:63//AQ108976

55 R-NT2RP2004594//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//5.3e-11:493:62//AC004605

R-NT2RP2004600//Homo sapiens chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//5.3e-11:493:62//AC004605

R-NT2RP2004602//Homo sapiens chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//5.3e-11:493:62//AC004605

R-NT2RP2004614

R-NT2RP2004655//Homo sapiens mRNA for leucine rich protein.//7.3e-117:587:96//AJ006291

R-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds.//1.8e-105:520:96//AB007929

R-NT2RP2004675//Human elastin (ELN) gene, partial cds, and LIM-kinase (LIMK1) gene, complete cds.//3.4e-22:197:79//U63721

R-NT2RP2004681//Rat notch 2 mRNA.//8.0e-30:276:78//M93661

R-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds.//1.6e-118:600:96//AB014525

R-NT2RP2004709//Homo sapiens full-length insert cDNA clone ZD42A08.//3.5e-14:139:86//AF086259

R-NT2RP2004710//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 126A5, WORKING DRAFT SEQUENCE.//6.9e-117:592:96//AL031447

R-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds.//4.2e-117:594:96//AB007947

R-NT2RP2004743//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.53:403:59//AC005505

R-NT2RP2004767//Human DNA sequence from PAC 491M17 on chromosome 1p36.2-1p36.3.//2.0e-81:568:84//Z97988

R-NT2RP2004775//Anopheles quadrimaculatus NADH dehydrogenase subunits (1-4, 4L, 5-6); cytochrome oxidase subunits (1-3); adenosine triphosphatase subunits (6,8); cytochrome b; transfer RNA; ribosomal RNA (large and small subunits).//4.0e-08:365:62//L04272

R-NT2RP2004791//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence.//7.8e-111:541:98//AC005216

R-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//2.5e-114:564:96//AF058953

R-NT2RP2004802

R-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds.//2.7e-118:584:97//AF054179

R-NT2RP2004841//Human BAC clone RG308B22 from 7q22-q31, complete sequence.//4.0e-46:447:72//AC002089

R-NT2RP2004861//Plasmodium falciparum MAL3P5, complete sequence.//0.19:189:66//AL034556

R-NT2RP2004897//Human Chromosome X clone bWXD187, complete sequence.//1.1e-08:330:61//AC004383

R-NT2RP2004936//CIT-HSP-2374L4.TF CIT-HSP Homo sapiens genomic clone 2374L4, genomic survey sequence.//0.99:129:65//AQ110571

R-nnnnnnnnnnnnn//Plasmodium falciparum MAL3P6, complete sequence.//0.014:402:61//Z98551

R-NT2RP2004961//RPC11-45P2.TK RPC11 Homo sapiens genomic clone R-45P2, genomic survey sequence.//9.3e-90:453:97//AQ202282

R-NT2RP2004962//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y40H4, WORKING DRAFT SEQUENCE.//0.017:291:61//AL022573

R-NT2RP2004967//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//4.6e-52:496:77//AC005077

R-NT2RP2004978//Homo sapiens chromosome 19, cosmid F23269, complete sequence.//0.088:322:63//AC005614

R-NT2RP2004982//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//0.025:339:61//AC003071

R-NT2RP2004985//T31H24TF TAMU Arabidopsis thaliana genomic clone T31H24, genomic survey sequence.//0.40:111:70//B78148

R-NT2RP2004999//Homo sapiens clone NH0084K19, WORKING DRAFT SEQUENCE, 30 unordered pieces.//0.23:157:68//AC005682

R-NT2RP2005000

R-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds.//3.0e-111:577:95//AB014515

R-NT2RP2005003//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//2.4e-21:246:77//AC004673

R-nnnnnnnnnnnnn//Homo sapiens SEC63 (SEC63) mRNA, complete cds.//9.5e-115:568:97//AF100141

R-NT2RP2005018//HS_3108_B1_E09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3108 Col=17 Row=J, genomic survey sequence.//1.9e-31:222:89//AQ104050

R-NT2RP2005020//Rattus norvegicus cationic amino acid transporter-1 (CAT-1) mRNA, complete cds.//6.6e-41:566:73//U70476

R-NT2RP2005003

R-NT2RP2005038//Sequence 5 from patent US 5552281 //2.2e-32:178:98//I25644

R-NT2RP2005108//Mus musculus orphan nuclear hormone receptor (CAR) gene, complete sequence //3.7e-23:475:67//AF009326

R-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds //8.4e-104:518:97//AB014564

5 R-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein) //1.4e-67:464:85//X98743

R-NT2RP2005139

R-NT2RP2005140//Leishmania mexicana amazonensis kinetoplast (clone 29) maxicircle A+T-rich repetitive DNA sequence //7.9e-08:460:60//U00101

10 R-NT2RP2005144//Homo sapiens chromosome 12p13.3 clone RPC11-372B4, WORKING DRAFT SEQUENCE, 129 ordered pieces //2.5e-103:519:96//AC005911

R-NT2RP2005147//Homo sapiens clone DJ1125K23, WORKING DRAFT SEQUENCE, 21 unordered pieces //0.068:100:75//AC004971

15 R-NT2RP2005159//CITBI-E1-2506A8.TF CITBI-E1 Homo sapiens genomic clone 2506A8, genomic survey sequence //0.90:113:71//AQ262104

R-NT2RP2005162//Homo sapiens chromosome 17, clone HCIT307A16, complete sequence //5.0e-14:183:75//AC003041

R-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein //7.5e-100:513:95//AJ007509

R-NT2RP2005204

20 R-NT2RP2005227//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence //7.2e-119:583:97//AC005189

R-NT2RP2005239//Homo sapiens mRNA for putative tRNA splicing protein, partial //8.4e-62:312:98//AJ010952

25 R-NT2RP2005254//Homo sapiens DNA sequence from PAC 262D12 on chromosome 1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neuronection, Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30S ribosomal protein S14-LIKE gene preceded by a CpG island. Contains ESTs, genomic marker D1S2691 and STSs //5.7e-09:328:62//Z99297

R-NT2RP2005270//Plasmodium falciparum MAL3P8, complete sequence //2.3e-05:355:61//AL034560

R-NT2RP2005276//Genomic sequence for Arabidopsis thaliana BAC F17F8, complete sequence //0.0014:541:58//AC000107

30 R-NT2RP2005287//Cavia porcellus zinc finger protein (zfoC1) mRNA, complete cds //4.4e-69:459:86//L26335

R-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds //7.4e-124:594:98//AF060219

R-NT2RP2005289//Homo sapiens mRNA for XRP2 protein //1.5e-110:545:96//AJ007590

35 R-NT2RP2005293//Leishmania mexicana amazonensis kinetoplast (clone 29) maxicircle A+T-rich repetitive DNA sequence //1.1e-12:554:61//U00101

R-NT2RP2005315//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS. CpG island, complete sequence //9.5e-15:218:77//AL022069

R-NT2RP2005325//Rattus norvegicus LIM homeodomain protein (LH-2) mRNA sequence //2.0e-72:478:88//L06804

40 R-NT2RP2005336//***ALU WARNING: Human Alu-J subfamily consensus sequence //7.3e-33:139:82//U14567

R-NT2RP2005344//Human DNA sequence from PAC 128N22 on chromosome Xq25-Xq26.3. contains STS //0.094:451:60//297629

R-NT2RP2005354//Homo sapiens mRNA for putative thioredoxin-like protein //1.3e-11:89:96//AJ010841

45 R-NT2RP2005360//Homo sapiens clone RG023115, WORKING DRAFT SEQUENCE, 1 unordered pieces //0.046:266:60//AC005049

R-NT2RP2005393//Homo sapiens chromosome 17, clone hRPK.85_B_7, complete sequence //6.0e-41:226:86//AC005695

R-NT2RP2005407

R-NT2RP2005436//Polistes annularis (clone pan117AAT) tandem repeat region //0.039:169:63//L10835

50 R-NT2RP2005441//CIT-HSP-2338P5.TR CIT-HSP Homo sapiens genomic clone 2338P5, genomic survey sequence //3.0e-38:263:88//AQ055548

R-NT2RP2005453//CIT-HSP-2367N1.TR CIT-HSP Homo sapiens genomic clone 2367N1, genomic survey sequence //0.67:409:59//AQ079845

R-NT2RP2005457//Homo sapiens partial XPGC gene, exon 2 //2.0e-42:315:82//X71342

55 R-NT2RP2005464//CIT-HSP-2359C16.TF CIT-HSP Homo sapiens genomic clone 2359C16, genomic survey sequence //1.0e-25:60//AQ075816

Sequence data from R-NT2RP2005464

Sequence data from R-NT2RP2005464

R-NT2RP2005472//Chlorarachnion CCMP621 small subunit ribosomal RNA, 5.8S ribosomal RNA, large subunit ribosomal RNA, U6 small nuclear RNA, small subunit ribosomal protein S13 (RPS13), pre-mRNA splicing factor PRP 6 homolog, small subunit ribosomal protein 4 (RPS4), small nucleolar ribonucleoprotein E homolog (snRNPE), ATP-dependent clip protease proteolytic subunit homolog (CLPP), putative RNA polymerase II subunit (RNA POLII), and RNA helicase homolog (RNAHEL) genes, complete cds.//1.0:356:59//U58510

R-NT2RP2005476//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P3, WORKING DRAFT SEQUENCE.//0.00092:421:60//AL031746

R-NT2RP2005490//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//6.2e-71:187:100//AC006030

R-NT2RP2005491//paramecium species 5,311 mt dna dimer: replication init. region.//1.6e-10:403:62//K00917

R-NT2RP2005495//Homo sapiens clone RG037F03, WORKING DRAFT SEQUENCE, 12 unordered pieces.//1.3e-25:208:82//AC005051

R-NT2RP2005496//Human DNA sequence from clone 354N19 on chromosome 6q22. Contains the 3' part of the gene for Mannosyl-Oligosaccharide Alpha-1,2-Mannosidase (Man(9)-alpha-mannosidase, EC 3.2.1.113), a Cytochrome C Oxidase Polypeptide I (EC 1.9.3.1) pseudogene and a pseudogene similar to 60S Ribosomal Protein L13A. Contains genomic markers D6S287 and D6S1696, ESTs, STSs, GSSs and two CA repeat polymorphisms, complete sequence.//1.5e-22:196:84//AL022722

R-NT2RP2005498

R-NT2RP2005501//Homo sapiens chromosome 17, clone hRPK.269_G_24, complete sequence.//7e-29:252:76//AC005828

R-NT2RP2005509//CIT-HSP-2060J6.TR CIT-HSP Homo sapiens genomic clone 2060J6, genomic survey sequence.//3.1e-53:402:84//B69979

R-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//9.9e-109:570:94//AF092563

R-NT2RP2005525//Human clone JkA2 mRNA induced upon T-cell activation, 3' end.//5.1e-32:175:98//U38432

R-NT2RP2005531//Homo sapiens PAC clone DJ0870F17 from 7q33-q36, complete sequence.//0.94:288:61//AC004911

R-NT2RP2005539//Homo sapiens mRNA for NSI-binding protein (NSI-BP).//2.7e-106:560:94//AJ012449

R-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds.//5.3e-114:583:96//AB007963

R-NT2RP2005549//Homo sapiens *** SEQUENCING IN PROGRESS *** , WORKING DRAFT SEQUENCE.//0.91:287:58//AJ011929

R-NT2RP2005555//Homo sapiens 12p13.3 PAC RPCIS-927J10 (Roswell Park Cancer Institute Human PAC library) complete sequence.//3.6e-05:222:66//AC004804

R-NT2RP2005557//Homo sapiens PAC clone DJ1200I23 from 7p15, complete sequence.//8.2e-22:236:76//AC004996

R-NT2RP2005581//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces.//7.2e-45:286:85//AC006146

R-NT2RP2005600//Human polymorphic microsatellite DNA.//0.043:304:58//M99148

R-NT2RP2005605//Human Cosmid g1572c190, complete sequence.//2.4e-17:163:77//AC000126

R-NT2RP2005620

R-NT2RP2005622//jd432 Trypanosome Shotgun M13 genomic Trypanosoma brucei brucei genomic clone 11B7, genomic survey sequence.//0.010:308:58//B13538

R-NT2RP2005637//Homo sapiens PAC clone DJ0555L14 from 7q34-q36, complete sequence.//2.5e-26:322:72//AC005996

R-NT2RP2005640//Mus musculus squamous cell carcinoma antigen 2 (Scca2) gene, complete cds.//0.030:370:60//AF063937

R-NT2RP2005645//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//3.2e-08:355:62//AE001398

R-NT2RP2005651

R-NT2RP2005654//Leishmania major Friedlin cosmid L5769, complete sequence.//0.96:216:66//AL031908

R-NT2RP2005669//Homo sapiens nitrilase homolog 1 (NIT1) gene, alternatively spliced product, complete cds.//6.7e-117:594:95//AF069984

R-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//1.8e-89:434:98//AF089814

R-NT2RP2005683//jd432 Trypanosome Shotgun M13 genomic Trypanosoma brucei brucei genomic clone 11B7

R-NT2RP2005694//*Plasmodium falciparum* DNA *** SEQUENCING IN PROGRESS *** from contig 3-106, complete sequence.//0.0026:414:57//AL010210

R-NT2RP2005701

R-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds.//4.1e-104:503:98//AB018342

R-NT2RP2005719//*Caenorhabditis elegans* cosmid LLC1, complete sequence.//0.83:275:61//Z82277

R-NT2RP2005722//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 228H13, WORKING DRAFT SEQUENCE.//1.2e-21:199:75//AL031985

R-NT2RP2005723

R-NT2RP2005726//Homo sapiens clone DJ0609N19, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.6e-64:503:82//AC004842

R-NT2RP2005741//Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE, 8 unordered pieces.//2.5e-09:261:64//AC000384

R-NT2RP2005748//RPC11-64K11.TK RPC11 Homo sapiens genomic clone R-64K11, genomic survey sequence.//0.00039:215:66//AQ239313

R-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds.//1.3e-40:223:96//AF068868

R-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//3.7e-103:494:98//AF082516

R-NT2RP2005763//Homo sapiens DNA sequence from PAC 510L9 on chromosome 6p24.1-p25.3.//9.7e-34:172:86//AL022098

R-NT2RP2005767//Human clone H3 mRNA.//2.5e-21:179:87//U03672

R-NT2RP2005773//HS_2168_B1_G12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2168 Col=23 Row=N, genomic survey sequence.//0.99:212:63//AQ086414

R-NT2RP2005775//Rabbit mRNA for endopeptidase, complete cds.//4.8e-98:591:88//D13310

R-NT2RP2005781//*Streptomyces* sp. genomic DNA for sarcosine oxidase.//0.019:384:59//D10623

R-NT2RP2005784//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1185N5, WORKING DRAFT SEQUENCE.//1.8e-102:490:99//AL034423

R-NT2RP2005804//Homo sapiens chromosome 17, clone hRPK.147_L_13, complete sequence.//6.3e-16:481:63//AC005332

R-NT2RP2005812//*Caenorhabditis elegans* cosmid F15810.//0.81:147:63//AF036696

R-NT2RP2005815

R-NT2RP2005835

R-NT2RP2005841//Human DNA sequence from cosmid U209G1 on chromosome X.//1.5e-26:512:64//Z68873

R-NT2RP2005853//Human DNA sequence from clone 1156N12 on chromosome X. Contains an STS and GSSs, complete sequence.//3.7e-16:340:64//AL009047

R-NT2RP2005857//Human DNA sequence from cosmid U246D9 on chromosome X. Contains a histone H2B like pseudogene.//1.3e-09:331:65//AL021308

R-NT2RP2005859//*Plasmodium falciparum* DNA *** SEQUENCING IN PROGRESS *** from contig 3-83, complete sequence.//0.0097:363:59//AL010152

R-NT2RP2005868//*Plasmodium falciparum* DNA *** SEQUENCING IN PROGRESS *** from contig 3-18, complete sequence.//1.1e-07:508:60//AL008971

R-NT2RP2005890//Mouse oncogene (ect2) mRNA, complete cds.//2.7e-31:500:67//AL11316

R-NT2RP2005901//Homo sapiens T-cell receptor alpha delta locus from bases 752679 to 1000555 (section 4 of 5) of the Complete Nucleotide Sequence.//0.89:276:60//AE000661

R-NT2RP2005908

R-NT2RP2005933//*Rattus norvegicus* nucleoporin p54 mRNA, complete cds.//1.2e-40:285:80//U63840

R-NT2RP2005942//Homo sapiens DNA sequence from PAC 142L7 on chromosome 6q21. Contains a Laminin Alpha 4 (LAMA4) LIKE gene coding for two alternatively spliced transcripts, a Tubulin Beta LIKE pseudogene, a Connective tissue growth factor (NOV, GIG) LIKE gene. A predicted CpG island, ESTs, STSs and genomic marker D6S416, complete sequence.//0.0011:480:58//Z99289

R-NT2RP2005980//Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence.//8.9e-21:136:78//AC004616

R-NT2RP2006023//HS_2176_B1_C10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2176 Col=19 Row=F, genomic survey sequence.//2.5e-66:369:95//AQ023148

R-NT2RP2006038//*Plasmodium falciparum* chromosome 2 section 6 of 73 of the complete sequence.//0.00029:414:57//AL010210

R-NT2RP2006043//*Forbesia annulata* 3.5 kb pac clone containing repeat region.//0.0021:199:75//AL031985

R-NT2RP2006052//*Plasmodium falciparum* 3B7 chromosome 2 section 4 of 42 of the complete sequence.//0.00029:414:57//AL010210

DRAFT SEQUENCE, 14 unordered pieces.//0.11:263:61//AC005140

R-NT2RP2006069

R-NT2RP2006071//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.00044:333:61//AC004709

R-NT2RP2006098//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-77, complete sequence.//4.1e-09:393:62//AL010151

R-NT2RP2006100//HS_2020_A2_H02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2020 Col=4 Row=O, genomic survey sequence.//8.3e-53:304:92//AQ228761

R-NT2RP2006103//Rat sodium-hydrogen exchange protein-isoform 3 (NHE-3) mRNA, complete cds.//1.5e-16:199:79//M85300

R-NT2RP2006141

R-NT2RP2006166//Human Chromosome 16 BAC clone CIT987SK-A-589H1, complete sequence.//8.2e-48:329:76//AC002045

R-NT2RP2006184//RPCI11-6O16.TP RPCI-11 Homo sapiens genomic clone RPCI-11-6O16, genomic survey sequence.//0.52:273:61//B49539

R-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds.//1.9e-108:553:95//AB014554

R-NT2RP2006196//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-57, complete sequence.//4.2e-05:420:59//AL008981

R-NT2RP2006200//Homo sapiens chromosome 12p13.3 clone RPCI1-96H9, WORKING DRAFT SEQUENCE, 66 unordered pieces.//2.1e-100:409:96//AC006057

R-NT2RP2006219//H.sapiens mRNA for DGCR6 protein.//3.8e-93:532:90//X96484

R-NT2RP2006237//P.falciparum PK1 gene.//2.9e-08:481:59//X83707

R-NT2RP2006238//Human chromosome 16 BAC clone CIT987SK-A-962B4, complete sequence.//3.5e-79:405:89//U91318

R-NT2RP2006258//Human PAC clone DJ0899B21 from 7p15-p21, complete sequence.//2.2e-08:283:63//AC004008

R-NT2RP2006261//H.sapiens mRNA for serine/threonine protein kinase EMK.//6.2e-13:234:68//X97630

R-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds.//2.0e-108:542:97//AF035262

R-NT2RP2006320//347J16.TVB CIT978SKA1 Homo sapiens genomic clone A-347J16, genomic survey sequence.//1.2e-27:215:65//B17768

R-NT2RP2006321//Human karyopherin beta 3 mRNA, complete cds.//1.7e-48:298:90//U72761

R-NT2RP2006323//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 702J19, WORKING DRAFT SEQUENCE.//2.8e-104:524:96//AL033531

R-NT2RP2006333//Homo sapiens PAC clone DJ0808A01 from 7q21.1-q31.1, complete sequence.//3.9e-33:298:78//AC004893

R-NT2RP2006334

R-NT2RP2006365//RPCI11-72I15.TK RPCI11 Homo sapiens genomic clone R-72I15, genomic survey sequence.//2.6e-35:217:92//AQ267043

R-NT2RP2006393//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone B13E4; HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//8.0e-40:317:81//AC004046

R-NT2RP2006436//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y738F9, WORKING DRAFT SEQUENCE.//3.2e-42:184:86//AL022345

R-NT2RP2006441//Plasmodium falciparum microsatellite TA80 sequence.//0.00021:188:68//AF010568

R-NT2RP2006454//Plasmodium falciparum chromosome 2, section 60 of 73 of the complete sequence.//0.30:265:60//AE001423

R-NT2RP2006456//Homo sapiens clone 23566 mRNA sequence.//2.5e-104:532:96//AF052098

R-NT2RP2006464//Homo sapiens mRNA for AND-1 protein.//6.6e-108:524:97//AJ006266

R-NT2RP2006467//Sequence 50 from patent US 5691147.//8.3e-22:235:74//I76222

R-NT2RP2006472//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1172A22, WORKING DRAFT SEQUENCE.//5.4e-12:407:62//AL034386

R-NT2RP2006534//Dictyostelium discoideum actin 8 gene, 3' UTR.//0.44:111:65//M25216

R-NT2RP2006554//Plasmodium falciparum chromosome 2, section 7 of 73 of the complete sequence.//0.19:392:58//AE001370

R-NT2RP2006565//Sus scrofa SCAMP 1 gene, exon 9.//1.5e-13:292:68//AJ223742

R-NT2RP2006571//Homo sapiens chromosome 19, cosmid F17972, complete sequence.//0.0024:409:58//M25666

R-NT2RP2006572//Homo sapiens chromosome 19, cosmid F17972, complete sequence.//0.0024:409:58//M25666

R-NT2RP2006573//Homo sapiens chromosome 19, cosmid F17972, complete sequence.//0.0024:409:58//M25666

448:64//J22015

R-NT2RP3000002//Human DNA sequence from cosmid N104C7 on chromosome 22, complete sequence//4.4e-14:501:63//Z82246

R-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//5.9e-115:560:97//AJ011972

R-NT2RP3000046//Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 20 unordered pieces//3.9e-57:402:83//AC005995

R-NT2RP3000047//Homo sapiens chromosome 17, clone hRPK.138_P_22, complete sequence//1.0:158:66//AC005697

R-NT2RP3000050//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 451B21, WORKING DRAFT SEQUENCE//2.7e-32:411:69//AL033522

R-NT2RP3000055//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1000N6, WORKING DRAFT SEQUENCE//7.9e-17:309:69//AL034378

R-NT2RP3000072//Brassica rapa DNA for S-locus glycoprotein, complete cds//2.9e-07:516:60//D88192

R-NT2RP3000080//Homo sapiens clone DJ1129D05, complete sequence//1.7e-27:186:90//AC005630

R-NT2RP3000085//Arabidopsis thaliana acetyl-CoA carboxylase biotin-containing subunit mRNA, nuclear gene encoding chloroplast protein, complete cds//0.0051:289:59//U-23155

R-NT2RP3000109//HS_3065_A2_D04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3065 Col=8 Row=G, genomic survey sequence//2.5e-62:304:100//AQ137776

R-NT2RP3000134//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P3, WORKING DRAFT SEQUENCE//0.027:414:57//AL031746

R-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds//3.8e-115:578:96//AB011164

R-NT2RP3000149//Homo sapiens chromosome 17, clone hRPK.332_H_18, complete sequence//1.3e-67:354:95//AC005746

R-NT2RP3000186

R-NT2RP3000197//Human DNA sequence from PAC 181N1 on chromosome X contains ESTs, STS polymorphic CA repeat*//2.5e-31:295:78//Z82899

R-NT2RP3000207//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-954B10, complete sequence//0.016:305:61//AC004514

R-NT2RP3000220//RPC111-63O7.TJ RPC111 Homo sapiens genomic clone R-63O7, genomic survey sequence//0.25:118:66//AQ201832

R-NT2RP3000233//Plasmodium falciparum mRNA for major merozoite surface antigen gp195//3.2e-11:440:59//X15063

R-NT2RP3000235//Mus musculus chromosome 6 clone TB6 subclone TB6pD1//0.81:114:64//U19530

R-NT2RP3000247//Homo sapiens DNA sequence from clone 326L12 on chromosome Xq27.1 27.3. Contains the cancer/testis antigen CT7 (melanoma-associated antigen MAGE-C1) gene, two MAGE family pseudogenes, STSs and a CA repeat polymorphism, complete sequence//4.8e-73:362:86//AL023279

R-NT2RP3000251//Homo sapiens chromosome 17, clone hRPK.192_H_23, complete sequence//0.025:131:66//AC005726

R-NT2RP3000252

R-NT2RP3000255//HS-1025-B2-F08-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 804 Col=16 Row=L, genomic survey sequence//0.67:119:66//B34879

R-NT2RP3000267

R-NT2RP3000299//Rattus norvegicus mRNA for Crk-associated substrate, p130, complete cds//1.2e-23:424:69//D29766

R-NT2RP3000312//Plasmodium falciparum MAL3P4, complete sequence//0.55:414:59//AL008970

R-NT2RP3000320//HS_3056_A1_C03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3056 Col=5 Row=E, genomic survey sequence//4.1e-32:214:89//AQ134064

R-NT2RP3000324//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds//1.5e-22:265:75//U78090

R-NT2RP3000333//Plasmodium falciparum MAL3P6, complete sequence//0.68:460:57//Z98551

R-NT2RP3000341//H.sapiens mRNA for TIM17 preprotein translocase//1.4e-19:137:90//X97544

R-NT2RP3000348//CITBI-E1-2513C11.TF CITBI-E1 Homo sapiens genomic clone 2513C11, genomic survey sequence//0.0014:118:72//AQ278177

R-NT2RP3000350

R-NT2RP3000359//Homo sapiens chromosome 17, clone hRPK.332_H_18, complete sequence//1.3e-67:354:95//AC005746

R-NT2RP3000366//CIT-HSP-2317H13.TF CIT-HSP Homo sapiens genomic clone 2317H13, genomic survey sequence.//6.7e-42:214:100//AQ041634

R-NT2RP3000397//HS-1012-B1-F01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone
Plate=CT 787 Col=1 Row=L, genomic survey sequence//0.015:184:63//B31814

R-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds.//1.3e-109:529:98//AF071185

R-NT2RP3000418//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 510B21, WORKING DRAFT SEQUENCE //6.2e-15:445:65//AL031885

R-NT2RP3000433

R-NT2RP3000439

R-NT2RP3000441

R-NT2RP3000449//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018D12, WORKING DRAFT SEQUENCE //1.6e-43:300:76//AL031650 R-NT2RP3000451//3'untranslated region of human mRNA for a K⁺ channel protein.//0.71:101:66//E13519

R-NT2RP3000456//Human Xq28 cosmids U126G1, U142F2, U69B6, U145C10, U169A5, U84H1, U24D12, U80A7, U153E6, L35485, and R7-163A8 containing iduronate 2-sulfatase gene and pseudogene, complete sequence.//5.2e-16:376:65//AF011889

R-NT2RP3000484//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 120G22, WORKING
DRAFT SEQUENCE.//0.61:326:58//AL031847

R-NT2RP3000487//Sequence 32 from patent US 5476781 //8.6e-08:409:61//116692

R-NT2RP3000512//RPC11-60F15.TK RPC11 Homo sapiens genomic clone R-60F15, genomic survey sequence.//2.2e-68:379:93//AQ201516

R-NT2RP3000526//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 377F16, WORKING DRAFT SEQUENCE.//4.1e-07:224:65//Z93783

R-NT2RP3000527//HS_3228_A1_H07_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3228 Col=13 Row=O, genomic survey sequence.//4.5e-30:184:93//AQ209131

R-NT2RP3000531//T6M24-Sp6 TAMU Arabidopsis thaliana genomic clone T6M24, genomic survey sequence//0.67:88:68//AQ248538

R-NT2RP3000542//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 126B4, WORKING DRAFT SEQUENCE.//2.0e-24:145:82//AL022316

R-NT2RP3000561//Homo sapiens PAC clone DJ0942116 from 7q11, complete sequence.//6.1e-107:548:95//AC006012

R-NT2RP3000562//HS_2041_B1_E08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2041 Col=15 Row=J, genomic survey sequence//9.6e-55:279:98//AQ230207

R-NT2RP3000578//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-105, complete sequence.//0.00060:356:58//AL010212

R-NT2RP3000582//Homo sapiens chromosome 17, clone hCIT.468_F_23, WORKING DRAFT SEQUENCE, 3 unordered pieces.//4.2e-29:282:67//AC004666

R-NT2RP3000584//Human PAC clone DJ222H05 from Xq25-q26, complete sequence.//7.4e-44:245:78//AC002377

R-NT2RP3000590//Arabidopsis thaliana chromosome II BAC T31E10 genomic sequence, complete sequence.
0.66:341:59//AC004077

R-NT2RP3000592//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.022:491:56//AC005505

R-nnnnnnnnnnnnn/HS_3025_A1_D11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3025 Col=21 Row=G, genomic survey sequence.//2.6e-21:161:88//AQ101452

R-NT2RP3000599//Plasmodium falciparum MAL3P8, complete sequence.//1.3e-09:543:58//AL034560

R-NT2RP3000605//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//5.6e-115:554:98//AC006128

R-NT2RP3000622//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 27 unordered pieces.//
0.15:233:63//AC005414

R-NT2RP3000624//CIT-HSP-2022D4.TR CIT-HSP Homo sapiens genomic clone 2022D4, genomic survey sequence//1 0:166:66/B64262

R-NT2RP3000628//Human BAC clone GS188P18, complete sequence.//5.3e-56:384:83//AC000115

R-NT2RP3000632//Human cyclin-selective ubiquitin carrier protein mRNA, complete cds.//4.0e-61:438:85//U73379

1720: 1720

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U72RP3000661: cDNAs cDNA sequence, clone 48022bB9, genomic survey sequence, 276 bp, 234 bp

AL005927

R-NT2RP3000665//Human chromosome 11 46b2 cosmid, complete sequence.//2.1e-42:526:72//U73645

R-NT2RP3000685//HS_3007_A2_F02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3007 Col=4 Row=K, genomic survey sequence.//1.6e-101:506:97//AQ118425

R-NT2RP3000690//Plasmodium falciparum MAL3P6, complete sequence.//1.3e-13:411:61//Z98551

R-NT2RP3000736

R-NT2RP3000742//Rattus norvegicus phospholipase C delta-4 mRNA, complete cds.//0.0071:231:65//U16655

R-NT2RP3000753//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//0.88:366:56//AL021368

R-NT2RP3000759//HS_2055_A2_D09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2055 Col=18 Row=G, genomic survey sequence.//0.45:251:60//AQ234828

R-NT2RP3000815//Homo sapiens chromosome 17, clone hRPK.209_J_20, complete sequence.//2.0e-20:293:72//AC005822

R-NT2RP3000825//Plasmodium falciparum MAL3P6, complete sequence.//0.0044:325:62//Z98551

R-NT2RP3000826//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 117715, WORKING DRAFT SEQUENCE.//5.3e-25:375:72//AL022315

R-NT2RP3000836//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y214H10, WORKING DRAFT SEQUENCE.//1.3e-19:181:81//AL022344

R-NT2RP3000841//Homo sapiens, clone hRPK.1_A_1, complete sequence.//0.20:226:61//AC006196

R-NT2RP3000845//Homo sapiens chromosome 19, cosmid R33632, complete sequence.//6.8e-91:512:92//AC005781

R-NT2RP3000847//***ALU WARNING: Human Alu-Sp subfamily consensus sequence.//7.9e-38:179:86//U14572

R-NT2RP3000850//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//4.4e-48:505:76//AC005014

R-NT2RP3000852//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 97P20, WORKING DRAFT SEQUENCE.//2.9e-82:311:98//AL031297

R-NT2RP3000859

R-NT2RP3000865//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS, GSS, complete sequence.//1.2e-15:482:63//AL022153 R-NT2RP3000868//Fruitfly strain g20 mitochondrial DNA, A+T-rich region, partial sequence.//0.00045:260:59//AB003097

R-NT2RP3000869//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 330012, WORKING DRAFT SEQUENCE.//0.0058:172:64//AL031731

R-NT2RP3000875//H.sapiens /Hepatitis B virus fusion mRNA for mevalonate kinase.//1.4e-99:531:93//X75311

R-NT2RP3000901

R-NT2RP3000904//Genomic sequence for Arabidopsis thaliana BAC T7N9, complete sequence.//0.32:261:57//AC000348

R-NT2RP3000917//Plasmodium falciparum MAL3P7, complete sequence.//0.00092:456:58//AL034559

R-NT2RP3000919

R-NT2RP3000968//H.sapiens mRNA for ribosomal protein S15a.//4.5e-24:375:71//X84407

R-NT2RP3000980//Homo sapiens chromosome 17, clone hRPK.855_D_21, complete sequence.//0.36:186:62//AC006079

R-NT2RP3000994//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.00052:413:60//AC005140

R-NT2RP3001004//Saccharomyces cerevisiae VAR1 gene, mitochondrial gene encoding mitochondrial protein, 3' processing site, partial sequence.//1.1e-07:330:64//U32857

R-NT2RP3001007//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-82, complete sequence.//0.045:286:61//AL010255

R-NT2RP3001055//Human DNA sequence from PAC 27K14 on chromosome Xp11.3-Xp11.4. Contains monoamine oxidase B (MAOB), ESTs and polymorphic CA repeats.//2.3e-56:348:91//Z95125

R-NT2RP3001057//H.sapiens HZF4 mRNA for zinc finger protein.//8.2e-84:531:86//X78927

R-NT2RP3001081//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P3, WORKING DRAFT SEQUENCE.//1.1e-08:537:60//AL031746

R-NT2RP3001084

R-NT2RP3001089

R-NT2RP3001100

R-nnnnnnnnnnnnn//Human Chromosome 15q26.1 PAC clone pDJ10k5 containing human DNA polymerase gamma (polg) gene, complete sequence.//7.4e-62:272:73//AC005316

R-NT2RP3001111

R-NT2RP3001113

R-NT2RP3001115//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//7.2e-112:550:97//AC005189

R-NT2RP3001116//CIT-HSP-2282K23.TR CIT-HSP Homo sapiens genomic clone 2282K23, genomic survey sequence.//0.000.13.160:69//AQ002011

R-NT2RP3001119//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//5.9e-99:497:96//AL031864

R-NT2RP3001120

R-NT2RP3001126//Plasmodium falciparum MAL3P7, complete sequence.//0.035:266:56//AL034559

R-NT2RP3001133

R-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds.//8.1e-114:549:97//AB018305

R-NT2RP3001147//Homo sapiens chromosome 17, clone HCIT187M2, complete sequence.//0.69:198:63//AC004448

R-NT2RP3001150//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE.//2.4e-108:542:97//AL034379

R-NT2RP3001155//Homo sapiens mRNA for AND-1 protein.//2.9e-116:563:98//AJ006266

R-NT2RP3001176//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.44:227:62//AC004688

R-NT2RP3001214//Borrelia burgdorferi plasmid lp25, complete plasmid sequence.//0.0023:381:61//AE000785

R-NT2RP3001216//RPCI11-18C15.TPC RPCI-11 Homo sapiens genomic clone RPCI-11-18C15, genomic survey sequence.//7.0e-29:167:97//B88077

R-NT2RP3001221//Homo sapiens clone 14503, WORKING DRAFT SEQUENCE, 1 ordered pieces.//0.020:211:63//AC005827

R-NT2RP3001232//Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence.//2.7e-08:390:62//AL021326

R-NT2RP3001236//RPCI11-25C17.TKBR RPCI-11 Homo sapiens genomic clone RPCI-11-25C17, genomic survey sequence.//9.5e-41:217:88//AQ014003

R-NT2RP3001239//Human microtubule-associated protein 1B (MAP1B) gene, complete cds.//2.9e-21:438:63//L06237

R-NT2RP3001245//Homo sapiens DNA sequence from PAC 964D12 on chromosome 1q24-q25. Contains EST, GSS.//0.00026:439:59//AL021398

R-NT2RP3001253//HS_3002_A2_H12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3002 Col=24 Row=O, genomic survey sequence.//0.98:190:63//AQ251982

R-NT2RP3001260

R-NT2RP3001268//Homo sapiens clone DJ0959C21, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.012:509:57//AC004936

R-NT2RP3001272//Homo sapiens BAC clone NH0161H12 from 7p14-p15, complete sequence.//2.2e-22:134:87//AC005589

R-NT2RP3001274//Sequence 11 from Patent WO9517522.//0.0058:133:66//A45341

R-NT2RP3001281//Human DNA sequence from PAC 52D1 on chromosome Xq21. Contains CA repeats, STS.//4.4e-55:558:76//Z96811

R-NT2RP3001307//HS_2058_A1_C06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=11 Row=E, genomic survey sequence.//7.2e-33:260:86//AQ305868

R-NT2RP3001318//Homo sapiens PAC clone DJ0649P17 from 7q11.23-q21, complete sequence.//0.27:210:65//AC004848

R-NT2RP3001325

R-NT2RP3001338//Rat tropoelastin gene, intron 17 (partial).//1.0:184:64//M86367

R-NT2RP3001339//Homo sapiens mRNA for KIAA0451 protein, complete cds.//1.2e-112:566:96//AB007920

R-NT2RP3001340//Homo sapiens HMG box factor SOX-13 mRNA, complete cds.//3.2e-86:450:95//AF083105

R-NT2RP3001355

R-NT2RP3001356//Homo sapiens clone DJ0959C21, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.012:509:57//AC004936

R-NT2RP3001357//Human DNA sequence from PAC 52D1 on chromosome Xq21. Contains CA repeats, STS.//4.4e-55:558:76//Z96811

R-NT2RP3001358//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.44:227:62//AC004688

279:63//AE001397

R-NT2RP3001384//Homo sapiens chromosome 19, cosmid R33907, complete sequence//4.4e-75:382:97//AC005785

R-NT2RP3001392//HS_3078_B2_D05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3078 Col=10 Row=H, genomic survey sequence//1.0:164:64//AQ140587

R-NT2RP3001396//RPC111-63N18.TJ RPC111 Homo sapiens genomic clone R-63N18, genomic survey sequence//0.14:242:61//AQ238544

R-NT2RP3001398//Mus musculus zinc finger protein (Zfp64) mRNA, complete cds//1.8e-10:193:72//U49046

R-NT2RP3001399

R-NT2RP3001407//Caenorhabditis elegans cosmid D1046, complete sequence//0.0011:392:60//Z68160

R-NT2RP3001420//Human BAC clone GS165104 from 7q21, complete sequence//3.7e-29:412:74//AC002379

R-NT2RP3001426//Homo sapiens clone 24616 mRNA sequence//1.1e-104:550:94//AF052158

R-NT2RP3001427//Caenorhabditis elegans cosmid K11D5//0.39:174:64//U53152

R-nnnnnnnnnnnn//Human nuclear pore complex-associated protein TPR (tpr) mRNA, complete cds//1.4e-94:533:91//U69668

R-NT2RP3001432//Homo sapiens DNA sequence from PAC 164C20 on chromosome 6q16.1-22.1. Contains ESTs and GSSs (BAC end sequences), complete sequence//2.5e-12:415:61//AL009029

R-NT2RP3001447//Homo sapiens PAC clone DJ0828B12 from 7q11.23-q21.1, complete sequence//5.6e-36:358:77//AC004903

R-NT2RP3001449//Homo sapiens clone 24497 mRNA sequence//1.5e-100:499:97//AF070630

R-NT2RP3001453//Homo sapiens clone DJ0852024, WORKING DRAFT SEQUENCE, 2 unordered pieces//4.0e-47:295:86//AC004906

R-NT2RP3001457

R-NT2RP3001459

R-NT2RP3001472//Crithidia fasciculata kinetoplast apocytochrome b gRNA-mRNA chimera, clone:24//0.33:150:66//D13030

R-NT2RP3001490//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-103, complete sequence//2.3e-08:483:60//AL010208

R-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds//4.4e-60:338:93//U13395

R-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds//2.1e-110:549:97//AF064801

R-NT2RP3001527//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1125A11, WORKING DRAFT SEQUENCE//5.3e-32:310:78//AL034549

R-NT2RP3001529//Human Chromosome X, complete sequence//5.5e-67:280:93//AC002420

R-NT2RP3001538

R-NT2RP3001554//Human microtubule-associated protein 1a (MAP1A) mRNA, complete cds//7.8e-16:391:62//U38292

R-NT2RP3001580//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces//0.00026:456:58//AC004688

R-NT2RP3001587//Homo sapiens HRIHFB2115 mRNA, partial cds//5.6e-08:86:88//AB015337

R-NT2RP3001589//Homo sapiens chromosome 17, clone hRPK.1096_G_20, complete sequence//0.066:360:60//AC005410

R-NT2RP3001607//CIT-HSP-2010M8.TR CIT-HSP Homo sapiens genomic clone 2010M8, genomic survey sequence//0.041:194:67//B53490

R-NT2RP3001608//Human DNA sequence from PAC 296K21 on chromosome X contains cytokeratin exon, delta-aminolevulinic synthase (erythroid); 5-aminolevulinic acid synthase (EC 2.3.1.37). 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (EC 2.7.1.105, EC 3.1.3.46), ESTs and STS//0.69:151:64//Z83821

R-NT2RP3001621//Human DNA sequence from clone 24o18 on chromosome 6p21:31-22.2 Contains zinc finger protein pseudogene, VNO-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST, STS, GSS, complete sequence//1.4e-46:354:83//AL021808

R-NT2RP3001629//H.sapiens simple DNA sequence region clone wg1a10//0.99:137:63//X76572

R-NT2RP3001634//Homo sapiens TRIAD1 type I mRNA, complete cds//8.5e-108:541:96//AF099149

R-NT2RP3001642

R-NT2RP3001646//HS_3218_A2_A01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=2 Row=A, genomic survey sequence//2.6e-32:215:91//AQ303003

R-NT2RP3001647//H.sapiens simple DNA sequence region clone wg1a10//0.99:137:63//X76572

R-NT2RP3001648//H.sapiens simple DNA sequence region clone wg1a10//0.99:137:63//X76572

R-NT2RP3001649

R-NT2RP3001676//Homo sapiens cosmid Q95D4, chromosome 21 5' of IFNAR2.//2.1e-48:413:77//AF039905
 R-NT2RP3001678//RPC111-50C17.TK RPC111 Homo sapiens genomic clone R-50C17, genomic survey se-
 quence.//0.15:232:62//AQ116359
 R-NT2RP3001679//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and
 non-small cell lung cancer, segment 3/11.//7.8e-104:549:95//AB020860
 R-NT2RP3001688//Homo sapiens PAC clone DJ1048B16 from 7q34-q36, complete sequence.//6.6e-41:291:86//
 AC006019
 R-NT2RP3001690//Plasmodium falciparum chromosome 2, section 52 of 73 of the complete sequence.//3.1e-07:
 433:59//AE001415
 R-NT2RP3001708//Homo sapiens allele 14 fragile site locus (FRA10B) minisatellite sequence.//6.0e-06:237:64//
 AF053523
 R-NT2RP3001712//CITBI-E1-2516N9.TF CITBI-E1 Homo sapiens genomic clone 2516N9, genomic survey se-
 quence.//1.5e-95:456:99//AQ279562
 R-NT2RP3001716//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//0.0012:346:58//
 AC004617
 R-NT2RP3001724//Human HepG2 3' region Mbol cDNA, clone hmd6a06m3.//1.3e-27:163:95//D17273
 R-NT2RP3001730//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 111B22, WORKING
 DRAFT SEQUENCE.//7.6e-43:409:76//Z98200
 R-NT2RP3001739
 R-NT2RP3001752//Human clone 23774 mRNA sequence.//1.9e-08:104:84//U79279
 R-NT2RP3001753//CIT-HSP-2379P21.TF CIT-HSP Homo sapiens genomic clone 2379P21, genomic survey se-
 quence.//8.8e-06:102:78//AQ113378
 R-NT2RP3001764
 R-NT2RP3001777//Human mRNA for heparan sulfate proteoglycan (glypican).//0.99:166:66//X54232
 R-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds.//1.3e-111:549:97//AB007928
 R-NT2RP3001792//Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds.//1.6e-32:266:83//
 U13262
 R-NT2RP3001799//H.sapiens mRNA for OX40 homologue.//8.5e-44:374:79//X75962
 R-NT2RP3001819
 R-NT2RP3001844//Caenorhabditis elegans cosmid C54G7.//0.0042:231:63//U40410
 R-NT2RP3001854//Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2),
 CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein
 (cg2), and CG7 (cg7) genes, complete cds.//1.0:404:59//AF030694
 R-NT2RP3001855
 R-NT2RP3001896//CIT978SK-A-686F10.TV CIT978SK Homo sapiens genomic clone A-636F10, genomic survey
 sequence.//0.0012:68:82//AQ116409
 R-NT2RP3001898//Homo sapiens Chromosome 11p15.5 PAC clone pDJ754h15 containing cdk-inhibitor p57/KIP2
 (CDKN1C) gene, complete sequence.//0.37:266:65//AC005950
 R-NT2RP3001915//Human BAC clone RG367O17 from 7p15-p21, complete sequence.//0.018:144:66//AC002486
 R-NT2RP3001926//Human polyadenylate binding protein (TIA-1) mRNA, complete cds.//2.4e-10:77:100//M77142
 R-NT2RP3001929
 R-NT2RP3001931//Homo sapiens full-length insert cDNA clone YU73B11.//1.0e-110:562:96//AF087969
 R-NT2RP3001938//Human DNA sequence from PAC 447B16 on chromosome Xq13.1-Xq13.3.//0.38:386:56//
 Z95328
 R-NT2RP3001943//Homo sapiens chromosome 5, P1 clone 1076B9 (LBNL H14), complete sequence.//0.87:298:
 61//AC004500
 R-NT2RP3001944//Bos taurus clone CSSM056 satellite DNA sequence.//0.0095:76:78//U03836
 R-NT2RP3001969//Homo sapiens chromosome 12p13.3 clone RPC111-350L7, WORKING DRAFT SEQUENCE,
 72 unordered pieces.//7.0e-109:552:96//AC005844
 R-NT2RP3001989//Caenorhabditis elegans cosmid C01A2, complete sequence.//0.15:111:68//Z81029
 R-NT2RP3002002//Plasmodium falciparum 14-3-3 protein gene, partial cds.//0.016:286:60//AF065987
 R-NT2RP3002004//H.sapiens mRNA for FAST kinase.//5.1e-41:335:82//X86779
 R-NT2RP3002007
 R-NT2RP3002014//Human DNA sequence from clone 228A9 on chromosome 22q12.3-13.32 Contains 85 KDA
 CALCIUM-INDEPENDENT PHOSPHOLIPASE A2, EST, GSS, CpG island, complete sequence.//6.6e-41:297:86//

R-NT2RP3002000

R-NT2RP3002045//Plasmodium falciparum 14-3-3 protein gene, partial cds.//0.016:286:60//AF065987

R-NT2RP3002054//*Caenorhabditis elegans* cosmid Y69H2, complete sequence.//0.82:362:57//Z98877
 R-NT2RP3002056//*F.rubripes* GSS sequence, clone 020E22bF7, genomic survey sequence.//0.010:185:63//Z87006
 R-NT2RP3002057
 5 R-NT2RP3002062//Human BAC clone RG356F09 from 7p21, complete sequence.//1.7e-17:164:81//AC004002
 R-NT2RP3002062
 R-NT2RP3002081//HS_3082_A1_G09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3082 Col=17 Row=M, genomic survey sequence.//4.2e-25:344:73//AQ122260
 R-NT2RP3002097//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//2.6e-23:212:80//AC006210
 10 R-NT2RP3002102//Homo sapiens BAC clone RG290G13 from 7q21, complete sequence.//0.43:168:64//AC004746
 R-NT2RP3002108//CIT-HSP-2346P16.TF CIT-HSP Homo sapiens genomic clone 2346P16, genomic survey sequence.//3.5e-08:110:78//AQ059071
 15 R-NT2RP3002146//*Streptococcus gordonii* competence factor (comC) and histidine protein kinase (comD) genes, complete cds, and response regulator (comE) gene, partial cds.//0.11:534:55//U80077
 R-NT2RP3002147//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 329F2, WORKING DRAFT SEQUENCE.//4.1e-108:551:96//AL031710
 R-NT2RP3002151//*Mus musculus* mRNA for Guanine Nucleotide Regulatory Protein, complete cds.//6.8e-62:347:80//AB003503
 20 R-NT2RP3002163//*Anolis pulchellus* vitellogenin mRNA, partial cds.//0.77:281:63//U46857
 R-NT2RP3002165
 R-NT2RP3002166//*D.sargus* satellite DNA (clone PSE3).//0.81:124:62//Z48711
 R-NT2RP3002173
 25 R-NT2RP3002181//HS-1042-A2-F01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 824 Col=2 Row=K, genomic survey sequence.//1.3e-35:305:81//B36980
 R-NT2RP3002244//*Caenorhabditis elegans* cosmid R11E3.//0.0024:393:61//AF100669
 R-NT2RP3002248//Human DNA sequence from PAC 170A21 on chromosome 22q12-qter contains ESTs.//0.30:217:63//Z82189
 30 R-NT2RP3002255
 R-NT2RP3002273//Homo sapiens BAC clone 393I22 from 8q21, complete sequence.//0.84:463:57//AF070717
 R-NT2RP3002276//HS_2260_A1_MF_E07 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2260 Col=13 Row=I, genomic survey sequence.//0.0017:198:63//AQ292491
 R-NT2RP3002303//Human HMG-17 gene for non-histone chromosomal protein HMG-17.//7.4e-93:510:93//X13546
 35 R-NT2RP3002304//Human BAC clone GS188P18, complete sequence.//6.3e-09:477:59//AC000115
 R-NT2RP3002330//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.087:388:58//AC004688
 R-NT2RP3002343
 40 R-NT2RP3002351//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//0.20:489:56//AC004617
 R-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A) gene.//2.4e-104:516:94//Y15164
 R-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds.//4.7e-102:524:95//AB014578
 R-NT2RP3002484
 R-NT2RP3002501//Human DNA sequence from PAC 92M18, BRCA2 gene region chromosome 13q12-13 contains BRCA2 exons 25, 26 and 27 ESTs and STS.//5.2e-17:232:75//Z73359
 45 R-NT2RP3002512
 R-NT2RP3002529//CIT-HSP-2340H2.TR CIT-HSP Homo sapiens genomic clone 2340H2, genomic survey sequence.//0.81:266:58//AQ057387
 R-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds.//3.3e-82:438:94//AB018272
 50 R-NT2RP3002549//*Medicago truncatula* ENBP1 gene, exons 1 to 12.//0.95:381:56//AJ002479
 R-NT2RP3002566//HS_2036_A1_D08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2036 Col=15 Row=G, genomic survey sequence.//0.18:162:64//AQ230627
 R-NT2RP3002587//Homo sapiens clone DJ1090E20, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.1e-15:213:73//AC004956
 55 R-NT2RP3002590//*Arabidopsis thaliana* genomic DNA: chromosome 5, P1 clone: MXK3 complete sequence.//0.11:13:59//AB013700
 R-NT2RP3002602//*Mus musculus* genomic DNA: chromosome 1, P1 clone: MXK3 complete sequence.//0.11:13:59//AB013700
 R-NT2RP3002603

- R-NT2RP3002631//Homo sapiens chromosome 21 PAC
 RPCIP704A9190Q2//1.0:241:59//AJ006997
 R-NT2RP3002659//Rat sodium-hydrogen exchange protein-isoform 3 (NHE-3) mRNA, complete cds//6.8e-24:
 331:76//M85300
- 5 R-NT2RP3002660//H.sapiens partial gene for progesterone receptor and Alu element DNA//9.8e-43:273:82//
 Z49816
 R-NT2RP3002663//Lymnaea stagnalis 16S ribosomal RNA gene, mitochondrial gene encoding ribosomal RNA,
 partial sequence//0.60:300:59//U82072
 R-NT2RP3002671//S.pombe chromosome III cosmid c553//1.2e-20:399:66//AL023704
- 10 R-NT2RP3002682//RPC111-44K6.TJ RPC111 Homo sapiens genomic clone R-44K6, genomic survey sequence//
 4.7e-09:122:77//AQ202481
 R-NT2RP3002687//P.falciparum complete gene map of plastid-like DNA (IR-B)//1.1e-07:494:59//X95276
 R-NT2RP3002688//Human 7SL RNA sequence//2.7e-32:290:79//X01037
 R-NT2RP3002701
- 15 R-NT2RP3002713//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 167A19, WORKING
 DRAFT SEQUENCE//0.95:334:59//AL031427
 R-NT2RP3002763//***ALU WARNING: Human Alu-J subfamily consensus sequence//3.9e-40:288:85//U14567
 R-NT2RP3002770//R.prowazekii genomic DNA fragment (clone A615F)//0.21:174:63//Z82710
 R-NT2RP3002785//Homo sapiens PAC clone DJ0170D19 from Xq23, complete sequence//0.78:354:59//
 AC004822
- 20 R-NT2RP3002799//Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flank-
 ing repeat regions//1.1e-20:161:77//AF003528
 R-NT2RP3002810//Caenorhabditis elegans cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3002818//HS_3053_A2_A08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3053 Col=16 Row=A, genomic survey sequence//0.19:220:60//AQ135025
- 25 R-NT2RP3002861//P.falciparum complete gene map of plastid-like DNA (IR-B)//9.3e-05:414:60//X95276
 R-NT2RP3002869//Homo sapiens chromosome 19, cosmid F21967, complete sequence//0.14:165:64//
 AC005256
 R-NT2RP3002876//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50024, WORKING
 DRAFT SEQUENCE//2.6e-59:311:96//AL034380
- 30 R-NT2RP3002877//Homo sapiens Xp22 bins 87-93 PAC RPC11-122K4 (Roswell Park Cancer Institute Human
 PAC Library) complete sequence//4.6e-24:422:63//AC003035
 R-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds//4.7e-109:570:95//AB018314
 R-NT2RP3002911//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence//3.1e-16:471:64//
 AC005014
- 35 R-NT2RP3002948//, complete sequence//4.5e-94:516:93//AC005500
 R-NT2RP3002953//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence//3.4e-111:
 566:96//AC005754
 R-NT2RP3002955//Plasmodium falciparum chromosome 2, section 28 of 73 of the complete sequence//0.19:424:
 58//AE001391
- 40 R-NT2RP3002969//Rat mRNA for brain acyl-CoA synthetase II, complete cds//1.1e-89:562:88//D30666
 R-NT2RP3002972//Stealth virus 5 clone C1311 T7 genomic sequence//1.0:122:67//AF067482
 R-NT2RP3002978//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 455J7, WORKING
 DRAFT SEQUENCE//4.8e-05:249:63//AL031733
- 45 R-NT2RP3002988//Human DNA sequence from PAC 106H8 on chromosome 1q24. Contains PHOSPHATI-
 DYLINISITOL-GLYCAN class C (PIG-C) and DYNAMIN-3 genes. Contains ESTs and STSs and a CpG island//
 0.0097:246:67//Z97195
 R-NT2RP3003008//Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP,
 G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes//1.9e-24:
 188:78//AF109905
- 50 R-NT2RP3003032//Arabidopsis thaliana (clone DW1) DNA retrotransposon Ta11-1 integration site//5.3e-07:376:
 63//L47211
 R-NT2RP3003059//Homo sapiens chromosome 3, clone hRPK.165_I_16, complete sequence//1.4e-13:323:66//
 AC005669
- 55 R-NT2RP3003061//Homo sapiens mRNA from HIV associated non-Hodgkin's lymphoma (clone hll-10)//3.8e-42:
 123:123:123
 R-NT2RP3003068//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003074//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003075//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003076//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003077//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003078//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003079//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003080//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003081//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003082//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003083//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003084//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003085//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003086//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003087//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003088//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003089//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003090//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003091//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003092//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003093//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003094//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003095//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003096//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003097//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003098//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003099//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003100//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003101//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003102//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003103//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003104//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003105//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003106//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003107//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003108//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003109//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003110//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003111//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003112//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003113//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003114//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003115//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003116//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003117//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003118//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003119//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003120//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003121//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003122//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003123//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003124//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003125//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003126//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003127//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003128//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003129//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003130//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003131//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003132//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003133//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003134//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003135//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
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 R-NT2RP3003137//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003138//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
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 R-NT2RP3003157//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003158//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003159//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
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 R-NT2RP3003164//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
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 R-NT2RP3003167//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
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 R-NT2RP3003169//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003170//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003171//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
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 R-NT2RP3003178//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
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 R-NT2RP3003180//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
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 R-NT2RP3003183//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
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 R-NT2RP3003186//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003187//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003188//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003189//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003190//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003191//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003192//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
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 R-NT2RP3003195//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003196//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003197//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003198//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003199//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003200//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003201//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003202//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003203//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003204//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003205//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003206//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003207//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003208//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003209//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003210//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003211//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003212//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003213//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003214//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003215//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003216//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003217//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003218//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003219//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003220//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003221//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003222//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003223//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003224//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003225//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003226//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003227//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003228//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003229//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003230//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003231//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003232//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003233//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003234//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003235//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003236//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003237//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003238//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003239//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003240//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003241//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003242//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003243//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003244//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003245//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003246//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003247//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003248//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003249//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003250//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003251//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003252//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003253//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003254//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003255//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003256//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003257//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003258//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003259//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003260//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003261//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003262//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003263//Homo sapiens chromosome 11, cosmid F10D2//0.28:441:56//AF022972
 R-NT2RP3003264//Homo sapiens chromosome 11, cosmid F1

- R-NT2RP3003071//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 510D11, WORKING DRAFT SEQUENCE.//0.00014:329:60//Z98044
- R-NT2RP3003078//T26A1TF TAMU Arabidopsis thaliana genomic clone T26A1, genomic survey sequence.//0.95:219:63//B27013
- 5 R-NT2RP3003101//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.4e-05:285:62//AC004153
- R-NT2RP3003121//Homo sapiens full-length insert cDNA clone ZD62D10.//2.1e-47:242:98//AF086348
- R-NT2RP3003133//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 228H13, WORKING DRAFT SEQUENCE.//1.4e-21:199:75//AL031985
- 10 R-NT2RP3003138//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//5.1e-14:287:68//D12646
- R-NT2RP3003139//Rattus norvegicus kappa opioid receptor gene, exon 4 and complete cds.//1.5e-13:122:80//U17995
- R-NT2RP3003150
- 15 R-NT2RP3003157//Homo sapiens 12q15 BAC GSHB-410F4 (Genome Systems Human Bac Library) complete sequence.//5.5e-42:289:74//AC005294
- R-NT2RP3003185//HS_2058_A1_H03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=5 Row=O, genomic survey sequence.//0.025:52:94//AQ231298
- R-NT2RP3003193//Homo sapiens chromosome 17, clone hRPK.628_E_12, complete sequence.//4.8e-40:349:79//AC005701
- 20 R-NT2RP3003197//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 36411, WORKING DRAFT SEQUENCE.//5.2e-10:180:71//AL031319
- R-NT2RP3003203//Mus musculus IFN alpha-treated embryonic fibroblast mRNA.//1.8e-11:148:77//U51904
- R-NT2RP3003204//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 892F13, WORKING DRAFT SEQUENCE.//6.6e-41:282:86//AL009183
- 25 R-NT2RP3003212//Homo sapiens full-length insert cDNA clone ZB91B11.//1.7e-68:363:95//AF086173
- R-NT2RP3003230//Caenorhabditis elegans cosmid T12B5.//0.0018:279:64//AF100307
- R-NT2RP3003242//Homo sapiens chromosome 7 clone UWGC:g3586a160 from 7p14-15, complete sequence.//1.0:346:57//AC005272
- 30 R-NT2RP3003251//Homo sapiens BAC clone RG060N22 from 7q21, complete sequence.//2.5e-10:436:62//AC003083
- R-NT2RP3003264//CIT-HSP-2296M7.TR CIT-HSP Homo sapiens genomic clone 2296M7, genomic survey sequence.//5.8e-05:308:61//AQ005862
- R-NT2RP3003278//Human HepG2 partial cDNA, clone hmd3b11m5.//9.4e-47:302:89//D17022
- 35 R-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds.//7.4e-101:550:93//L36983
- R-NT2RP3003290//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 460J8, WORKING DRAFT SEQUENCE.//3.0e-22:228:78//AL031662
- R-NT2RP3003301
- R-NT2RP3003302//CIT-HSP-2319H19.TR CIT-HSP Homo sapiens genomic clone 2319H19, genomic survey sequence.//1.5e-69:367:95//AQ034950
- 40 R-NT2RP3003311//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//5.1e-08:398:64//AC005505
- R-NT2RP3003313//Caenorhabditis elegans cosmid F39B1, complete sequence.//0.00022:436:58//Z69660
- R-NT2RP3003327//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-237H1 ~complete genomic sequence, complete sequence.//1.5e-16:334:70//AC002287
- 45 R-NT2RP3003330//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003344//HS_3235_B2_H09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3235 Col=18 Row=P, genomic survey sequence.//4.1e-18:197:80//AQ303203
- R-NT2RP3003346
- 50 R-NT2RP3003353//CITBI-E1-2523B18.TR CITBI-E1 Homo sapiens genomic clone 2523B18, genomic survey sequence.//8.3e-06:130:73//AQ278834
- R-NT2RP3003377//Homo sapiens clone DJ0919J22, WORKING DRAFT SEQUENCE, 34 unordered pieces.//1.9e-97:481:94//AC005519
- R-NT2RP3003384//Homo sapiens clone DJ0038I10, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.3e-10:226:71//AC004820
- 55 R-NT2RP3003385
- R-NT2RP3003400//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003401//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003402//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003403//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003404//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003405//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003406//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003407//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003408//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003409//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003410//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003411//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003412//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003413//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003414//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003415//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003416//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003417//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003418//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003419//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003420//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003421//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003422//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003423//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003424//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003425//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003426//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003427//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003428//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003429//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003430//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003431//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003432//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003433//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003434//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003435//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003436//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003437//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003438//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003439//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003440//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003441//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003442//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003443//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003444//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003445//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003446//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003447//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003448//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003449//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003450//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003451//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003452//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003453//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003454//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003455//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003456//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003457//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003458//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003459//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003460//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003461//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003462//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003463//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003464//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003465//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003466//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003467//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003468//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003469//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003470//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003471//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003472//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003473//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003474//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003475//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003476//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003477//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003478//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003479//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003480//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003481//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003482//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003483//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003484//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003485//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003486//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003487//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003488//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003489//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003490//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003491//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003492//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003493//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003494//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003495//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003496//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003497//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003498//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003499//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015
- R-NT2RP3003500//Homo sapiens full-length insert cDNA YI24C02.//4.4e-96:458:99//AF075015

72//AL031585

R-NT2RP3003409//Rat POU domain factor (Brn-5) mRNA//1.5e-20:375:68//L23204

R-NT2RP3003411//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 438L4, WORKING DRAFT SEQUENCE//1.0:180:61//Z97635

5 R-NT2RP3003427//RPC11-45J23.TJ RPC11 Homo sapiens genomic clone R-45J23, genomic survey sequence//0.82:162:69//AQ195566

R-NT2RP3003433//Homo sapiens BAC clone NH0044G14 from 7q11.23-21.1, complete sequence//1.1e-10:379:61//AC006031

10 R-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//1.1e-95:479:96//AF004828

R-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds//1.3e-100:527:93//AB018268

R-NT2RP3003491//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence//4.0e-08:495:59//AE001398

R-NT2RP3003500//W.suaveolens mitochondrial ATP9 gene//0.0074:514:59//X77238

15 R-NT2RP3003543//Human clone A9A2BRB7 (CAC)n/(GTG)n repeat-containing mRNA//1.3e-31:217:88//U00952

R-NT2RP3003552

R-NT2RP3003555//Dictyostelium discoideum interaptin (abpD) gene, complete cds//0.98:321:61//AF057019

R-NT2RP3003564

20 R-NT2RP3003572//Human DNA sequence from BAC 992D9 on chromosome 22q12.1 contains STS//0.0015:507:59//AL008638

R-NT2RP3003576//Human Chromosome 16 BAC clone CIT987SK-A-61E3, complete sequence//1.2e-39:359:79//AC003007

R-NT2RP3003589//Plasmodium falciparum MAL3P8, complete sequence//0.014:539:58//AL034560

25 R-NT2RP3003625//Human DNA sequence from clone 1042K10 on chromosome 22q13.1-13.2. Contains the AD-SL gene for Adenylosuccinate lyase (EC 4.3.2.2, Adenylosuccinase, ASL) and 4 novel genes (one with probable rabGAP domains and Src homology domain 3). Contains ESTs, STSs, GSSs and a putative CpG island, complete sequence//1.8e-44:448:77//AL022238

30 R-NT2RP3003656//Homo sapiens chromosome 17, clone hRPK.401_O_9, complete sequence//0.34:257:62//AC005291

R-NT2RP3003659//O.fuscipennis 16S rRNA gene, partial//0.021:145:65//Z93701

R-NT2RP3003665//HS_3078_B2_C09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3078 Col=18 Row=F, genomic survey sequence//1.3e-75:397:95//AQ140580

R-NT2RP3003672

35 R-NT2RP3003686

R-NT2RP3003701//Human BAC clone GS310A05 from 7q21-q22, complete sequence//6.4e-17:464:62//AC002452

R-NT2RP3003716//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 774G10, WORKING DRAFT SEQUENCE//0.00072:425:62//AL034410

40 R-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds//1.7e-101:492:97//AB018300

R-NT2RP3003746//Homo sapiens Chromosome 16 BAC clone CIT987-SK502C10, complete sequence//3.7e-07:217:66//AC003009

R-NT2RP3003795//Human DNA sequence from clone 505B13 on chromosome 1p36.2-36.3 Contains CA repeat and GSSs, complete sequence//8.1e-26:456:68//Z98052

45 R-NT2RP3003799//cSRL-138g10-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-138g10, genomic survey sequence//4.9e-09:117:77//B01736

R-NT2RP3003800//Homo sapiens tyrosine kinase pp60c-src (SRC) gene, exon 12 and partial cds//2.8e-106:551:95//AF077754

R-NT2RP3003805

50 R-NT2RP3003809//Homo sapiens full-length insert cDNA clone YZ95A01//3.6e-106:533:97//AF086107

R-NT2RP3003819//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 34606, WORKING DRAFT SEQUENCE//6.0e-44:288:81//Z84487

R-NT2RP3003825//Mus domesticus interleukin 1 receptor antagonist (IL-1RA) mRNA//0.0014:410:58//M64404

R-NT2RP3003828

55 R-NT2RP3003831//****ALU WARNING: Human Alu-J subfamily consensus sequence//2.3e-41:289:85//U14567

R-NT2RP3003833//Homo sapiens X22.1A (22q11.21) genomic systems BAC clone, complete sequence

R-NT2RP3003842//Homo sapiens X22.1A (22q11.21) genomic systems BAC clone, complete sequence//6.4e-17:447:64//AC002980

R-NT2RP3003846//Plasmodium falciparum MAL3P3, complete sequence.//3.5e-06:356:62//Z98547
R-NT2RP3003870//Homo sapiens full-length insert cDNA clone ZD75H11 //8.2e-09:68:98//AF086402
R-NT2RP3003876//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018D12, WORKING DRAFT SEQUENCE.//0.0027:180:66//AL031650
R-NT2RP3003914//Dictyostelium discoideum DNA for transposable element Tdd-3 tandem array.//0.029:234:62//X53439
R-NT2RP3003918
R-NT2RP3003932//Mus musculus MRC OX-2 antigen homolog gene, exons 2-5, and complete cds.//0.00087:164:67//AF029215
R-NT2RP3003989
R-NT2RP3003992//Sequence 1 from patent US 5591825.//0.56:235:59//I33465
R-NT2RP3004013//HS_3018_A1_G09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=17 Row=M, genomic survey sequence.//0.00026:421:60//AQ119904
R-NT2RP3004016//Drosophila melanogaster DNA sequence (P1s DS03465 (D149) and DS08544 (D187)), complete sequence.//4.8e-12:308:62//AC004532
R-NT2RP3004041//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 598F2, WORKING DRAFT SEQUENCE.//0.42:190:64//AL021579
R-NT2RP3004051//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//3.6e-21:332:69//AC006130
R-NT2RP3004070//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.0e-05:476:57//AC005308
R-NT2RP3004078//Homo sapiens chromosome 19, cosmid R30335, complete sequence.//2.0e-86:486:93//AC005784
R-NT2RP3004093//Human PAC clone 257C22A from 13q12-q13, complete sequence.//5.3e-11:230:69//AC002525
R-NT2RP3004095//Homo sapiens clone NH0486I22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//7.5e-93:551:92//AC005038
R-NT2RP3004110//Homo sapiens 12p13.3 PAC RPCI5-940J5 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.6e-104:317:100//AC006064
R-NT2RP3004125//Pongo pygmaeus CT microsatellite, clone #3, from the tandemly repeated genes encoding U2 small nuclear RNA (RNU2 locus).//0.73:168:60//U36532
R-NT2RP3004145//Homo sapiens full-length insert cDNA clone ZE09H03.//2.3e-89:427:99//AF086542
R-NT2RP3004148//Arabidopsis thaliana chromosome II BAC T1B8 genomic sequence, complete sequence.//0.013:134:70//U78721
R-NT2RP3004155//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence.//3.8e-10:101:87//AC004081
R-NT2RP3004206//Homo sapiens clone DJ0794K21, complete sequence.//1.5e-06:442:57//AC005533
R-NT2RP3004207//Mouse mRNA for seizure-related gene product 6.//1.7e-07:220:69//D29763
R-NT2RP3004209//Human cosmid Q7A10 (D21S246) insert DNA, complete sequence.//7.3e-89:504:92//D42052
R-NT2RP3004215//Caenorhabditis elegans cosmid F11A6, complete sequence.//0.018:353:59//Z81498
R-NT2RP3004242//Plasmodium falciparum chromosome 2, section 52 of 73 of the complete sequence.//4.5e-06:407:60//AE001415
R-NT2RP3004246//Homo sapiens chromosome 10 clone CIT987SK-1010K1 map 10q25, complete sequence.//2.8e-105:534:97//AC005385
R-NT2RP3004253//RPCI11-78J12.TJ RPCI11 Homo sapiens genomic clone R-78J12, genomic survey sequence.//4.0e-64:382:90//AQ281324
R-NT2RP3004258//Rattus norvegicus Zis mRNA, complete cds.//7.0e-60:417:84//AF013967
R-NT2RP3004262//Mus musculus heat shock protein hsp40-3 gene, complete cds.//2.7e-43:528:73//AF092536
R-NT2RP3004334//Homo sapiens chromosome 17, clone hRPC.1110_E_20, complete sequence.//1.4e-06:435:62//AC004231
R-NT2RP3004341//CITBI-E1-2503F11.TR CITBI-E1 Homo sapiens genomic clone 2503F11, genomic survey sequence.//0.0018:210:65//AQ263365
R-NT2RP3004348//Homo sapiens chromosome 17, clone hRPK.85_B_7, complete sequence.//7.1 e-46:340:83//AC005695
R-NT2RP3004349//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 117O3, WORKING DRAFT SEQUENCE.
R-NT2RP3004378//Human DNA sequence from PAC clone H1010A10 chromosome X; contains exon 1 of the cytochrome oxidase B (MAOB), ESIS and polymorphic CA repeats.//2.0e-07:422:90//Z95123

R-NT2RP3004399//HS_3046_A1_E02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3046 Col=3 Row=1, genomic survey sequence.//0.00014:186:67//AQ137619
 R-NT2RP3004424//RPC111-59114.TJ RPC111 Homo sapiens genomic clone R-59114, genomic survey sequence.//7.4e-71:370:95//AQ201461

5 R-NT2RP3004428//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y66A7, WORKING DRAFT SEQUENCE.//0.096:205:64//AL022282
 R-NT2RP3004451//Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence.//0.0029:396:60//AC005824
 R-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds.//2.9e-106:526:98//AB007917

10 R-NT2RP3004466
 R-NT2RP3004470//Homo sapiens chromosome 5, Bac clone 5m9 (LBNL H220), complete sequence.//8.3e-06:229:64//AC005895
 R-NT2RP3004472//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.87:442:59//AC005504

15 R-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds.//1.6e-105:521:97//AB007925
 R-NT2RP3004480//Mus musculus maternal-embryonic 3 (Mem3) mRNA, complete cds.//3.9e-38:322:81//U47024
 R-NT2RP3004490//Homo sapiens PAC clone 166H1 from 12q, complete sequence.//4.2e-96:527:92//AC003982
 R-NT2RP3004498//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//2.3e-43:342:82//AC006023

20 R-NT2RP3004503//Human cosmid g1572c101, complete sequence.//2.3e-25:392:68//AC000357
 R-NT2RP3004504//M.musculus mRNA for CPEB protein.//1.8e-28:387:70//Y08260
 R-NT2RP3004507
 R-NT2RP3004527//Homo sapiens chromosome 14, BAC CITB-135H17 containing the RAD51L1 gene, complete sequence.//0.68:244:62//AC004518

25 R-ntnnnnnnnnnnnn//Mouse oncogene (ect2) mRNA, complete cds.//2.6e-79:525:84//L11316
 R-NT2RP3004544
 R-NT2RP3004566
 R-NT2RP3004569//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.96:296:58//AC004709

30 R-NT2RP3004572//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence.//8.2e-12:457:63//AC005083
 R-NT2RP3004578//Homo sapiens mRNA for KIAA0477 protein, complete cds.//2.4e-97:488:96//AB007946
 R-NT2RP3004594//Homo sapiens BAC clone NH0436H22 from 2, complete sequence.//1.7e-10:368:61//AC005234

35 R-NT2RP3004617
 R-NT2RP3004618//F2H16TF IGF Arabidopsis thaliana genomic clone F2H16, genomic survey sequence.//0.96:212:64//B26414
 R-NT2RP3004670//Homo sapiens GN6ST mRNA for N-acetylglucosamine-6-O-sulfotransferase (GlcNAc6ST), complete cds.//2.2e-55:291:95//AB014679

40 R-NT2RP4000008//H.sapiens polyA site DNA sequence.//2.5e-25:202:85//Z24749
 R-NT2RP4000023//CIT-HSP-2372A9.TF CIT-HSP Homo sapiens genomic clone 2372A9, genomic survey sequence.//3.6e-51:313:89//AQ112388
 R-NT2RP4000035//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//4.3e-69:536:81//AC005015

45 R-NT2RP4000049//Homo sapiens TRAIL receptor 2 mRNA, complete cds.//2.1e-58:289:82//AF016266
 R-NT2RP4000051//Homo sapiens Chromosome 22q11.2 Cosmid Clone 20b In DGCR Region, complete sequence.//0.56:462:58//AC000074
 R-NT2RP4000078//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.00021:460:60//AC005506

50 R-NT2RP4000102//Homo sapiens chromosome 5, PAC clone 17e19 (LBNL H148), complete sequence.//1.6e-08:518:58//AC004648
 R-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds.//3.5e-106:536:96//AB011538
 R-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds.//1.1e-110:554:97//AB007952
 R-NT2RP4000147

55 R-NT2RP4000150//Rat proto-oncogene (Ets-1) mRNA, complete cds.//3.5e-46:395:83//L20681
 R-NT2RP4000154//Caenorhabditis elegans cosmid R221.1, genomic survey sequence.//1.1e-10:368:61//AC005234
 R-NT2RP4000167//RPC111-59114.TJ RPC111 Homo sapiens genomic clone R-59114, genomic survey sequence.//7.4e-71:370:95//AQ201461

6.2e-26:163:93//AQ200049

R-NT2RP4000185

R-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds.//4.6e-99:505 :96//AB014600

R-NT2RP4000212//, complete sequence.//1.0e-106:538:96//AC005300

5 R-NT2RP4000214//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//1.2e-39:272:88//AC005261

R-NT2RP4000218//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence.//1.6e-09:457:60//AC004081

R-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP).//9.0e-69:354:96//AJ006470

10 R-NT2RP4000246//Mus musculus mRNA for NDPP-1 protein, complete cds.//2.0e-27:344:73//D10727

R-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence.//9.7e-78:381:99//AF091092

R-NT2RP4000263//CIT-HSP-2336N24.TF CIT-HSP Homo sapiens genomic clone 2336N24, genomic survey sequence.//0.26:124:69//AQ043515

15 R-nnnnnnnnnnnnn//ORF 5' of ECLF2...ECRF3=G protein-coupled receptor homolog [herpesvirus saimiri HVS, host-squirrel monkey, Genomic, 4 genes, 3720 nt].//0.12:326:61//S76368

R-NT2RP4000312//Human DNA sequence from clone 523E19 on chromosome 6p11.2-12.3 Contains ESTs STS and GSSs, complete sequence.//2.2e-111:538:98//AL033384

R-NT2RP4000321//Homo sapiens clone 24453 mRNA sequence.//1.4e-108:515:99//AF070524

R-NT2RP4000323//S.cerevisiae telomeric sequence DNA, clone YLP108CA-2-i.//0.048:107:69//M34311

20 R-NT2RP4000355//Homo sapiens clone DJ1136A10, WORKING DRAFT SEQUENCE, 4 unordered pieces.//4.3e-39:350:79//AC004972

R-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds.//2.4e-109:520:99//AB018281

R-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//8.7e-109:527:98//AF044195

25 R-NT2RP4000370//Homo sapiens PAC clone DJ0777O23 from 7p14-p15, complete sequence.//9.9e-25 :348:72//AC005154

R-NT2RP4000376//Rattus norvegicus phospholipase A-2-activating protein (plap) mRNA, complete cds.//2.2e-69:391:89//U17901

30 R-NT2RP4000381//Homo sapiens chromosome 17, clone hRPK.394_K_10, complete sequence.//0.066:197:63//AC006080

R-NT2RP4000415//345F19.TV CIT978SKA1 Homo sapiens genomic clone A-345F19, genomic survey sequence.//0.10:79:75//B15527

R-NT2RP4000417//Homo sapiens full-length insert cDNA clone ZD52B10.//9.6e-96:468:97//AF086313

35 R-NT2RP4000424//Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethylaniline Monooxygenase (N-Oxide 3, EC1.14.13.8, Dimethylaniline Oxidase 3, FMO II, FMO 3), and a gene for another, unknown, Flavin-containing Monooxygenase family protein. Contains ESTs and GSSs, complete sequence.//1.8e-08:489:59//AL021026

40 R-NT2RP4000448//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//3.3e-07:510:60//AC005505

R-NT2RP4000449//HS_2037_B2_A09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2037 Col=18 Row=B, genomic survey sequence.//1.3e-58:375:88//AQ243047

R-NT2RP4000455//Phocine herpesvirus type 1 glycoprotein D (gD) gene, partial cds.//0.62:133:63//U92271

R-nnnnnnnnnnnnn

45 R-NT2RP4000480//cSRL-54b11-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone CSRL-54b11, genomic survey sequence.//2.1e-19:145:88//B05082

R-nnnnnnnnnnnnn

R-NT2RP4000500

50 R-NT2RP4000515//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//1.4e-05:411:59//AC005140

R-NT2RP4000517//Human Chromosome 16 BAC clone CIT987SK-A-61E3, complete sequence.//2.7e-21:230:77//AC003007

55 R-NT2RP4000518//Homo sapiens DNA sequence from PAC 206D15 on chromosome 1q24. Contains a Reduced Folate Carrier protein (RFC) LIKE gene, a mitochondrial ATP Synthetase protein 8 (ATP8, MTATP8) LIKE pseudogene, an unknown gene and the last exon of the JEM1 gene coding for the Basic-Leucine Zipper nuclear factor

PM104441.1 Homo sapiens: reduced folate carrier protein 1 (RFC1) gene, complete cds. PM104441.1 Homo sapiens: reduced folate carrier protein 1 (RFC1) gene, complete cds.

PM104441.1 Homo sapiens: reduced folate carrier protein 1 (RFC1) gene, complete cds.

PM104441.1 Homo sapiens: reduced folate carrier protein 1 (RFC1) gene, complete cds.

R-NT2RP4000528//Homo sapiens chromosome 17, clone hRPK.138_P_22, complete sequence.//0.99:158:66//AC005697

R-NT2RP4000541//Homo sapiens Chromosome 22q11.2 Cosmid Clone 33e In DGCR Region, complete sequence.//1.0:309:59//AC000078

5 R-NT2RP4000556//Rattus norvegicus cell cycle protein p55CDC gene, complete cds.//0.0031:126:72//AF052695

R-NT2RP4000588//Homo sapiens BAC clone RG208K23 from 7q31, complete sequence.//1.0:186:64//AC004161

R-NT2RP4000614//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-62, complete sequence.//1.4e-06:526:58//AL009013

10 R-NT2RP4000638//Homo sapiens chromosome 17, clone hCIT.468_F_23, WORKING DRAFT SEQUENCE, 3 unordered pieces.//6.9e-48:497:75//AC004666

R-NT2RP4000648//CIT-HSP-230017.TR CIT-HSP Homo sapiens genomic clone 230017, genomic survey sequence.//0.22:110:68//AQ012747

R-NT2RP4000657//Lycodichthys dearborni type III antifreeze peptide gene, clone 5'LD-1/NotI-EcoRI subclone SphI-XbaI, partial cds.//0.0065:189:63//U20443

15 R-NT2RP4000704//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 409J21, WORKING DRAFT SEQUENCE.//0.22:334:60//Z83824

R-NT2RP4000724//Homo sapiens Chromosome 22q11.2 Cosmid Clone 56c In DGCR Region, complete sequence.//2.2e-70:448:88//AC000080

R-NT2RP4000728//CIT-HSP-2310K14.TF CIT-HSP Homo sapiens genomic clone 2310K14, genomic survey sequence.//0.00013:289:61//AQ019669

20 R-NT2RP4000739//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 21 unordered pieces.//0.53:254:61//AC004765

R-NT2RP4000781//P.cepacia fusaric acid-resistance genes encoding 5 proteins, complete cds.//1.0:392:59//D12503

25 R-NT2RP4000817//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.//0.59:378:58//AC003037

R-NT2RP4000833//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING DRAFT SEQUENCE.//3.4e-53:307:85//AL023808

R-NT2RP4000837//Homo sapiens T-cell receptor alpha delta locus from bases 501613 to 752736 (section 3 of 5) of the Complete Nucleotide Sequence.//7.0e-50:367:77//AE000660

30 R-NT2RP4000855

R-NT2RP4000865//Homo sapiens chromosome 17, clone HRPC905N1, complete sequence.//1.5e-78:479:88//AC003098

R-NT2RP4000878//Mus musculus mRNA for myeloid associated differentiation protein.//4.5e-09:186:69//AJ001616

35 R-NT2RP4000879//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//7.8e-08:364:60//AC004153

R-nnnnnnnnnnnn//Human S-adenosylmethionine decarboxylase (AMD1) gene, exons 5-9.//3.5e-90:459:96//M88006

40 R-nnnnnnnnnnnn//H.sapiens ung gene for uracil DNA-glycosylase.//7.6e-09:392:61//X89398

R-NT2RP4000925//Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds.//5.8e-45:264:92//U42975

R-nnnnnnnnnnnn//epstein-barr virus simple repeat array (ir3).//0.00012:367:61//J02079

45 R-NT2RP4000928//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCL19, complete sequence.//1.0:138:68//AB006698

R-NT2RP4000929//Human DNA sequence from PAC 293L6 on chromosome 22, complete sequence.//0.45:288:62//Z82197

R-NT2RP4000955//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 633O19, WORKING DRAFT SEQUENCE.//1.1e-09:322:62//AL022302

50 R-NT2RP4000973//Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions.//2.3e-06:326:62//AF003528

R-NT2RP4000975

R-NT2RP4000979//HS_3009_B1_F08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3009 Col=15 Row=L, genomic survey sequence.//2.3e-14:117:89//AQ090957

55 R-NT2RP4000984//Human immunodeficiency virus type 1 envelope glycoprotein (env) gene, C2-V3 region, isolate

R-NT2RP4000989//Sequence from patent US 5552253

R-NT2RP4000996//Plasmodium falciparum strain Dd2 heat shock protein 80 (HSP80)

CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein (cg2), and CG7 (cg7) genes, complete cds.//3.8e-07:421:59//AF030694

R-NT2RP4000997//Homo sapiens chromosome 17, clone 104H12, complete sequence.//4.2e-37:499:72//AC000003

R-NT2RP4001004//HS_3163_A2_H02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3163 Col=4 Row=O, genomic survey sequence.//2.8e-38:241:90//AQ168515

R-NT2RP4001006//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.
7.1e-55:372:73//AC006023

R-NT2RP4001010//Homo sapiens full-length insert cDNA clone ZD38E12.//3.3e-09:153:74//AF086247

R-NT2RP4001029//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds//2.1e-34:361:78//U20086

R-NT2RP4001041//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence//9.9e-84:435:96//AC005216

R-NT2RP4001057//Homo sapiens KIAA0399 mRNA, partial cds.//6.2e-50:282:94//AB007859

R-NT2RP4001064//H.sapiens NOS2 gene, exon 15.//0.71:183:61//X85771

R-NT2RP4001078//Human D-site binding protein gene, exon 4 and complete cds.//1.9e-114:569:97//U48213

R-NT2RP4001079//Homo sapiens mRNA for putative Ca²⁺-transporting ATPase, partial.//2.4e-118:574:98//AJ010953

R-NT2RP4001080//Plasmodium falciparum chromosome 2, section 66 of 73 of the complete sequence//0.013:430:58//AE001429

R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0592 protein, partial cds.//1.8e-119:548:95//AB011164

R-NT2RP4001095//Homo sapiens cosmid IM0525, LC1233, Qc3C1, LB1439, Qc12C11 and 220B3 from Xq28, complete sequence.//2.8e-39:312:81//AF003626

R-NT2RP4001100//Human DNA sequence from cosmid U85A3, between markers DXS366 and DXS87 on chromosome X contains *rad21* and T-cell cyclophorin pseudogenes, STS//8.7e-41:389:78/Z78021

R-NT2RP4001117//Canis familiaris sec61 homologue mRNA, complete cds.//2.8e-12:292:68//M96629

R-NT2RP4001122//Caenorhabditis elegans cosmid F44D12, complete sequence.//0.97:129:66//Z68298

R-NT2RP4001126//HS_3146_A1_805_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3146 Col=9 Row=C, genomic survey sequence.//0.013:268:63//AQ141093

R-NT2RP4001138

R-NT2RP4001143//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 64K7, WORKING DRAFT SEQUENCE.//1.8e-31:380:68//AL031668

R-NT2RP4001148//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces//1.2e-83:325:92//AC005095

R-NT2RP4001149//Mouse mRNA for thymic epithelial cell surface antigen, complete cds.//8.1e-32:553:67//D67067

R-NT2RP4001150//AK011 Genomic DNA *Hordeum vulgare* genomic clone tel44a similar to barley TAS, genomic survey sequence//0.91:132:63//AQ248412

R-NT2RP4001159//Cloning vector pAP3neo DNA, complete sequence.//4.0e-118:437:97//AB003468

R-NT2RP4001174//Homo sapiens 12q24 BAC RPC11-162P23 (Roswell Park Cancer Institute Human BAC library) complete sequence//1.7e-33:289:82//AC002996

R-nnnnnnnnnnnnn//P.falciparum mRNA for AARP2 protein.//0.93:187:64/Y08924

R-NT2RP4001207

R-NT2RP4001210//CIT-HSP-2042D13.TF CIT-HSP Homo sapiens genomic clone 2042D13, genomic survey sequence.//3.8e-06:268:63//B74772

R-NT2RP4001213//Human zinc finger protein 20 (ZNF20) pentanucleotide repeat polymorphism.//4.7e-16:371:66/M99593

R-NT2RP4001219//HS_2190_A1_A06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2190 Col=11 Row=A, genomic survey sequence//2.4e-06:288:61//AQ216635

R-NT2RP4001228//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P2, WORKING DRAFT SEQUENCE.//0.024:357:58//AL031745

R-NT2RP4001235//HS_3047_A1_E07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=13 Row=L, genomic survey sequence//0.0033:301:63//AQ126918

R-NT2RP4001256//HS_3007_A2_B06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3007 Col=12 Row=C, genomic survey sequence.//1.5e-11:140:80//AQ118389

R-NT2RP4001260//Plasmodium falciparum chromosome 2, section 63 of 73 of the complete sequence//0 0013-186 59//AF001426

Accession number: J04021 (42,449-AQ01388)

R-nnnnnnnnnnnnn/Homo sapiens full-length insert cDNA clone ZD55D10//1.2e-10:90:92//AF086334
R-NT2RP4001313//Mus musculus orphan nuclear hormone receptor (CAR) gene, complete sequence//7.7e-23:466:66//AF009326
R-NT2RP4001315//CIT-HSP-2312C6.TR CIT-HSP Homo sapiens genomic clone 2312C6, genomic survey sequence//0.98:305:62//AQ018036
R-NT2RP4001339
R-NT2RP4001345
R-NT2RP4001351//Fruitfly strain g20 mitochondrial DNA, A+T-rich region, partial sequence//0.00082:260:59//AB003097
R-NT2RP4001353//RPC111-55N17.TJ RPC111 Homo sapiens genomic clone R-55N17, genomic survey sequence//0.74:106:66//AQ081821
R-NT2RP4001372
R-NT2RP4001373//Homo sapiens chromosome 17, clone hRPK.394_K_10, complete sequence//1.5e-09:473:60//AC006080
R-NT2RP4001375
R-NT2RP4001379//CIT-HSP-2335A10.TF CIT-HSP Homo sapiens genomic clone 2335A10, genomic survey sequence//9.4e-41:441:75//AQ040083
R-NT2RP4001389//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence//2.4e-22:276:73//AC004691
R-NT2RP4001407//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces//0.49:254:61//AC005140
R-NT2RP4001414
R-NT2RP4001433//Human prohibitin (PHB) gene, exons 1-7//6.6e-66:357:90//L14272
R-NT2RP4001442//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces//0.11:307:59//AC005308
R-NT2RP4001447//cSRL-58d2-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-58d2, genomic survey sequence//0.0039:112:71//B05220
R-NT2RP4001474
R-NT2RP4001483
R-NT2RP4001498//Plasmodium falciparum (clone Dd2) heat shock protein 86 gene, complete cds//1.2e-07:339:61//L34027
R-NT2RP4001502//HS_2187_B1_C10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2187 Col=19 Row=F, genomic survey sequence//1.3e-20:183:81//AQ214108
R-NT2RP4001507//Arabidopsis thaliana chromosome 1 BAC T17H3 sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces//0.15:333:62//AC005916
R-NT2RP4001524//Genomic sequence from Human 13, complete sequence//0.96:159:65//AC001226
R-NT2RP4001529//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds//9.5e-34:337:80//U20086
R-NT2RP4001547//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces//0.00027:336:63//AC004710
R-nnnnnnnnnnnnn//Arabidopsis thaliana BAC T12H20//1.5e-11:517:60//AF080119
R-NT2RP4001555//Human DNA sequence from PAC 481A17 on chromosome X contains ESTs//0.0069:305:62//Z82212
R-NT2RP4001567//RPC111-61A2.TJ RPC111 Homo sapiens genomic clone R-61A2, genomic survey sequence//0.0072:180:60//AQ200771
R-NT2RP4001568
R-NT2RP4001571//Trypanoplasma borreli kinetoplast ribosomal protein S12 (RPS12), putative cryptogene (GR11), 12S ribosomal RNA, and apocytochrome b (CYb) genes, primary transcripts, and cytochrome c oxidase subunit III (COIII) gene, complete cds//1.6e-09:555:58//U14181
R-NT2RP4001574//HS_2247_B1_B05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2247 Col=9 Row=D, genomic survey sequence//1.1e-41:254:90//AQ182345
R-NT2RP4001575//Human DNA sequence from clone 1033B10 on chromosome 6p21.2-21.31. Contains the BING5 gene, exons 11 to 15 of the BING4 gene, the gene for GalT3 (beta3-Galactosyltransferase), the RPS18 (40S ribosomal protein S18) gene, the SACM2L (suppressor of actin mutation 2, yeast, homolog) gene, a pseudogene similar to TAT-SF1, a Pseudogene similar to zinc finger genes, the RING1 gene, the gene for HKE6 (RING2), the gene for HKE4 (RING5), the RXRB (Retinoid X receptor beta) gene, the COL11A2 (collagen type I alpha 2(I) chain) gene, the COL11A1 (collagen type I alpha 1(I) chain) gene, the COL11A3 (collagen type I alpha 3(I) chain) gene, the COL11A4 (collagen type I alpha 4(I) chain) gene, the COL11A5 (collagen type I alpha 5(I) chain) gene, the COL11A6 (collagen type I alpha 6(I) chain) gene, the COL11A7 (collagen type I alpha 7(I) chain) gene, the COL11A8 (collagen type I alpha 8(I) chain) gene, the COL11A9 (collagen type I alpha 9(I) chain) gene, the COL11A10 (collagen type I alpha 10(I) chain) gene, the COL11A11 (collagen type I alpha 11(I) chain) gene, the COL11A12 (collagen type I alpha 12(I) chain) gene, the COL11A13 (collagen type I alpha 13(I) chain) gene, the COL11A14 (collagen type I alpha 14(I) chain) gene, the COL11A15 (collagen type I alpha 15(I) chain) gene, the COL11A16 (collagen type I alpha 16(I) chain) gene, the COL11A17 (collagen type I alpha 17(I) chain) gene, the COL11A18 (collagen type I alpha 18(I) chain) gene, the COL11A19 (collagen type I alpha 19(I) chain) gene, the COL11A20 (collagen type I alpha 20(I) chain) gene, the COL11A21 (collagen type I alpha 21(I) chain) gene, the COL11A22 (collagen type I alpha 22(I) chain) gene, the COL11A23 (collagen type I alpha 23(I) chain) gene, the COL11A24 (collagen type I alpha 24(I) chain) gene, the COL11A25 (collagen type I alpha 25(I) chain) gene, the COL11A26 (collagen type I alpha 26(I) chain) gene, the COL11A27 (collagen type I alpha 27(I) chain) gene, the COL11A28 (collagen type I alpha 28(I) chain) gene, the COL11A29 (collagen type I alpha 29(I) chain) gene, the COL11A30 (collagen type I alpha 30(I) chain) gene, the COL11A31 (collagen type I alpha 31(I) chain) gene, the COL11A32 (collagen type I alpha 32(I) chain) gene, the COL11A33 (collagen type I alpha 33(I) chain) gene, the COL11A34 (collagen type I alpha 34(I) chain) gene, the COL11A35 (collagen type I alpha 35(I) chain) gene, the COL11A36 (collagen type I alpha 36(I) chain) gene, the COL11A37 (collagen type I alpha 37(I) chain) gene, the COL11A38 (collagen type I alpha 38(I) chain) gene, the COL11A39 (collagen type I alpha 39(I) chain) gene, the COL11A40 (collagen type I alpha 40(I) chain) gene, the COL11A41 (collagen type I alpha 41(I) chain) gene, the COL11A42 (collagen type I alpha 42(I) chain) gene, the COL11A43 (collagen type I alpha 43(I) chain) gene, the COL11A44 (collagen type I alpha 44(I) chain) gene, the COL11A45 (collagen type I alpha 45(I) chain) gene, the COL11A46 (collagen type I alpha 46(I) chain) gene, the COL11A47 (collagen type I alpha 47(I) chain) gene, the COL11A48 (collagen type I alpha 48(I) chain) gene, the COL11A49 (collagen type I alpha 49(I) chain) gene, the COL11A50 (collagen type I alpha 50(I) chain) gene, the COL11A51 (collagen type I alpha 51(I) chain) gene, the COL11A52 (collagen type I alpha 52(I) chain) gene, the COL11A53 (collagen type I alpha 53(I) chain) gene, the COL11A54 (collagen type I alpha 54(I) chain) gene, the COL11A55 (collagen type I alpha 55(I) chain) gene, the COL11A56 (collagen type I alpha 56(I) chain) gene, the COL11A57 (collagen type I alpha 57(I) chain) gene, the COL11A58 (collagen type I alpha 58(I) chain) gene, the COL11A59 (collagen type I alpha 59(I) chain) gene, the COL11A60 (collagen type I alpha 60(I) chain) gene, the COL11A61 (collagen type I alpha 61(I) chain) gene, the COL11A62 (collagen type I alpha 62(I) chain) gene, the COL11A63 (collagen type I alpha 63(I) chain) gene, the COL11A64 (collagen type I alpha 64(I) chain) gene, the COL11A65 (collagen type I alpha 65(I) chain) gene, the COL11A66 (collagen type I alpha 66(I) chain) gene, the COL11A67 (collagen type I alpha 67(I) chain) gene, the COL11A68 (collagen type I alpha 68(I) chain) gene, the COL11A69 (collagen type I alpha 69(I) chain) gene, the COL11A70 (collagen type I alpha 70(I) chain) gene, the COL11A71 (collagen type I alpha 71(I) chain) gene, the COL11A72 (collagen type I alpha 72(I) chain) gene, the COL11A73 (collagen type I alpha 73(I) chain) gene, the COL11A74 (collagen type I alpha 74(I) chain) gene, the COL11A75 (collagen type I alpha 75(I) chain) gene, the COL11A76 (collagen type I alpha 76(I) chain) gene, the COL11A77 (collagen type I alpha 77(I) chain) gene, the COL11A78 (collagen type I alpha 78(I) chain) gene, the COL11A79 (collagen type I alpha 79(I) chain) gene, the COL11A80 (collagen type I alpha 80(I) chain) gene, the COL11A81 (collagen type I alpha 81(I) chain) gene, the COL11A82 (collagen type I alpha 82(I) chain) gene, the COL11A83 (collagen type I alpha 83(I) chain) gene, the COL11A84 (collagen type I alpha 84(I) chain) gene, the COL11A85 (collagen type I alpha 85(I) chain) gene, the COL11A86 (collagen type I alpha 86(I) chain) gene, the COL11A87 (collagen type I alpha 87(I) chain) gene, the COL11A88 (collagen type I alpha 88(I) chain) gene, the COL11A89 (collagen type I alpha 89(I) chain) gene, the COL11A90 (collagen type I alpha 90(I) chain) gene, the COL11A91 (collagen type I alpha 91(I) chain) gene, the COL11A92 (collagen type I alpha 92(I) chain) gene, the COL11A93 (collagen type I alpha 93(I) chain) gene, the COL11A94 (collagen type I alpha 94(I) chain) gene, the COL11A95 (collagen type I alpha 95(I) chain) gene, the COL11A96 (collagen type I alpha 96(I) chain) gene, the COL11A97 (collagen type I alpha 97(I) chain) gene, the COL11A98 (collagen type I alpha 98(I) chain) gene, the COL11A99 (collagen type I alpha 99(I) chain) gene, the COL11A100 (collagen type I alpha 100(I) chain) gene, the COL11A101 (collagen type I alpha 101(I) chain) gene, the COL11A102 (collagen type I alpha 102(I) chain) gene, the COL11A103 (collagen type I alpha 103(I) chain) gene, the COL11A104 (collagen type I alpha 104(I) chain) gene, the COL11A105 (collagen type I alpha 105(I) chain) gene

R-NT2RP4001614

R-NT2RP4001634//Homo sapiens full-length insert cDNA clone YU73B11.//5.8e-101:526:94//AF087969

R-NT2RP4001638//Homo sapiens clone 23967 unknown mRNA, partial cds//5.4e-115:559:97//AF007151

R-NT2RP4001644//M.musculus mRNA for map kinase interacting kinase, Mnk2.//6.8e-33:286:79//Y11092

R-NT2RP4001656//Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE, 8 unordered pieces//2.2e-109:515:99//AC000384

R-NT2RP4001677//Genomic sequence from Human 9q34, complete sequence.//0.19:504:58//AC000397

R-NT2RP4001696//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence.//4.5e-115:583:96//U96629

R-NT2RP4001725//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//
0.98:301:60//AC000380

R-nnnnnnnnnnnnn//Caenorhabditis elegans cosmid F48E3./2.2e-17:328:64//U28735

R-NT2RP4001739//RPC111-74E7.TJ RPC111 Homo sapiens genomic clone R-74E7, genomic survey sequence.// 1.1e-08;141:65//AQ268408

R-NT2RP4001753//H.sapiens HZF3 mRNA for zinc finger protein.//1.7e-111:552:96//X78926

R-NT2RP4001760//Mouse oncogene (ect2) mRNA, complete cds//9.3e-27:358:72//L11316

R-NT2RP4001790//Homo sapiens clone GS259H13, WORKING DRAFT SEQUENCE, 4 unordered pieces//1.7e-99:484:98//AC005020

R-NT2RP4001803//HS_3087_B2_B05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3087 Col=10 Row=D, genomic survey sequence.//2.7e-96:471:97//AQ121405

H-NI 2KP4001822

R-NT2RP4001823

R-NT2RP4001828//Human DNA sequence from PAC 179115, BRCA2 gene region chromosome 13q12-q13 contains Klotho ESTs and CpG island.//4.1e-14:136:83/Z92540

R-NT2RP4001838//Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence.//2.5e-06:418:60//AE001372

R-NT2RP4001849//P.falciparum serine rich protein (SERP I) gene//0.64:135:67//J03983

R-NT2RP4001889//Homo sapiens PAC clone DJ1182N03 from 7q11.23-q21.1, complete sequence.//4.3e-26:212:82//AC004548

R-NT2RP4001893//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//1.8e-111:570:96//AC005014

R-NT2RP4001896

R-NT2RP4001901

R-NT2RP4001927//*Borrelia burgdorferi* (section 32 of 70) of the complete genome.//1.0:242:60//AE001146

R-NT2RP4001938//Human aminopeptidase N gene, exon 1//3.3e-42:195:85//M55523

R-NT2RP4001946//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.97:371:57//AC004157

R-NT2RP4001950//RPC11-69C18.TJ RPC11 Homo sapiens genomic clone R-69C18, genomic survey sequence.//4.7e-91:552:89//AQ236641

R-NT2RP4001953//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//6.6e-70:325:84//Z93023

R-NT2RP4001966//Rat mRNA for growth potentiating factor, complete cds.//5.5e-37:141:86//D42148

R-NT2RP4001975//Human Newcastle disease virus inducible protein mRNA, partial 3'UTR region//1.0e-46:242:98//U25276

R-NT2RP4002018//RPCI11-76I23.TV RPCI11 Homo sapiens genomic clone R-76I23, genomic survey sequence.//
7.9e-89:438:97//AQ268536

R-NT2RP4002047//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 97P20, WORKING DRAFT SEQUENCE//4.1e-07:325:62//AL031297

R-NT2RP4002052//Human DNA sequence from clone 352E11 on chromosome 22q13.1-13.31. Contains GSSs, complete sequence //0.31:452:57//AL022353

R-NT2RP4002058//RPC11-69O1.TJ RPC11 Homo sapiens genomic clone R-69O1, genomic survey sequence.//
0.23:163:64//AQ268418

NITROBENZENE

0-7-98447-6

^a 1994 GenBank human cDNA sequence from clone 2101 on chromosome 6p11.2 contains part of an exon.

of a putative new gene and STSs and GSSs, complete sequence.//0.085:350:61//AL033375

R-NT2RP4002078//RPCI11-79I16.TV RPCI11 Homo sapiens genomic clone R-79I16, genomic survey sequence.//
3.3e-87:452:95//AQ283131

R-oooooooooooo

R-NT2RP4002083//Homo sapiens mineralocorticoid receptor (MLR), exon 5.//0.50:256:61//AF068619

R-NT2RP4002408//CIT-HSP-2376023.TF CIT-HSP Homo sapiens genomic clone 2376O23, genomic survey sequence.//6.8e-62:320:96//AQ111163

R-NT2RP4002791//Human PAC clone DJ318C15 from Xq23, complete sequence.//0.022:435:61//AC002476

R-NT2RP4002888//Homo sapiens BAC clone RG067E13 from 7q21, complete sequence.//6.0e-56:660:71//AC002383

R-NT2RP4002905//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-20, complete sequence.//0.0017:533:57//AL008972

R-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds.//8.7e-114:605:94//AB007934

R-OVARC1000004//Homo sapiens chromosome 4 clone B368A9 map 4q25, complete sequence//2.1e-43:326:74//AC005510

R-OVARC1000006//HS_2253_B1_F01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2253 Col=1 Row=L, genomic survey sequence//3.7e-35:191:98//AQ069124

R-OVARC1000013//HS_2212_A2_G06_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2212 Col=12 Row=M, genomic survey sequence.//0.14:212:63//AQ210584

R-OVARC1000014//Human DNA sequence from PAC 463A9, on chromosome Xq25 contains STS //0.0053:356:62//Z80232

R-OVARC1000017

R-OVARC1000035//RPCI11-65E1.TJ RPCI11 Homo sapiens genomic clone R-65E1, genomic survey sequence.//
3.3e-05:236:63//AQ237194

R-OVARC1000058//Homo sapiens DNA sequence from BAC 390C10 on chromosome 22q11.21-12.1. Contains an Immunoglobulin LIKE gene and a pseudogene similar to Beta Crystallin. Contains ESTs, STSs, GSSs and taga and tat repeat polymorphisms, complete sequence.//2.7e-48:325:82//AL008721

R-OVARC1000060//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 27K12, WORKING DRAFT SEQUENCE.//5.0e-21:297:70//AL033397

R-OVARC1000068//P.falciparum complete gene map of plastid-like DNA (IR-B)//0.00038:553:58//X95276

R-OVARC1000071//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 596C15, WORKING DRAFT SEQUENCE.//5.1e-110:599:93//AL031387

R-OVARC1000085//DNA encoding component HC5 of human proteasome.//2.7e-65:366:92//E03413

R-nnnnnnnnnnnn//CIT-HSP-2172N17.TF CIT-HSP Homo sapiens genomic clone 2172N17, genomic survey sequence.//0.80:285:59//B94391

R-OVARC1000091

R-OVARC1000092//CIT-HSP-2373J20.TR CIT-HSP Homo sapiens genomic clone 2373J20, genomic survey sequence.//1.4e-17:141:85//AQ111520

R-OVARC 1000106

R-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds //2.6e-100:495:97//AF069250

R-OVARC1000114//Homo sapiens partial XPGC gene, exon 2//9.5e-49:392:80//X71342

R-OVARC1000133/Human Chromosome 16 BAC clone CIT987SK-A-362G6, complete sequence.//0.00020:243:65//U95740

R-OVARC1000145//Homo sapiens chromosome 10 clone CIT987SK-1010K1 map 10q25, complete sequence.//
1.8e-16:370:67//AC005385

R-OVARC1000148//CIT-HSP-2386P14.TF.1 CIT-HSP Homo sapiens genomic clone 2386P14, genomic survey sequence.//1.1e-05:55:98//AQ240492

R-OVARC1000151//M.musculus GEG-154 mRNA.//9.8e-21:192:81//X71642

R-OVARC1000168//CIT-HSP-2336F6.TR CIT-HSP Homo sapiens genomic clone 2336F6, genomic survey sequence.//0.050:176:62//AQ042932

R-OVARC1000191//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE. 7 unordered pieces.//3.7e-08:534:58//AC005506

R-OVARC1000198/** SEQUENCING IN PROGRESS ** Homo sapiens chromosome 4, BAC clone C0366H07; HTGS phase 1. WORKING DRAFT SEQUENCE. 28 unordered pieces.//5 2e-111:556:96//AC004604

[illegible]

YAH, Y. and M. S. Y. 1999. The effect of Cd on the growth of *Hydrilla verticillata* L. f. *Hydrobiologia* 406: 149-154.

✓A40100C240: nucleotide sequence of the complete sequence 5' to 3' (100%)

AC005670

R-OVARC1000241//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds.//1.1e-25:312:73//AF060194

R-OVARC1000288//Human HepG2 3' region Mbol cDNA, clone hmd1d01m3.//5.4e-07:128:70//D17131

5 R-OVARC1000302//Homo sapiens chromosome 17, clone hRPK.651_L_9, complete sequence.//1.7e-10:100:88//AC005971

R-OVARC1000304//Mouse mRNA from Mov10 locus.//7.9e-66:379:81//X52574

R-OVARC 1000309

10 R-OVARC1000321//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces.//6.5e-83:453:94//AC005236

R-OVARC1000326//Rattus norvegicus lamina-associated polypeptide 1C (LAP1C) mRNA, complete cds.//5.0e-58:455:81//U19614

R-OVARC1000335//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0483I23; HTGS phase 1, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.034:429:60//AC005690

15 R-OVARC1000347//Mus musculus HRS gene, complete cds.//4.6e-06:339:61//AF020308

R-OVARC1000384//D.discoideum glycoprotein 24 A and B (GP24A and GP24B) genes, complete cds.//0.48:296:62//M27588

R-OVARC1000408//Homo sapiens DNA from chromosome 19-cosmid R27740 containing MEF2B and RSRFR2 genes, genomic sequence.//9.4e-39:286:87//AD000812

20 R-OVARC1000411//CIT-HSP-2303H10.TF CIT-HSP Homo sapiens genomic clone 2303H10, genomic survey sequence.//1.5e-07:94:84//AQ016720

R-OVARC1000414//Homo sapiens genomic DNA, 21q region, clone: 149C3X10, genomic survey sequence.//1.8e-32:296:75//AG002388

R-OVARC1000420//Homo sapiens clone DJ113/M13, complete sequence.//2.0e-48:354:77//AC005378

25 R-OVARC1000427//D.discoideum vegetative specific gene V18 gene for ribosomal protein.//2.5e-09:370:59//X15382

R-OVARC1000431//HS_2199_A2_E02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2199 Col=4 Row=1, genomic survey sequence.//1.3e-34:186:98//AQ093722

R-OVARC1000437//Gallus gallus tensin mRNA, 3' end.//1.3e-15:160:80//L06662

30 R-OVARC1000440//Homo sapiens BAC clone NH0538D15 from 7q11.23-q21.1, complete sequence.//0.0054:337:61//AC006043

R-OVARC1000442//CIT-HSP-2335L20.TR CIT-HSP Homo sapiens genomic clone 2335L20, genomic survey sequence.//1.0e-45:322:86//AQ037381

R-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds.//1.1e-77:418:94//AB014583

35 R-OVARC1000461//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 215D11, WORKING DRAFT SEQUENCE.//0.62:333:59//AL034417

R-OVARC1000465//Bos taurus guanine nucleotide-exchange protein (ARF-GEP1) mRNA, complete cds.//1.1e-81:489:91//AF023451

40 R-OVARC1000466//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence.//0.0088:98:72//AC004526

R-OVARC1000473//Homo sapiens full-length insert cDNA clone YI53C10.//3.2e-92:317:100//AF085851

R-OVARC1000479//Rattus norvegicus mRNA for TIP120, complete cds.//2.7e-70:502:84//D87671

R-OVARC1000486//Dictyostelium discoideum FusC (fusC) gene, partial cds.//0.52:411:58//AF019984

R-OVARC1000496

45 R-OVARC1000520//Homo sapiens PAC clone DJ412A9 from 22, complete sequence.//3.8e-17:294:71//AC005005

R-OVARC1000526//Homo sapiens clone GS438P06, WORKING DRAFT SEQUENCE, 17 unordered pieces.//4.5e-109:547:96//AC005024

R-OVARC1000533//Homo sapiens chromosome 19, cosmid R30385, complete sequence.//3.0e-46:264:93//AC004510

50 R-OVARC1000543//Caenorhabditis elegans cosmid F10C1.//0.00063:417:59//U49831

R-OVARC1000556//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS. CpG island, complete sequence.//1.5e-39:144:92//AL022069

R-OVARC1000557//Homo sapiens chromosome 19, cosmid R32469, complete sequence.//1.5e-81:429:96//AC005197

55 R-OVARC1000564//Homo sapiens chromosome 17, clone HRPC837J1, complete sequence.//0.83:301:58//AC004223

R-OVARC1000565//Homo sapiens chromosome 17, clone hRPK.651_L_9, complete sequence.//1.7e-10:100:88//AC005971

(IDH), and translocon-associated protein delta (TRAP) genes, complete cds, plexin related protein (PLEXR) and serine kinase (SK) genes, partial cds, Xq28lu1 gene and cytochrome C (CCp) pseudogene.//2.4e-44:300:88//U52111

5 R-OVARC1000578//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//6.4e-48:436:78//AF001549

R-OVARC1000588//Homo sapiens chromosome 19, cosmid F19847, complete sequence.//2.7e-32:313:78//AC005952

R-OVARC 1000605

10 R-OVARC1000622//Homo sapiens PAC clone DJ0942116 from 7q11, complete sequence.//6.2e-43:328:83//AC006012

R-OVARC1000640//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//1.9e-47:514:73//AC005840

R-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds.//1.6e-29:162:100//AB011162.

15 R-OVARC1000678//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.50:270:60//AC005140

R-nnnnnnnnnnnn//Rattus norvegicus mRNA for myosin-RhoGAP protein Myr 7.//1.4e-83:549:86//AJ001713

R-OVARC1000681//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 257E24, WORKING DRAFT SEQUENCE.//3.2e-13:160:76//AL034424

20 R-OVARC1000689//Schistocerca americana Antennapedia homeotic protein (Antp) mRNA, complete cds.//0.90:230:61//U32943

R-OVARC1000700//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//5.1e-15:133:85//AC005754

R-OVARC1000703//Homo sapiens chromosome 22, clone hRPC.130_H_16, complete sequence.//6.9e-48:525:73//AC005585

25 R-OVARC1000730//HS_3018_B1_H10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=19 Row=P, genomic survey sequence.//0.00019:198:63//AQ093513

R-OVARC1000746//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.98:154:65//X95276

R-OVARC1000769//Human coagulation factor XI gene, intron 2, partial, clone pTZ18R.//2.0e-30:187:78//M21185

R-OVARC1000771

30 R-OVARC1000781//Sequence 5 from Patent WO9722695.//8.4e-47:401:77//A63552

R-OVARC1000787//Homo sapiens PAC clone DJ430N08 from 22q12.1-qter, complete sequence.//7.8e-111:567:96//AC004542

R-OVARC1000800//Homo sapiens mitochondrial HSP75 mRNA, complete cds.//1.3e-17:119:95//L15189

35 R-OVARC1000802//Homo sapiens chromosome 5, BAC clone 120c13 (LBNL H171), complete sequence.//2.3e-51:482:78//AC005574

R-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CALC.//3.6e-105:536:95//Y1771

R-OVARC1000846//Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence.//2.7e-107:538:96//AC004494

R-OVARC1000850//Homo sapiens PB39 mRNA, complete cds.//3.6e-114:579:96//AF045584

40 R-OVARC1000862//M.musculus F1f mRNA.//2.3e-20:346:73//X71978

R-OVARC1000876//Plasmodium falciparum chromosome 2, section 53 of 73 of the complete sequence.//9.1e-08:427:58//AE001416

R-OVARC1000883//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//5.6e-34:357:78//U20086

45 R-OVARC1000885//Lycopersicon esculentum alcohol dehydrogenase homolog (GAD3) mRNA, partial cds.//0.47:305:60//U21801

R-OVARC 1000886

R-OVARC1000891//HS_3082_A2_F04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3082 Col=8 Row=K, genomic survey sequence.//1.1e-16:187:79//AQ122500

50 R-OVARC1000897//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudogene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//7.2e-07:476:60//AL020989

R-OVARC1000912

R-OVARC1000915//Homo sapiens chromosome 17, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

55 R-OVARC1000924//Homo sapiens Chromosome 22q11.2 Cosmid Clone cosk In NF1 Region complete sequence.//1.8e-37:185:73//U32943

R-OVARC1000925//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000926//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000927//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000928//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000929//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000930//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000931//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000932//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000933//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000934//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000935//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000936//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000937//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000938//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000939//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000940//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000941//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000942//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000943//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000944//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000945//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000946//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000947//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000948//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000949//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000950//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000951//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000952//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000953//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000954//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000955//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000956//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000957//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000958//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000959//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000960//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000961//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000962//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000963//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000964//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000965//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000966//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000967//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000968//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000969//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000970//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000971//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000972//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000973//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000974//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000975//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000976//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000977//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000978//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000979//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000980//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000981//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000982//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000983//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000984//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000985//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000986//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000987//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000988//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000989//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000990//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000991//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000992//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000993//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000994//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000995//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000996//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000997//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000998//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000999//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1001000//Homo sapiens chromosome 22, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000937//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 250D10, WORKING DRAFT SEQUENCE.//0.0028:161:65//Z99716

R-OVARC1000945//Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds.//3.5e-62:526:78//AB005549

5 R-OVARC1000948//Hypera postica NADH dehydrogenase subunit 1 (ND1) gene, partial cds, tRNA-Leu gene, complete sequence, and 16S ribosomal gene, partial sequence, mitochondrial genes encoding mitochondrial products.//0.018:212:61//U61169

R-OVARC1000959//CIT-HSP-2371K16.TR CIT-HSP Homo sapiens genomic clone 2371K16, genomic survey sequence.//1.1e-45:303:87//AQ111323

10 R-OVARC1000960//Homo sapiens BAC clone GS293C05 from 7q21-q22, complete sequence.//7.5e-44:353:81//AC005021

R-OVARC1000971//H.sapiens DNA for repeat unit locus D18S51(285 bp).//2.2e-07:223:70//X91255

R-OVARC1000984

15 R-OVARC1000996//Human DNA sequence from clone 272L16 on chromosome 1q32.1-32.3. Contains the 3' end of the LAMB3 gene for Laminin, Beta 3 (Nicein, Kalinin, BM600) and a novel Rat Ca²⁺/Calmodulin dependent Protein Kinase LIKE gene. Contains ESTs, STSs, GSSs, genomic marker D1S491 and a ca repeat polymorphism, complete sequence.//1.3e-06:179:70//AL023754

R-OVARC1000999//Homo sapiens chromosome 17, clone hCIT.457_L_16, complete sequence.//5.8e-71:332:87//AC003957

20 R-OVARC1001000//HS_3032_B1_G11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3032 Col=21 Row=N, genomic survey sequence.//5.1e-51:257:99//AQ096695

R-OVARC1001004//Homo sapiens from UWGC:y18c282 from 6p21, complete sequence.//5.6e-92:473:96//AC004190

25 R-OVARC1001010//RPCI11-10P1.TV RPCI-11 Homo sapiens genomic clone RPCI-11-10P1, genomic survey sequence.//4.1e-05:201:65//B71813

R-OVARC1001011//Homo sapiens clone DJ1021I20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//7.9e-18:219:69//AC005520

R-OVARC1001032//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y738F9, WORKING DRAFT SEQUENCE.//2.7e-89:464:86//AL022345

30 R-OVARC1001034//Homo sapiens chromosome 20, BAC clone 99 (LBNL H80), complete sequence.//1.4e-18:451:64//AC005220

R-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds.//1.3e-99:501:96//AF099149

R-OVARC1001040//Homo sapiens chromosome 17, clone hRPK.1096_G_20, complete sequence.//9.7e-17:180:78//AC005410

35 R-OVARC1001044

R-OVARC1001051//H.sapiens mRNA for homologue to yeast ribosomal protein L41.//3.7e-15:124:88//Z12962

R-OVARC1001055//Homo sapiens, clone hRPK.15_A_1, complete sequence.//2.0e-30:292:76//AC006213

R-OVARC1001062//Sequence 65 from patent US 5691147.//2.6e-54:312:92//I76237

40 R-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds.//2.3e-95:463:98//AF082657

R-OVARC1001072//Gallus gallus chicken brain factor-2 (CBF-2) mRNA, complete cds.//0.92:272:59//U47276

R-OVARC1001074//HS_2205_A1_D07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2205 Col=13 Row=G, genomic survey sequence.//1.3e-35:205:94//AQ184530

R-OVARC1001085

45 R-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin)).//4.5e-95:325:98//AJ005897

R-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds.//1.0e-73:386:95//AF051782

R-OVARC1001117//Homo sapiens chromosome 7 clone UWGC:g3586a160 from 7p14-15, complete sequence.//6.1e-37:314:81//AC005272

50 R-OVARC1001118//Homo sapiens chromosome 5, P1 clone 1195e2 (LBNL H73), complete sequence.//1.5e-44:390:77//AC005372

R-OVARC1001129//Rickettsia prowazekii strain Madrid E, complete genome; segment 1/4.//0.81:461:57//AJ235270

55 R-OVARC1001161//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 850H21, WORKING DRAFT SEQUENCE.//4.6e-08:342:64//AL031680

R-OVARC1001162//Homo sapiens chromosome 17, clone hRPK.1096_G_20, complete sequence.//9.7e-17:180:78//AC005410

R-OVARC1001163//Homo sapiens chromosome 17, clone hRPK.1096_G_20, complete sequence.//9.7e-17:180:78//AC005410

R-OVARC1001164//Homo sapiens chromosome 17, clone hRPK.1096_G_20, complete sequence.//9.7e-17:180:78//AC005410

1.3e-28:427:70//AC004963

R-OVARC1001169//RPCI11-36P6.TV RPCI-11 Homo sapiens genomic clone RPCI-11-36P6, genomic survey sequence.//0.56:113:72//AQ045859

R-OVARC1001170//Homo sapiens Xp22 BAC GS-377014 (Genome Systems Human BAC library) complete sequence.//8.8e-39:301:85//AC002549

R-OVARC1001173//Human clone HS2.30 Alu-Ya5 sequence.//2.4e-35:183:83//U67213

R-OVARC1001180//Homo sapiens 12q24.1 NOVECTOR P443K8 () complete sequence.//9.1e-41:516:72//AC005907

R-OVARC1001188//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g4, complete sequence.//1.2e-14:134:85//AC004796

R-OVARC1001200//ALS=85 kda insulin-like growth factor binding protein-3 complex acid-labile subunit [baboons, liver, mRNA Partial, 1818 nt].//0.12:345:60//S83462

R-OVARC1001232//Bovine tyrosine hydroxylase mRNA, complete cds.//0.66:257:59//M36794

R-OVARC1001240//Homo sapiens chromosome 17, clone hCIT.124_H_2, complete sequence.//1.4e-41:284:87//AC006071

R-OVARC1001243//HS_2055_B2_C01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2055 Col=2 Row=F, genomic survey sequence.//0.59:83:75//AQ243142

R-OVARC1001261//Crocodylus porosus mRNA for transthyretin.//0.93:121:66//AJ223148

R-OVARC1001268

R-OVARC1001270//Plasmodium falciparum MAL3P6, complete sequence.//0.0031:295:62//Z98551

R-OVARC1001271//Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence.//1.6e-107:544:97//AC004494

R-OVARC1001282//Homo sapiens Xp22-39-47 PAC RPCI1-199J3 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.025:402:59//AC006062

R-OVARC1001296//Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA, complete cds.//1.1e-05:319:62//U97018

R-nnnnnnnnnnnn//Sequence 13 from patent US 5624818.//5.4e-85:577:84//I41142

R-OVARC1001329//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 30G7, WORKING DRAFT SEQUENCE.//4.2e-71:282:88//AL034402

R-OVARC1001330//Homo sapiens PAC clone DJ0697H17 from 7q11.23-q21.1, complete sequence.//0.19:256:59//AC004862

R-OVARC1001339//Homo sapiens 12q13 PAC RPCI1-316M24 (Roswell Park Cancer Institute Human PAC library) complete sequence.//2.5e-49:366:83//AC004242

R-OVARC1001341//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 695O20, WORKING DRAFT SEQUENCE.//4.8e-26:447:69//AL032818

R-OVARC1001342//Homo sapiens chromosome 10 clone CIT987SK-1175G20 map 10q25.2-10q25.3, complete sequence.//5.5e-86:569:86//AC005874

R-OVARC1001344//Homo sapiens chromosome 5, BAC clone 261j17 (LBNL H190), complete sequence.//2.8e-46:424:78//AC005350

R-OVARC1001357//Sequence 1 from patent US 5597707.//3.0e-42:250:93//I34297

R-OVARC1001360//Homo sapiens chromosome 17, clone hRPK.786_O_4, complete sequence.//0.20:335:60//AC005863

R-OVARC 1001369

R-OVARC1001372//S.scrofa DNA for myogenin 3'flanking region (285 bp).//6.9e-29:249:83//X89210

R-OVARC1001376//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//2.1e-50:491:73//AC004491

R-OVARC1001381//Homo sapiens chromosome 17, clone hRPK.156_L_14, complete sequence.//9.3e-20:422:60//AC005821

R-OVARC1001391

R-nnnnnnnnnnnn

R-OVARC1001417//Homo sapiens EXLM1 mRNA, complete cds.//9.9e-110:561:95//AB00665

R-OVARC1001419//CIT-HSP-2362F16.TR CIT-HSP Homo sapiens genomic clone 2362F16, genomic survey sequence.//7.6e-47:242:98//AQ074668

R-OVARC1001425//Homo sapiens PAC clone DJ1108A12 from 14q24.3, complete sequence.//2.3e-20:211:66//AC005157

R-OVARC 1001430

R-OVARC 1001430

R-OVARC1001430//Homo sapiens BAC clone D00251N14 from Xp22, complete sequence.//2.3e-18:181:81//AC002086

R-OVARC1001476//CITBI-E1-2517B6.TR CITBI-E1 Homo sapiens genomic clone 2517B6, genomic survey sequence.//0.24:308:59//AQ278655

R-OVARC1001480//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 753D4, WORKING DRAFT SEQUENCE.//0.99:294:62//AL031676

5 R-OVARC1001489//E.caballus microsatellite DNA marker (clone ASB32).//0.87:81:71//X93546

R-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds.//9.3e-116:585:96//AF016507

R-OVARC1001506//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-13F4 ~complete genomic sequence, complete sequence.//2.6e-40:285:86//AC002039

10 R-OVARC1001525//Homo sapiens clone NH0215P16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.0:320:59//AC006036

R-OVARC1001542//Homo sapiens hJTB mRNA, complete cds.//5.0e-110:566:95//AB016488

R-OVARC1001547

R-OVARC1001577//Homo sapiens SRp46 splicing factor transcribed retropseudogene.//5.9e-33:216:92//AF031165

15 R-OVARC1001600//Human Chromosome X, complete sequence.//3.0e-22:157:89//AC002418

R-OVARC1001610//HS_3070_A2_A06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3070 Col=12 Row=A, genomic survey sequence.//0.47:107:66//AQ103523

R-OVARC1001611//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1185N5, WORKING DRAFT SEQUENCE.//0.17:236:63//AL034423

20 R-OVARC1001615//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 310O13, WORKING DRAFT SEQUENCE.//1.3e-19:248:70//AL031658

R-OVARC1001668//HS_3228_A2_E12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3228 Col=24 Row=I, genomic survey sequence.//4.6e-13:156:76//AQ188379

25 R-OVARC1001702//CITBI-E1-2501P16.TR.1 CITBI-E1 Homo sapiens genomic clone 2501P16, genomic survey sequence.//1.6e-41:217:99//AQ241965

R-OVARC1001703

R-OVARC1001711//CITBI-E1-2502N10.TF CITBI-E1 Homo sapiens genomic clone 2502N10, genomic survey sequence.//2.0e-14:220:72//AQ266194

30 R-OVARC1001726//CIT-HSP-2320O1.TF CIT-HSP Homo sapiens genomic clone 2320O1, genomic survey sequence.//0.021:170:62//AQ038145

R-OVARC1001731//Human mRNA for fibroblast tropomyosin TM30 (pl).//2.5e-72:422:90//X05276

R-OVARC1001745//Human DNA sequence from clone 796I11 on chromosome 20q12. Contains ESTs, an STS and GSSs, complete sequence.//7.6e-44:314:84//AL031257

35 R-nnnnnnnnnnnn//S.cerevisiae N-acetyltransferase (AAA1) mRNA, complete cds.//1.6e-08:396:60//M23166

R-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//3.5e-108:567:94//U97670

R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0675 protein, complete cds.//6.3e-108:529:97//AB014575

R-OVARC1001768//Caenorhabditis elegans cosmid Y57G11A, complete sequence.//0.24:205:64//Z99279

40 R-OVARC1001791//Homo sapiens BAC clone RG118P15 from 8q21, complete sequence.//4.6e-58:558:76//AC005066

R-OVARC1001795

R-OVARC1001802//Human HLA class III region containing cAMP response element binding protein-related protein (CREB-RP) and tenascin X (tenascin-X) genes, complete cds, complete sequence.//1.1e-37:346:78//U89337

45 R-OVARC1001805//Human DNA sequence from clone 511E16 on chromosome 6p24.3-25.1. Contains the last coding exon of the gene for P18 component of aminoacyl-tRNA synthetase complex, part of an unknown gene downstream of a putative CpG island, and an STS with a CA repeat polymorphism, complete sequence.//3.0e-112:581:95//AL023694

R-OVARC1001812//Human DNA sequence from clone 227L5 on chromosome Xp11.22-11.3. Contains a Keratin, Type 1 Cytoskeletal 18 (KRT18, CYK18, K18, CK18) pseudogene and an STS, complete sequence.//6.6e-41:345:81//AL031585

50 R-OVARC1001813//CITBI-E1-2508J18.TR CITBI-E1 Homo sapiens genomic clone 2508J18, genomic survey sequence.//1.6e-72:386:95//AQ263046

R-OVARC1001820//Human PAC clone DJ525N14 from Xq23, complete sequence.//4.8e-41:320:83//AC002086

55 R-OVARC1001828//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE.//0.0045:165:67//B58905

R-OVARC1001846//CIT-HSP-2014O1.TF CIT-HSP Homo sapiens genomic clone 2014O1, genomic survey sequence.//0.0045:165:67//B58905

R-OVARC1001861//M.musculus mRNA for pMEM2 protein.//9.5e-28:405:68//X95350
 R-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence.//5.9e-104:571:91//AF070611
 R-OVARC1001879//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from
 5 gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island,
 complete sequence.//9.1e-20:206:80//AL031864
 R-OVARC1001880//RPC111-42115.TJ RPC111 Homo sapiens genomic clone R-42115, genomic survey se-
 quence.//3.9e-50:287:88//AQ052700
 R-OVARC1001883//Homo sapiens chromosome 17, clone hCIT.123_J_14, complete sequence.//6.1e-13:457:63//
 AC003950
 10 R-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//
 2.5e-86:346:90//AF061749
 R-OVARC1001901//Homo sapiens testis specific methyl-CpG binding protein MBD2 (MBD2) mRNA, partial cds.//
 7.2e-89:421:100//AF072246
 R-OVARC1001911//Homo sapiens full-length insert cDNA clone ZD52F10.//8.2e-106:510:98//AF086315
 15 R-OVARC1001916
 R-OVARC1001928
 R-OVARC1001942//S.cerevisiae N-acetyltransferase (AAA1) mRNA, complete cds.//0.0013:231:63//M23166
 R-OVARC1001943//Human immunodeficiency virus type 1, strain FRMP329, envelope glycoprotein V3 region
 (env) gene, partial cds.//0.14:173:64//U58826
 20 R-OVARC1001949//Human zinc finger protein 20 (ZNF20) pentanucleotide repeat polymorphism.//1.3e-09:306:
 63//M99593
 R-OVARC1001950//Homo sapiens chromosome 17, clone hRPK.112_H_10, complete sequence.//8.2e-38:385:
 75//AC005666
 R-OVARC1001987
 25 R-OVARC1001989//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y57G11,
 WORKING DRAFT SEQUENCE.//6.3e-08:355:60//Z92841
 R-OVARC1002044//Human DNA sequence from clone 681J21 on chromosome 1q23.2-24.3 Contains CpG island,
 complete sequence.//5.0e-42:298:86//AL031286
 R-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds.//1.4e-107:542:96//AB007934
 30 R-OVARC1002066//Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence.//
 0.23:210:61//AC004411
 R-OVARC1002082//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//
 5.4e-99:546:92//AC006015
 R-OVARC1002107//Human DNA sequence from PAC 417G15 on chromosome Xq25-Xq26. Contains glypican-3
 35 precursor (intestinal protein OCI-5) (GTR2-2), pseudogene, ESTs.//4.4e-34:375:74//AL009174
 R-OVARC1002127
 R-OVARC1002138//CIT-HSP-2290O18.TF CIT-HSP Homo sapiens genomic clone 2290O18, genomic survey se-
 quence.//2.4e-07:316:62//AQ003988
 R-OVARC1002143//RPC111-54M8.TJ RPC111 Homo sapiens genomic clone R-54M8, genomic survey sequence.//
 40 2.3e-35:220:90//AQ083241
 R-OVARC1002156
 R-OVARC1002158//CITBI-E1-2514D4.TF CITBI-E1 Homo sapiens genomic clone 2514D4, genomic survey se-
 quence.//1.6e-12:140:79//AQ265720
 R-OVARC1002165//CIT-HSP-2307C9.TF CIT-HSP Homo sapiens genomic clone 2307C9, genomic survey se-
 45 quence.//5.0e-59:291:99//AQ020420
 R-OVARC1002182//P. falciparum SD17 gene for knob-associated histidine-rich protein.//0.74:161:65//Y00060
 R-PLACE1000004//D.discoideum gene for protein kinase.//0.00081:263:59//Z37981
 R-PLACE1000005//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING
 DRAFT SEQUENCE, 9 unordered pieces.//0.0082:477:58//AC005507
 50 R-PLACE1000007//Homo sapiens clone 24422 mRNA sequence.//1.2e-14:100:97//AF070557
 R-PLACE1000014//Homo sapiens genomic DNA, chromosome 21q22.2, p1 clone: T1212 and T1601, WORKING
 DRAFT SEQUENCE.//2.8e-44:405:77//D83253
 R-PLACE1000031//Homo sapiens clone UWGC:y23c049 from 6p21, complete sequence.//1.8e-24:291:73//
 AC006162
 55 R-PLACE1000040//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y105C5
 (a) 1000040 Human BAC clone RG21004 complete sequence.//1.0e-13:54:8//Z0246
 R-PLACE1000048//Human BAC clone RG21004 complete sequence.//1.0e-13:54:8//Z0246
 R-PLACE1000050//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING

DRAFT SEQUENCE, 8 unordered pieces.//0.98:73:76//AC005505
 R-PLACE1000061//Human ribosomal protein L37a mRNA sequence.//5.9e-21:125:98//L22154
 R-PLACE1000066
 R-PLACE1000078//Homo sapiens chromosome 11 clone CIT987SK-1012F4, WORKING DRAFT SEQUENCE, 6
 5 unordered pieces.//1.2e-87:456:95//AC005848
 R-PLACE1000081
 R-PLACE1000094//RPC111-91K6.TV RPC111 Homo sapiens genomic clone R-91K6, genomic survey sequence.//
 2.3e-83:409:98//AQ282619
 R-PLACE1000133//Homo sapiens chromosome 17, clone hRPK.746_E_8, complete sequence.//1.8e-06:420:57//
 10 AC005358
 R-PLACE1000142
 R-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds.//1.3e-112:594:94//
 AF058291
 R-PLACE1000185
 R-PLACE1000213//CIT-HSP-2308A18.TR CIT-HSP Homo sapiens genomic clone 2308A18, genomic survey se-
 15 quence.//8.2e-80:410:97//AQ022149
 R-PLACE1000214//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-09, complete
 sequence.//1.6e-05:548:59//AL008989
 R-PLACE1000236//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 695O20, WORKING
 20 DRAFT SEQUENCE.//2.2e-16:118:91//AL032818
 R-PLACE1000246//X.laevis mRNA for XLCL2 protein.//6.5e-13:66:95//Z14122
 R-PLACE1000292//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 111B22, WORKING
 DRAFT SEQUENCE.//6.6e-41:322:84//Z98200
 R-PLACE1000332//Homo sapiens chromosome 17, clone hCIT.281_F_24, complete sequence.//1.8e-16:598:62//
 25 AC004706
 R-PLACE1000347//Homo sapiens PAC clone DJ1090P18 from 7q21-q22, complete sequence.//2.3e-11:237:69//
 AC005326
 R-PLACE1000374//Arabidopsis thaliana chromosome 1 BAC F15K9 sequence, complete sequence.//8.7e-09:
 492:58//AC005278
 R-PLACE1000380//Plasmodium falciparum chromosome 2, section 1 of 73 of the complete sequence.//0.59:354:
 30 59//AE001364
 R-PLACE1000383//Mus musculus myotubularin related protein 1 (Mtmr1) mRNA, complete cds.//0.55:65:84//
 AF073997
 R-PLACE1000401//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.6e-
 35 17:152:83//AC005015
 R-PLACE1000406//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21H1, complete sequence.//
 0.51:346:58//AB020742
 R-PLACE1000420//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 2/15,
 WORKING DRAFT SEQUENCE.//1.5e-25:243:79//AP000009
 R-PLACE1000421//HS_2251_B2_G12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 40 nomic clone Plate=2251 Col=24 Row=N, genomic survey sequence.//1.4e-82:430:95//AQ192807
 R-PLACE1000424//Human PAC clone DJ515N1 from 22q11.2-q22, complete sequence.//1.8e-36:483:71//
 AC002073
 R-PLACE1000435//Homo sapiens chromosome 21q22.2 cosmid clone Q71A3, complete sequence.//2.6e-37:371:
 45 76//AF015724
 R-PLACE1000444//Homo sapiens chromosome 17, clone hRPK.227_G_15, complete sequence.//1.0e-54:429:
 81//AC005899
 R-PLACE1000453//Murine genomic DNA; partially digested Sau3A fragment, cloned into cosmid vector
 pEMBLcos2, complete sequence.//0.66:103:72//AF059580
 R-PLACE1000481//Human DNA sequence from clone 960O17 on chromosome Xp11.21-11.22 Contains EST, CA
 50 repeat(DXS991), STS, GSS, complete sequence.//0.019:171:66//AL022166
 R-PLACE1000492//Rat vacuolar protein sorting homolog vps33b mRNA, complete cds.//3.2e-17:221:72//
 U35245
 R-PLACE1000540//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING
 55 DRAFT SEQUENCE 5 unordered pieces //0.00045:480:60//AC005308
 R-PLACE1000562// complete sequence //1.8e-45:280:92//AC005405

R-PLACE1000564//Human chromosome 16 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds.//0.0079:180:65//U41302

R-PLACE1000583//Homo sapiens chromosome 17, clone hRPK.799_N_11, complete sequence.//1.5e-37:414:74//AC005323

5 R-nnnnnnnnnnnnn//Human guanylate binding protein isoform I (GBP-2) mRNA, complete cds.//1.9e-77:542:82//M55542

R-PLACE1000596//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.00019:482:59//AC005506

10 R-PLACE1000599//Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S2A1T, TCRBV6S5A1N1, TCRBV30S1P, TCRBV31S1, TCRBV13S5, TCRBV6S1A1N1, TCRBV32S1P, TCRBV5S5P, TCRBV1S1A1N1, TCRBV12S2A1T, TCRBV21S1, TCRBV8S4P, TCRBV12S3, TCRBV21S3A2N2T, TCRBV8S5P, TCRBV13S1 genes from bases 1 to 267156 (section 1 of 3).//5.6e-51:369:85//U66059

15 R-PLACE1000610//HS_3071_A1_C05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=9 Row=E, genomic survey sequence.//0.051:147:65//AQ103341

R-PLACE1000636//HS_3220_B2_E09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3220 Col=18 Row=J, genomic survey sequence.//0.010:253:64//AQ181157

20 R-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//1.6e-99:506:96//AF102265

R-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNLc110F1857Q7 (RZPD Berlin)).//4.5e-101:559:92//AJ005896

R-PLACE1000706//nuclear protein TIF1 [mice, mRNA, 3951 nt].//9.1e-10:331:63//S78219

R-PLACE1000712//Homo sapiens full-length insert cDNA clone ZD76G10.//1.0e-69:345:98//AF086408

25 R-PLACE1000716//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//1.0:174:62//AC002300

R-PLACE1000748//Plasmodium falciparum MAL3P3, complete sequence.//1.0e-06:337:60//Z98547

R-PLACE1000749//cSRL-15g9-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-15g9, genomic survey sequence.//8.8e-26:236:80//B02791

30 R-PLACE1000755//HS_2183_B1_H11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=21 Row=P, genomic survey sequence.//0.47:151:65//AQ064202

R-PLACE1000769//Homo sapiens clone DJ0647J21, WORKING DRAFT SEQUENCE, 10 unordered pieces.//7.0e-38:492:74//AC004847

R-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds.//2.6e-101:513:96//AB014548

35 R-PLACE1000786//Human putative outer mitochondrial membrane 34 kDa translocase hTOM34 mRNA, complete cds.//0.078:180:68//U58970

R-nnnnnnnnnnnnn

R-PLACE1000798//Homo sapiens cosmid D66B10, chromosome 21 5' of IFNAR1.//5.1e-26:348:72//AF039904

40 R-PLACE1000841//Human guanine nucleotide regulatory protein (NET1) mRNA, complete cds.//1.4e-26:110:95//U02081

R-nnnnnnnnnnnnn//Homo sapiens full-length insert cDNA clone ZD55D10.//1.4e-13:93:96//AF086334

R-PLACE1000856//Anopheles quadrimaculatus NADH dehydrogenase subunits (1-4, 4L, 5-6); cytochrome oxidase subunits (1-3); adenosine triphosphatase subunits (6,8); cytochrome b; transfer RNA; ribosomal RNA (large and small subunits).//2.7e-09:484:59//L04272

45 R-PLACE1000863

R-PLACE1000909//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//3.0e-05:274:60//AC005505

50 R-PLACE1000931//RPCI11-66P7.TK RPCI11 Homo sapiens genomic clone R-66P7, genomic survey sequence.//3.4e-73:369:97//AQ237489

R-PLACE1000948//RPCI11-64K15.TK RPCI11 Homo sapiens genomic clone R-64K15, genomic survey sequence.//6.6e-06:258:62//AQ239337

R-PLACE1000972//Homo sapiens chromosome 17, clone hRPK.112_J_9, complete sequence.//8.3e-20:223:76//AC005553

55 R-PLACE1000977//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 10 unordered pieces.//0.00019:482:59//AC005506

R-nnnnnnnnnnnnn

R-PLACE1000978//Homo sapiens cosmid D66B10, chromosome 21 5' of IFNAR1.//5.1e-26:348:72//AF039904

R-PLACE1000979//Homo sapiens cosmid D66B10, chromosome 21 5' of IFNAR1.//5.1e-26:348:72//AF039904

quence.//7.0e-07:64:95//AQ004997

R-PLACE1001007//Human endothelial nitric oxide synthase gene, complete cds.//0.0078:215:64//D26607

R-PLACE1001010

R-PLACE1001015//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 150C2, WORKING

DRAFT SEQUENCE.//1.5e-16:452:63//AL022318

R-PLACE1001024//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 417M14, WORKING

DRAFT SEQUENCE.//0.99:186:63//AL024498

R-PLACE1001036//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.5e-15:313:68//AC005377

R-PLACE1001062//Homo sapiens chromosome 17, clone hCIT54K19, complete sequence.//7.3e-16:119:84//AC003664

R-PLACE1001076

R-PLACE1001088//Human DNA sequence from cosmid 203C2, between markers DXS6791 and DXS8038 on chromosome X contains ESTs.//0.97:332:59//Z74696

R-PLACE1001092//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//6.2e-07:302:62//AC005139

R-PLACE1001104//Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence.//0.057:280:60//AE001372

R-PLACE1001118//Homo sapiens DNA sequence from PAC 418A9 on chromosome 6q21. Contains the first (5') two exons of a CDK8 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and STSs, complete sequence.//4.9e-06:334:60//Z84480

R-PLACE1001136//Homo sapiens chromosome 17, clone hRPK.22_N_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//1.1e-31:331:75//AC005412

R-PLACE1001168//HS_2036_A1_H04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2036 Col=7 Row=O, genomic survey sequence.//0.40:144:63//AQ230662

R-PLACE1001171

R-PLACE1001185

R-PLACE1001238//Human coxVIb gene, last exon and flanking sequence.//3.4e-36:349:76//X58139

R-PLACE1001241//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-20, complete sequence.//0.11:258:61//AL008972

R-PLACE1001257//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone B4P3; HTGS phase 1, WORKING DRAFT SEQUENCE, 9 unordered pieces.//1.9e-46:484:73//AC000016

R-PLACE1001272//Homo sapiens chromosome 21q22.3 PAC 191P10, complete sequence.//0.89:119:65//AF045448

R-PLACE1001279//Caenorhabditis elegans cosmid Y39A1C, complete sequence.//0.99:95:69//AL023839

R-PLACE1001280//CIT-HSP-2328B24.TF CIT-HSP Homo sapiens genomic clone 2328B24, genomic survey sequence.//5.4e-24:147:76//AQ042129

R-PLACE1001294//M.musculus GEG-154 mRNA.//1.3e-22:472:65//X71642

R-PLACE1001304//Homo sapiens chromosome 19, overlapping cosmids F18547, F11133, R27945, R28830 and R32804, complete sequence.//2.2e-22:139:77//AC003682

R-PLACE1001311//Loligo pealei repeat region.//0.84:232:64//Z18286

R-PLACE1001323//Homo sapiens DNA sequence from PAC 418A9 on chromosome 6q21. Contains the first (5') two exons of a CDK8 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and STSs, complete sequence.//7.2e-39:308:83//Z84480

R-PLACE1001351//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y39B6, WORKING DRAFT SEQUENCE.//0.0018:408:59//Z95399

R-PLACE1001366//Human Na+/phosphate co-transporter gene, exon 1, partial sequence.//2.2e-46:369:82//D89927

R-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds.//7.1e-80:431:93//AF009615

R-PLACE1001383//Homo sapiens clone 24538 mRNA sequence.//3.6e-35:192:97//AF055030

R-PLACE1001384//Homo sapiens mRNA for multi PDZ domain protein.//2.6e-86:456:94//AJ001319

R-PLACE1001387

R-PLACE1001395//Nyctalus leisleri mitochondrial D-loop, partial sequence.//0.054:148:68//U95355

R-PLACE1001399//Homo sapiens chromosome 17, clone hRPK.22_N_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//6.7e-70:352:98//AC005412

R-PLACE1001400//Homo sapiens chromosome 17, clone hRPK.22_N_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//6.7e-70:352:98//AC005412

R-PLACE1001401//Homo sapiens chromosome 17, clone hRPK.22_N_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//6.7e-70:352:98//AC005412

- R-PLACE1001440//Homo sapiens Xq28 genomic DNA in the region of the ALD locus containing the genes for creatine transporter (SLC6A8), CDM, adrenoleukodystrophy (ALD), Na⁺-isocitrate dehydrogenase gamma subunit (IDH), and translocon-associated protein delta (TRAP) genes, complete cds, plexin related protein (PLEXR) and serine kinase (SK) genes, partial cds, Xq281u1 gene and cytochrome C (CCp) pseudogene.//1.0:250:61//U52111
- 5 R-PLACE1001456//Borrelia burgdorferi (section 16 of 70) of the complete genome.//0.0077:173:62//AE001130
- R-PLACE1001468//HS_3050_A2_D07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3050 Col=14 Row=G, genomic survey sequence.//0.00023:202:65//AQ133920
- R-PLACE1001484//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence.//7.2e-17:180:80//AC002368
- 10 R-PLACE1001502//RPCI11-24F2.TP RPCI-11 Homo sapiens genomic clone RPCI-11-24F2, genomic survey sequence.//0.15:203:66//B84401
- R-PLACE1001503//HS_2183_A1_B10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=19 Row=C, genomic survey sequence.//1.3e-38:181:82//AQ022613
- R-PLACE1001517//Homo sapiens hGAA1 mRNA, complete cds.//6.4e-56:339:90//AB006969
- 15 R-PLACE1001534//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 620E11, WORKING DRAFT SEQUENCE.//8.6e-59:304:97//AL031667
- R-PLACE1001545//Homo sapiens chromosome 3, clone hRPK.165_L_16, complete sequence.//2.6e-18:171:82//AC 005669
- R-PLACE1001551
- 20 R-PLACE1001570//M.capricolum DNA for CONTIG MC188.//0.0043:305:57//Z33135
- R-PLACE1001602//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11.//2.5e-82:408:98//AB020860
- R-PLACE1001603//Homo sapiens KE05 protein mRNA, complete cds.//1.5e-40:295:84//AF064605
- R-PLACE1001610//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.5e-39:307:82//AC005037
- 25 R-PLACE1001611//Homo sapiens histone macroH2A1.2 mRNA, complete cds.//4.9e-41:217:97//AF054174
- R-PLACE1001632//Human DNA binding protein (HPF2) mRNA, complete cds.//1.4e-08:178:65//M27878
- R-PLACE1001634//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone H06C16, WORKING DRAFT SEQUENCE.//0.00026:221:62//Z92791
- 30 R-PLACE1001640//Homo sapiens chromosome 17, clone hRPK.651_L_9, complete sequence.//2.6e-83:441:95//AC005971
- R-PLACE1001672//H.sapiens flow-sorted chromosome 6 TaqI fragment, SC6pA26H8.//0.91:115:69//Z79253
- R-PLACE1001691//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds.//1.5e-111:545:97//AF069250
- 35 R-PLACE1001692//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.0e-46:478:75//AC005077
- R-PLACE1001705//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 250D10, WORKING DRAFT SEQUENCE.//0.79:91:73//Z99716
- R-PLACE1001716//Homo sapiens Xp22 PAC RPCI1-167A22 (from Roswell Park Cancer Center) complete sequence.//0.96:172:66//AC002349
- 40 R-PLACE1001720
- R-PLACE1001729//Human interleukin-13 (IL-13) precursor gene, complete cds.//0.79:280:60//U31120
- R-PLACE1001739//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//1.0:109:65//AC005261
- 45 R-PLACE1001740//Homo sapiens BAC clone GS114I09 from 7p14-p15, complete sequence.//5.3e-11:249:67//AC006027
- R-PLACE1001745
- R-PLACE1001746//Homo sapiens chromosome 4 clone B200N5 map 4q25, complete sequence.//6.0e-05:337:61//AC005509
- 50 R-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//1.3e-91:540:89//AF061243
- R-PLACE1001756//Human BAC clone RG302F04 from 7q31, complete sequence.//0.074:344:62//AC002463
- R-PLACE1001761
- R-PLACE1001771//Homo sapiens full-length insert cDNA clone ZD79C11.//4.4e-57:298:96//AF086426
- R-PLACE1001781//T.thermophila micronuclear DNA containing to chromosomal breakage sequence Cbs-1, clone Ti819.//4.6e-05:282:61//M15711
- 55 R-PLACE1001782//Homo sapiens A1 P-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.

4.1e-92:463:95//AF058953

R-PLACE1001821//***ALU WARNING: Human Alu-J subfamily consensus sequence.//3.6e-36:281:82//U14567

R-PLACE1001845//Mus musculus Paneth cell enhanced expression PCEE mRNA, complete cds.//9.1e-26:313:73//U37351

R-PLACE1001869

R-PLACE1001897//Mus musculus homeobox protein (D1x5) mRNA, complete cds.//0.0043:207:64//AF033011

R-PLACE1001912//RPCI11-25F23.TKBR RPCI-11 Homo sapiens genomic clone RPCI-11-25F23, genomic survey sequence.//6.3e-33:248:67//AQ013567

R-PLACE1001920//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds.//5.0e-73:363:98//AF070671

R-PLACE1001928//Homo sapiens chromosome 17, clone hRPK.642_C_21, complete sequence.//0.98:248:60//AC005245

R-PLACE1001983//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y40H7, WORKING DRAFT SEQUENCE.//0.12:157:61//AL021389

R-PLACE1001989//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 968D22, WORKING DRAFT SEQUENCE.//1.4e-44:376:80//AL023755

R-PLACE1002046//CITBI-E1-2520J24.TF CITBI-E1 Homo sapiens genomic clone 2520J24, genomic survey sequence.//4.5e-20:144:89//AQ280117

R-PLACE1002052//Human DNA sequence from cosmid U160A4, between markers DXS366 and DXS87 on chromosome X contains STS.//0.025:362:57//Z80900

R-PLACE1002066//Leishmania tarentolae maxicircle DNA fragment.//0.0034:197:62//X02438

R-PLACE1002072//Homo sapiens chromosome 5, P1 clone 854b11 (LBNL H44), complete sequence.//9.7e-06:414:60//AC004763

R-PLACE1002073

R-PLACE1002090//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-345G4 ~complete genomic sequence, complete sequence.//1.8e-06:278:63//AC002302

R-PLACE1002115//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y214H10, WORKING DRAFT SEQUENCE.//6.0e-12:327:64//AL022344

R-PLACE1002119//Mus musculus IERS (Ier5) mRNA, complete cds.//5.1e-67:442:86//AF079527

R-PLACE1002140//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1.

Contains ESTs, STSs and GSSs, complete sequence.//2.2e-80:403:97//AL022162 R-PLACE1002150//Human DNA sequence from PAC 145B12 on chromosome Xq27-Xq28. Contains EST, CA repeat and STS.//0.043:455:59//AL008706

R-PLACE1002157//Human DNA sequence from Fosmid 65B7 on chromosome 22q11.2-qter. Contains exons 6-12 of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter), complete sequence.//9.8e-58:384:79//Z83849

R-PLACE1002163//Canis familiaris MHC class IIA DLA-DQA (DQA 1 allele) gene, exon 2, partial cds.//0.82:96:70//U44785

R-PLACE1002171//Homo sapiens PAC clone DJ1100F23 from 7q31, complete sequence.//0.83:196:65//AC004456

R-PLACE1002205//Human DNA sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked, juvenile) 1 (XLRS1). Contains ESTs, an STS and GSSs, complete sequence.//0.0017:193:61//Z94056

R-PLACE1002213//Homo sapiens chromosome 19, fosmid 37308, complete sequence.//8.0e-42:330:81//AC004152

R-PLACE1002227//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//2.1e-10:126:80//AC003071

R-PLACE1002256//Homo sapiens clone DJ0853H20, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.7e-06:478:57//AC004907

R-PLACE1002259//Human DNA sequence from cosmid U75A4 on chromosome X.//6.5e-81:501:88//Z82255

R-PLACE1002319//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00023:549:58//AC005505

R-PLACE1002342//Homo sapiens mRNA for KIAA0728 protein, partial cds.//4.9e-94:501:93//AB018271

R-PLACE1002395//Homo sapiens chromosome 19, cosmid R34382, complete sequence.//1.4e-69:385:93//AC005329

R-PLACE1002433//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y214H10, WORKING DRAFT SEQUENCE.//0.85:176:63//AL031984

R-PLACE1002437//Human BAC clone RG114A06 from 7q31, complete sequence.//0.0040:213:63//AC002542
 R-PLACE1002438//CITBI-E1-2501M20.TF.1 CITBI-E1 Homo sapiens genomic clone 2501M20, genomic survey
 sequence.//0.70:247:61//AQ242104
 5 R-PLACE1002450//Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3.//
 0.00060:471:59//AJ229041
 R-PLACE1002465//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//
 2.5e-10:98:81//AC004854
 R-PLACE1002474//Mus musculus matrilin-2 precursor mRNA, complete cds.//1.7e-25:199:71//U69262
 10 R-PLACE1002477//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE
 LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs.
 Contains polymorphic CA repeat.//1.2e-11:382:63//Z92545
 R-PLACE1002493//Homo sapiens signal transducing adaptor molecule 2A (STAM2) mRNA, complete cds.//1.1e-
 53:307:91//AF042273
 R-PLACE1002499//Plasmodium falciparum MAL3P6, complete sequence.//0.56:270:60//Z98551
 15 R-PLACE1002500//CIT-HSP-2337C20.TR CIT-HSP Homo sapiens genomic clone 2337C20, genomic survey se-
 quence.//3.2e-42:297:85//AQ037614
 R-PLACE1002514//Human DNA Sequence *** SEQUENCING IN PROGRESS *** from clone 212A2, WORKING
 DRAFT SEQUENCE.//7.8e-16:221:73//Z95114
 R-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds.//1.6e-86:582:85//AB018256
 20 R-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1, complete sequence.//9.0e-91:453:97//
 AC004774
 R-PLACE1002537//Hansenula wingei mitochondrial gene for NADH dehydrogenase subunit 5, complete cds.//
 0.0042:489:60//D16253
 R-PLACE1002571//Apis mellifera ligustica complete mitochondrial genome.//0.034:493:55//L06178
 25 R-PLACE1002578//Homo sapiens chromosome 5, Pac clone 9c13 (LBNL H127), complete sequence.//2.5e-44:
 292:84//AC006084
 R-PLACE1002583//Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete
 cds.//3.1e-17:517:61//AF045555
 R-PLACE1002591
 30 R-PLACE1002598//Caenorhabditis elegans cosmid Y37D8A, complete sequence.//0.080:308:60//AL032626
 R-PLACE1002604//Human cosmid LL12NC01-88A9, ETV6 gene, exons 6, 7 and 8 and partial cds.//0.0013:176:
 65//U63313
 R-PLACE1002625//HS_2233_B2_H04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=2233 Col=8 Row=P, genomic survey sequence.//5.2e-13:137:79//AQ146663
 35 R-PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//5.8e-46:272:94//
 AF079765
 R-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds.//1.2e-
 77:390:97//AF068180
 R-PLACE1002714//Mus musculus clone OST2473, genomic survey sequence.//1.3e-35:328:78//AF046656
 40 R-PLACE1002722//Sequence 1 from patent US 5686597.//1.7e-42:276:89//I73723
 R-PLACE1002768//Homo sapiens Xp22 bins 169-171 BAC GSHB-383H3 (Genome Systems Human BAC Library)
 complete sequence.//0.0098:197:64//AC005185
 R-PLACE1002772//Homo sapiens PAC clone DJ0560O14 from 7q21.1-q21.2, complete sequence.//6.7e-49:378:
 82//AC006145
 45 R-PLACE1002782
 R-PLACE1002794
 R-PLACE1002811//CIT-HSP-2316H11.TF CIT-HSP Homo sapiens genomic clone 2316H11, genomic survey se-
 quence.//6.0e-50:250:100//AQ034981
 R-PLACE1002815//Sequence 2 from patent US 5747660.//2.7e-59:312:84//AR005279
 50 R-PLACE1002816//Homo sapiens 12q13.1 PAC RPCI5-1057I20 (Roswell Park Cancer Institute Human PAC li-
 brary) complete sequence.//6.3e-59:339:93//AC004466
 R-PLACE1002834//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//1.4e-78:413:95//
 M27877
 R-PLACE1002839//Homo sapiens PAC clone DJ0015I23 from 22, complete sequence.//6.5e-25:301:74//
 55 AC004819
 R-PLACE1002853//Human interleukin 6 (IL6) gene, 5' flanking 358-bp 327-bp 300304.3

R-PLACE1002881

R-PLACE1002908//HS_3064_A1_D04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=7 Row=G, genomic survey sequence.//1.9e-09:156:72//AQ142985

R-PLACE1002941

R-PLACE1002962

R-PLACE1002968//Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF127 LIKE gene, and the PPAR for Peroxisome Proliferator Activated Receptor Delta (PPAR-Delta, PPAR-Beta, Nuclear Hormone Receptor 1, NUC1, NUCI, PPARB). Contains three putative CpG islands, ESTs, STSs, GSSs and a ca repeat polymorphism, complete sequence.//1.9e-32:314:77//AL022721

R-PLACE1002991//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 968D22, WORKING DRAFT SEQUENCE.//1.6e-42:343:81//AL023755

R-PLACE1002993//Homo sapiens PAC clone DJ0899E09 from 7q11.23-q21.1, complete sequence.//0.56:88:72//AC004921

R-PLACE1002996//HS_2064_A1_A05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2064 Col=9 Row=A, genomic survey sequence.//4.9e-18:117:95//AQ243211

R-PLACE1003025//Homo sapiens PAC clone DJ0560O14 from 7q21.1-q21.2, complete sequence.//0.26:428:58//AC006145

R-PLACE1003027//Homo sapiens chromosome 17, clone hRPK.700_H_6, complete sequence.//1.3e-95:465:98//AC005920

R-PLACE1003044

R-PLACE1003092//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-89, complete sequence.//3.6e-05:358:60//AL010266

R-PLACE1003100//HS_2244_A2_H12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2244 Col=24 Row=O, genomic survey sequence.//2.3e-42:288:86//AQ084224

R-PLACE1003108//Homo sapiens clone DJ0781A18, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.00066:233:61//AC004885

R-PLACE1003136//Plasmodium falciparum MAL3P2, complete sequence.//0.019:429:57//AL034558

R-PLACE1003145

R-PLACE1003153//Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence.//3.2e-05:390:58//AC004616

R-PLACE1003174//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTE17, complete sequence.//2.4e-06:390:60//AB015479

R-PLACE1003176

R-PLACE1003190//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces.//4.0e-78:406:81//AC005095

R-PLACE1003200//Plasmodium falciparum MAL3P6, complete sequence.//0.016:411:57//Z98551

R-PLACE1003205//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.00084:288:61//AC005139

R-PLACE1003238//Homo sapiens full-length insert cDNA clone ZD79H11 //7.6e-114:567:96//AF086432

R-PLACE1003249//Human Chromosome X, complete sequence.//1.3e-45:317:85//AC002416

R-PLACE1003256//Homo sapiens chromosome 17, clone HCIT421K24, complete sequence.//1.0e-45:328:85//AC004099

R-PLACE1003258

R-PLACE1003296//Diphtheria sp. 16S ribosomal RNA gene, mitochondrial gene encoding mitochondrial rRNA, partial sequence.//0.050:228:59//U39952

R-PLACE1003302//Figure 2. Nucleotide and translated protein sequences of HPF1, 2, and-9.//1.7e-91:458:96//M27877

R-PLACE1003334//Homo sapiens DNA sequence from BAC 217C2 on chromosome 22q13-q13.33. Contains a gene for the presumptive isolog of Rat RTP60 (nuclear pore complex protein Npap60). Contains ESTs, complete sequence.//4.3e-34:370:71//Z82243

R-PLACE1003342//CIT-HSP-2311D21.TF CIT-HSP Homo sapiens genomic clone 2311D21, genomic survey sequence.//1.0:159:68//AQ020460

R-PLACE1003343//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.1e-05:330:61//AC004153

R-PLACE1003366//Homo sapiens CAG repeated sequence//0.018:319:61//AJ006805
 R-PLACE1003369//T18H17-T7 TAMU Arabidopsis thaliana genomic clone T18H17, genomic survey sequence//0.050:155:63//B20174
 R-PLACE1003373//Homo sapiens chromosome 17, clone hRPC.1050_D_4, complete sequence//1.2e-62:434:83//AC004771
 R-PLACE1003375//Dictyostelium discoideum golvesin (gol) gene, complete cds//0.042:263:57//J89350
 R-PLACE1003383//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 10/10//1.7e-83:429:96//AB020878
 R-PLACE1003401//Homo sapiens chromosome 17, clone hRPK.85_B_7, complete sequence//2.4e-13:175:76//AC005695
 R-PLACE1003420//Homo sapiens PAC clone DJ0988G15 from 7q33-q35, complete sequence//2.1e-05:340:61//AC005587
 R-PLACE1003454//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-64, complete sequence//0.47:411:58//AL009014
 R-PLACE1003478//M.capricolum DNA for CONTIG MC175//0.51:253:59//Z33125
 R-PLACE1003493//Homo sapiens chromosome 17, clone hRPK.394_K_10, complete sequence//4.6e-37:319:81//AC006080
 R-PLACE1003516//CIT-HSP-2295M19.TF CIT-HSP Homo sapiens genomic clone 2295M19, genomic survey sequence//1.0e-40:251:90//AQ007480
 R-PLACE1003519//Homo sapiens chromosome 21q22.3 PAC 141B3, complete sequence, containing ribosomal protein homologue pseudogene L23a//2.7e-29:163:89//AF064859
 R-PLACE1003521//HS_3252_A2_G05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=10 Row=M, genomic survey sequence//0.00017:274:60//AQ221562
 R-PLACE1003528//HS_2041_B1_B07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2041 Col=13 Row=D, genomic survey sequence//6.6e-40:219:83//AQ230483
 R-PLACE1003537//Drosophila melanogaster mitochondrial cytochrome c oxidase subunits, ATPase6, 7 tRNAs (Trp, Cys, Tyr, Leu(UUR), Lys, Asp, Gly) genes, and unidentified reading frames A61, 2 and 3//8.3e-05:300:61//J01404
 R-PLACE1003553//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 97P20, WORKING DRAFT SEQUENCE//2.7e-87:450:96//AL031297
 R-PLACE1003566
 R-PLACE1003575//Homo sapiens chromosome 16, cosmid clone 325D7, complete sequence//4.7e-20:148:78//AC003965
 R-PLACE1003583//Human DNA sequence from PAC 388N15 on chromosome Xq21.1//3.5e-18:287:68//Z99571
 R-PLACE1003584
 R-PLACE1003592//Homo sapiens cosmid 223D9 from Xq28, complete sequence//2.5e-10:153:73//AF061032
 R-PLACE1003593//Human BAC clone RG030H15 from 7q31, complete sequence//6.9e-07:240:65//AC002066
 R-PLACE1003596//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y87G2, WORKING DRAFT SEQUENCE//0.13:393:60//AL022597
 R-PLACE1003602//Homo sapiens mRNA expressed in placenta//2.4e-95:576:88//D83200
 R-PLACE1003605//Homo sapiens BAC clone RG331C24 from 7q21, complete sequence//2.9e-19:302:71//AC002081
 R-nnnnnnnnnnnnn
 R-PLACE1003618//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 191E19, WORKING DRAFT SEQUENCE//8.3e-57:469:80//AL034451
 R-PLACE1003625//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces//2.1e-05:339:62//AC004688
 R-PLACE1003638//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1104E15, WORKING DRAFT SEQUENCE//2.5e-38:279:84//AL022312
 R-PLACE1003669//HS_3054_A2_E07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=14 Row=I, genomic survey sequence//0.014:265:61//AQ132713
 R-PLACE1003704//HS_3213_A1_D12_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=23 Row=G, genomic survey sequence//0.80:195:61//AQ176784
 R-PLACE1003709//Human BAC clone RG126M09 from 7q21-q22, complete sequence//0.018:152:61//AC002067
 R-PLACE1003720//Homo sapiens DNA sequence from clone RG126M09 on chromosome 22q11.2, contains a putative steroid-binding protein (SBRP) LIKE gene. Contains GSSs and an SFS, complete sequence//2.7e-19:302:71//AC002081

- 44:505:73//AL022336
 R-PLACE1003738//H.sapiens DNA sequence//0.93:185:60//Z22357
 R-PLACE1003760//Human globin gene//5.9e-97:538:91//M69023
 R-PLACE1003762//Homo sapiens chromosome 17, clone HCIT39G8, complete sequence//4.6e-13:134:79//
 5 AC003070
 R-PLACE1003768//Homo sapiens chromosome 17, clone hRPK.142_H_19, complete sequence//5.4e-12:189:
 71//AC005919
 R-PLACE1003771//Homo sapiens BAC clone GS164B05 from 7p21-p22, complete sequence//1.7e-119:619:95//
 AC004160
 10 R-PLACE1003783
 R-PLACE1003784//Homo sapiens chromosome 19, CIT-HSP-87m17 BAC clone, complete sequence//5.6e-15:
 204:74//AC004659
 R-PLACE1003795//CIT-HSP-2374C8.TR CIT-HSP Homo sapiens genomic clone 2374C8, genomic survey se-
 quence//7.0e-37:234:89//AQ114933
 15 R-PLACE1003833//Homo sapiens full-length insert cDNA clone ZE15C06//4.4e-59:313:95//AF086558
 R-PLACE1003850
 R-PLACE1003858
 R-nnnnnnnnnnnnn
 R-PLACE1003870//Homo sapiens Chromosome 22q11.2 Cosmid Clone 15a10 In DGCR Region, complete se-
 20 quence//8.7e-33:285:81//AC000072
 R-nnnnnnnnnnnnn
 R-PLACE1003886
 R-PLACE1003888//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence//0.73:127:65//
 AC004069
 25 R-PLACE1003900//Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds//1.9e-05:239:59//L78810
 R-PLACE1003903//Homo sapiens full-length insert cDNA clone ZD78D11//8.1e-74:369:97//AF086422
 R-PLACE1003915//Mus musculus bone morphogenetic protein-6 (BMP-6) gene, exons 6 and 7 and complete
 cds//0.56:247:61//U73520
 R-PLACE1003923//Caenorhabditis elegans cosmid Y57G11C, complete sequence//0.67:213:63//Z99281
 30 R-PLACE1003932//Human DNA sequence from cosmid U90B3, on chromosome Xp11, contains ESTs//8.7e-49:
 342:85//Z74022
 R-PLACE1003936//H.sapiens gene for ventricular myosin light chain 2//2.6e-09:394:61//Z15030
 R-PLACE1003968//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-62, complete
 sequence//1.3e-07:245:65//AL010247
 35 R-PLACE1004104
 R-PLACE1004114//Human PAC clone RG212D03, complete sequence//5.0e-07:336:61//AC002485
 R-PLACE1004118//HS_3092_B1_B01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3092 Col=1 Row=D, genomic survey sequence//0.80:207:60//AQ128151
 R-PLACE1004128//Rattus norvegicus guanine nucleotide binding protein beta 4 subunit mRNA, partial cds//1.8e-
 40 06:193:66//AF022085
 R-PLACE1004149//HS_2253_A2_F11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=2253 Col=22 Row=K, genomic survey sequence//2.4e-59:315:95//AQ129711
 R-PLACE1004156//Homo sapiens Xp22 bins 3-5 PAC RPC14-617A9 (Roswell Park Cancer Institute Human PAC
 Library) containing Arylsulfatase D and E genes, complete sequence//8.3e-53:299:76//AC005295
 45 R-PLACE1004161
 R-PLACE1004183//Homo sapiens for TOM1-like protein//1.3e-80:434:93//AJ010071
 R-PLACE1004197//RPC11-69N15.TK RPC11 Homo sapiens genomic clone R-69N15, genomic survey se-
 quence//0.0078:170:65//AQ265515
 R-PLACE1004203//Homo sapiens semaphorin L (SEMA1) mRNA, complete cds//3.4e-105:501:98//AF030698
 50 R-PLACE1004242//Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic
 marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence//6.1e-65:373:86//
 AL021326
 R-PLACE1004256//Homo sapiens BAC clone NH0044G14 from 7q11.23-21.1, complete sequence//0.011:383:
 61//AC006031
 55 R-PLACE1004257//Homo sapiens Xp22 BAC GSHB-433024 (Genome Systems Human BAC library) complete
 sequence//1.4e-59:315:95//AQ129711
 R-PLACE1004258//HS_3034_B1_B01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
 nomic clone Plate=3034 Col=23 Row=D, genomic survey sequence//1.4e-35:359:77//AQ128936

R-PLACE1004270//CITBI-E1-2504K14.TR CITBI-E1 Homo sapiens genomic clone 2504K14, genomic survey sequence.//2.7e-06:150:74//AQ261108

R-PLACE1004274//Homo sapiens BAC clone NH0436H22 from 2, complete sequence //0.025:116:72//AC005234

R-PLACE1004277//Homo sapiens two pore domain K⁺ channel (TASK-2) mRNA, complete cds //4.4e-106:581:91//AF084830

R-PLACE1004284//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.59:231:60//AC005308

R-FLACE1004289//Homo sapiens chromosome 17, clone hRPK.700_H_6, complete sequence.//5.8e-31:340:75//AC005920

R-PLACE1004302//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces //6.4e-90:572:86//AC005095

R-PLACE1004316//H.sapiens mRNA for apoptosis specific protein.//1.9e-113:590:94/Y11588

R-PLACE1004336//Human DNA sequence*** SEQUENCING IN PROGRESS *** from clone 1013A10, WORKING DRAFT SEQUENCE.//2.3e-65:292:82//AL033383

R-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds//2.4e-70:379:93/AF100153

R-PLACE1004376//CIT-HSP-2287M8.TF CIT-HSP Homo sapiens genomic clone 2287M8, genomic survey sequence.//0.47:173:61//AQ000837

R-PLACE1004384//CIT-HSP-2316J11.TF CIT-HSP Homo sapiens genomic clone 2316J11, genomic survey sequence.//0.035:109:69//AQ037817

R-PLACE1004388//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-82, complete sequence.//4.2e-06:381:60//AL010149

R-PLACE1004405//Homo sapiens clone GS512I21. WORKING DRAFT SEQUENCE, 9 unordered pieces //0.20:270.60//AC005027

R-PLACE1004425//Homo sapiens PAC clone DJ0733B09 from 7p14-p13, complete sequence.//1.3e-96:516:94//AC005532

R-PLACE1004428//Human DNA sequence from clone 888M10 on chromosome 1p36.11-36.31 Contains part of gene KIAA0453, EST, STS, GSS, complete sequence.//5.8e-10:279:65//AL031296

R-PLACE1004437//Human NAD⁺-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds//2.9e-88:516:88//U49283

R-PLACE1004451//HS_2258_B2_F01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2258 Col=2 Row=L, genomic survey sequence//0.82:172:61//AQ221189

R-PLACE1004460

R-PLACE1004467//Syrian hamster carbamoylphosphate synthetase-aspartate transcarbamylasedihydroorotase (CAD) gene, exons 1 and 2//1.2e-24;311:62//M31621

R-PLACE1004471//Homo Sapiens Chromosome X clone bWXD75, complete sequence.//2.1e-34:333 :70//
AC004389

R-PLACE1004473

R-PLACE1004491//Drosophila melanogaster Oregon-R mitochondrial A+T region//1.0e-08:485:60//U11584

R-PLACE1004506

R-PLACE1004510//Plasmodium falciparum chromosome 2, section 64 of 73 of the complete sequence.//0.0094:543:56//AE001427

R-PLACE1004516//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//0.00011:343:59//AC003071

R-PLACE1004518

R-PLACE1004548//Homo sapiens Xp22 BAC GS-551O19 (Genome Systems Human BAC library) and cosmid U199A7 and U209F2 (Lawrence Livermore X chromosome cosmid library) containing part of human chloride channel 4 gene, complete sequence.//4.9e-40:245:80//AC003666

R-PLACE1004550

R-PLACE1004564//B.taurus mRNA for cleavage and polyadenylation specificity factor//2.7e-82:532:86//X75931
R-PLACE1004629//Homo sapiens chromosome 7 clone 1JWG3:c3586a230 from 7p14-15, complete sequence //

0.015:437:59//AC004800

R-PLACE1004645//CIT-HSP-2370D6.TR CIT-HSP Homo sapiens genomic clone 2370D6, genomic survey sequence.//0.033:76:75//AQ110136

R-PLACE1004646//Homo sapiens cosmid 120C12 from Xq28 complete sequence //2 0e-23 237 79//AF036876

U5A: primary complete sequence. <https://doi.org/10.1093/nar/gaa877> A000534

nnnnnnnnnnnn//RPCI11-79G23 TV RPCI11 Homo sapiens genomic clone R-79G23 genomic survey seq

quence.//2.2e-81:433:94//AQ283692

R-PLACE1004672//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds.//2.7e-24:263:74//U07561

R-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds.//1.1e-89:513:91//AF035606

R-PLACE1004681//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11.//1.3e-96:498:95//AB020860

R-PLACE1004686

R-PLACE1004691//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 2/11.//2.1e-33:290:80//AB020859

R-PLACE1004693//Caenorhabditis elegans cosmid Y2H9A, complete sequence.//1.0:195:60//AL021448

R-PLACE1004716//CITBI-E1-2519C14. TR CITBI-E1 Homo sapiens genomic clone 2519C14, genomic survey sequence.//5.0e-43:245:93//AQ276965

R-PLACE1004722//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0022:360:60//AC005507

R-PLACE1004736

R-PLACE1004740

R-nnnnnnnnnnnn//Homo sapiens ubiquitin-protein ligase E3-alpha (UBR1) mRNA, partial cds.//5.4e-105:575:92//AF061556

R-PLACE1004751//Homo sapiens Xq28 BACs 360 F12, GSHB-555C13, complete sequence.//9.0e-26:317:76//AC002523

R-PLACE1004773//Homo sapiens inversin protein mRNA, complete cds.//8.5e-88:437:96//AF084367

R-PLACE1004777//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 3/15, WORKING DRAFT SEQUENCE.//0.050:138:65//AP000010

R-PLACE1004793//Human endogenous retrovirus HERV-K(HML6) proviral clone HML6.17 putative polymerase and envelope genes, partial cds, and 3'LTR.//5.1e-58:313:80//U60269

R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0606 protein, partial cds.//5.8e-98:580:88//AB011178

R-PLACE1004813//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//5.3e-09:256:64//AC005140

R-PLACE1004814//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds.//3.5e-107:358:99//AF069250

R-PLACE1004815//Human Chromosome 11q12.2 PAC clone pDJ606g6, complete sequence.//3.8e-61:353:89//AC004126

R-PLACE1004824//Homo sapiens chromosome 17, clone hCIT.468_F_23, WORKING DRAFT SEQUENCE, 3 unordered pieces.//5.7e-42:364:79//AC004666

R-PLACE1004827//Homo sapiens Xp22 BAC GS-594A7 (Genome Systems Human BAC library) contains Bmx gene, complete sequence.//2.7e-14:156:79//AC003669

R-PLACE1004836//HS_2270_A2_H10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2270 Col=20 Row=O, genomic survey sequence.//8.6e-51:267:96//AQ164110

R-PLACE1004838//CIT-HSP-2343E10. TR CIT-HSP Homo sapiens genomic clone 2343E10, genomic survey sequence.//0.071:168:63//AQ058544

R-PLACE1004840//Sequence 4 from patent US 5728819.//1.6e-26:150:98//I92820

R-PLACE1004868//Human Chromosome X clone bWDX342, complete sequence.//0.57:344:59//AC004072

R-PLACE1004885//HS_3235_B2_E07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3235 Col=14 Row=J, genomic survey sequence.//1.1e-38:175:78//AQ210193

R-PLACE1004900//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.0e-44:334:84//AL022577

R-PLACE1004902

R-nnnnnnnnnnnn//Human DNA sequence from clone J428A131, WORKING DRAFT SEQUENCE.//7.7e-58:377:87//Z82209

R-PLACE1004918//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//0.00084:373:60//AC004605

R-PLACE1004930//Homo sapiens MDC-3 13 isoform 1 mRNA complete cds.//2.0e-100:532:93//AF099936

R-PLACE1004931//Homo sapiens MDC-3 13 isoform 2 mRNA complete cds.//1.3e-100:532:93//AF099937

R-PLACE1004937//Caenorhabditis elegans SEL-10 (sel-10) mRNA complete cds.//1.3e-13:367:61//AF020788

R-PLACE1004969//Human DNA sequence from clone LUC7 on chromosome 3, complete sequence.//0.97:116:71//Z84494
R-PLACE1004972
R-PLACE1004979//Plasmodium falciparum MAL3P4, complete sequence.//0.74:304:60//AL008970
R-PLACE1004982//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.7e-05:495:57//AC005308
R-PLACE1004985//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 451B21, WORKING DRAFT SEQUENCE.//2.5e-10:410:60//AL033522
R-PLACE1005026//Homo sapiens PAC clone DJ0907C10 from 7q31-3q32, complete sequence.//2.7e-56:158:99//AC004925
R-PLACE1005027
R-PLACE1005046//Homo sapiens chromosome 19, cosmid F20237, complete sequence.//3.1e-63:438:86//AC005775
R-PLACE1005052//Homo sapiens chromosome Xp22-135-136 clone GSHB-567I1, WORKING DRAFT SEQUENCE, 35 unordered pieces.//6.1e-87:301:98//AC005867
R-PLACE1005066//Human DNA sequence from clone 67K17 on chromosome 6q24.1-24.3. Contains the HIVEP2 (Schnurri-2) gene for HIV type 1 Enhancer-binding Protein 2, and a possible pseudogene in an intron of this gene. Contains STSs and GSSs and an AAAT repeat polymorphism, complete sequence.//1.1e-09:453:61//AL023584
R-PLACE1005077//H.sapiens genes for semenogelin I and semenogelin II.//2.6e-05:199:66//Z47556
R-PLACE1005085//Homo sapiens chromosome 17, clone hRPK.293_K_20, complete sequence.//2.1e-42:384:69//AC005495
R-PLACE1005086//RPCI11-30H10.TV RPCI-11 Homo sapiens genomic clone RPCI-11-30H10, genomic survey sequence.//0.13:112:67//B87788
R-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds.//2.5e-97:531:92//L40401
R-PLACE1005102//Homo sapiens chromosome 19, cosmid R29388, complete sequence.//1.3e-91:504:92//AC004476
R-PLACE1005108//Homo sapiens BAC129, complete sequence.//4.0e-28:232:84//U85195
R-PLACE1005111//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 566H6, WORKING DRAFT SEQUENCE.//3.0e-18:174:74//AL031845
R-PLACE1005128
R-PLACE1005146
R-PLACE1005162//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//2.4e-07:273:61//AC005140
R-NNNNNNNNNNNN//Rat alternatively spliced mRNA.//8.1e-20:185:82//M93018
R-PLACE1005181//HS_2182_B2_B05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=10 Row=D, genomic survey sequence.//4.9e-05:193:65//AQ030787
R-PLACE1005187//Arabidopsis thaliana chromosome II BAC T14A4 genomic sequence, complete sequence.//0.00073:264:60//AC006161
R-PLACE1005206//Homo sapiens full-length insert cDNA YN66A06.//6.3e-64:343:93//AF075043
R-PLACE1005232//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 25J6, WORKING DRAFT SEQUENCE.//1.3e-34:286:81//Z84476
R-PLACE1005243
R-PLACE1005261//Caenorhabditis elegans cosmid ZK666, complete sequence.//0.66:180:60//Z49132
R-PLACE1005266//Homo sapiens clone RG122E10, complete sequence.//1.3e-15:166:78//AC005067
R-PLACE1005277//CITBI-E1-2514D4.TF CITBI-E1 Homo sapiens genomic clone 2514D4, genomic survey sequence.//2.5e-34:358:74//AQ265720
R-PLACE1005287//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P1, WORKING DRAFT SEQUENCE.//4.1e-07:495:60//AL031744
R-PLACE1005305//HS_3180_B2_D02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3180 Col=4 Row=H, genomic survey sequence.//1.1e-42:308:85//AQ169443
R-PLACE1005308
R-PLACE1005313//Human Chromosome 11 pac pDJ227b23, WORKING DRAFT SEQUENCE, 19 unordered pieces.//0.00048:320:60//AC000383
R-PLACE1005327//chromosome 1 specific transcript KIAA0491.//5.4e-103:537:94//AB007960
R-PLACE1005331//Homo sapiens chromosome 19 cosmid F20569 complete sequence.//2.2e-94:536:91//

- R-PLACE1005373//Homo sapiens BAC129, complete sequence.//8.8e-10:229:68//U85195
 R-PLACE1005374//Homo sapiens chromosome 17, clone hRPK.401_O_9, complete sequence.//3.0e-44:434:77//AC005291
- 5 R-PLACE1005409//Human BAC clone RG167B05 from 7q21, complete sequence.//8.8e-105:529:96//AC003991
 R-PLACE1005453//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//4.7e-39:302:82//AC002477
- R-PLACE1005467//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 167P19, WORKING DRAFT SEQUENCE.//1.1e-40:328:81//Z93014
- 10 R-PLACE1005471//Human DNA sequence from clone 395P12 on chromosome 1q24-25. Contains the TXGP1 gene for tax-transcriptionally activated glycoprotein 1 (34kD) (OX40 ligand, OX40L) and a GOT2 (Aspartate Amino-transferase, mitochondrial precursor, EC 2.6.1.1, Transaminase A, Glutamate Oxaloacetate Transaminase-2) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//6.4e-68:409:90//AL022310
 R-PLACE1005477//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 32B1, WORKING DRAFT SEQUENCE.//0.020:216:66//AL023693
- 15 R-PLACE1005480//Homo sapiens chromosome 19, CIT-HSP BAC 490g23 (BC338531), complete sequence.//2.8e-44:327:70//AC005392
 R-PLACE1005481//Homo sapiens-chromosome 17, clone hRPC.1164_O_3, complete sequence.//4.2e-23:284:74//AC004703
- R-PLACE1005494//Danio rerio homeobox protein LIM-3 (lim3) gene, exon 4.//0.19:468:60//AF031631
- 20 R-PLACE1005502//Homo sapiens formin binding protein 21 mRNA, complete cds.//1.6e-55:277:98//AF071185
 R-PLACE1005526//Human mRNA for alpha-1 type II collagen.//0.10:227:63//X16468
 R-PLACE1005528//Homo sapiens genomic DNA, chromosome 21q11.1, segment 9/28, WORKING DRAFT SEQUENCE.//2.3e-76:395:96//AP000038
- R-PLACE1005530//C.familiaris CA repeat sequence (isolate).//0.023:90:75//X86184
- 25 R-PLACE1005550//Fugu rubripes GSS sequence, clone 048A08bH1, genomic survey sequence.//2.0e-09:235:64//AL025928
 R-PLACE1005554//Homo sapiens chromosome 17, clone hRPK.215_P_18, complete sequence.//0.069:305:60//AC005969
- R-PLACE1005557//Homo sapiens chromosome 17, clone hRPC.117_B_12, complete sequence.//4.3e-105:587:91//AC004707
- 30 R-PLACE1005574//Human BAC 367D17 from chromosome 18, complete sequence.//1.5e-17:274:67//AC003971
 R-PLACE1005584//Homo sapiens PAC clone DJ1186C01 from 7q21.2-q31.1, complete sequence.//2.7e-15:191:77//AC004991
- R-PLACE1005595//Human Chromosome 11q12.2 PAC clone pDJ606g6, complete sequence.//6.4e-90:453:96//AC004126
- 35 R-PLACE1005603//Homo sapiens cosmid clone U169D2 from Xp22.1-22.2, complete sequence.//0.69:322:61//U72788
 R-PLACE1005611//Borrelia burgdorferi plasmid cp18, OspE (ospE) gene, partial cds.//0.059:473:56//U42599
- R-PLACE1005623//Homo sapiens full-length insert cDNA clone ZD76B03.//1.6e-113:575:95//AF086405
- 40 R-PLACE1005630//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.6e-79:270:94//AC005840
 R-PLACE1005639//Human BAC clone RG022J17 from 7q21, complete sequence.//8.2e-56:441:83//AC002382
- R-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds.//3.2e-110:585:93//AF083255
- 45 R-PLACE1005656//Homo sapiens chromosome 17, clone hRPK.628_E_12, complete sequence.//8.6e-08:505:58//AC005701
 R-PLACE1005666//Human DNA sequence from PAC 360E18 on chromosome X contains EST, CpG island and polymorphic CA repeat.//3.2e-27:307:72//Z82203
- R-PLACE1005698//344B22.TV CIT978SKA1 Homo sapiens genomic clone A-344B22, genomic survey sequence.//0.030:91:70//B15144
- 50 R-PLACE1005727//Human variable number tandem repeat (VNTR) region, allele 17R1 3' to collagen type II (COL2A1) gene.//5.2e-10:587:59//L10171
 R-PLACE1005730//Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds.//0.0039:239:58//L78810
- R-PLACE1005739//Mus musculus IFN-gamma induced (Mg11) mRNA, complete cds.//2.2e-21:270:72//U15635
- 55 R-PLACE1005755//Caenorhabditis elegans cosmid M03F4 //6.9e-08:219:64//U64601
 R-PLACE1005799//Human X chromosome mRNA for CD24 protein (CD24) cell proliferation (CD24) (X00000)
 R-PLACE1005802//Homo sapiens PAC clone DJ044L15 from Xq25, complete sequence.//1.4e-69:391:92

AC004827

R-PLACE1005803

R-PLACE1005804//Human BAC clone RG341D10 from 7p15-p21, complete sequence.//1.8e-21:175:75//AC002530

5 R-PLACE1005828//Homo sapiens chromosome 17, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//2.9e-56:333:91//AC004150

R-PLACE1005834//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P2, WORKING DRAFT SEQUENCE.//0.020:513:55//AL031745

R-PLACE1005845//Rabbit mRNA for protein phosphatase 2A-beta.//1.8e-10:182:69//Y00763 R-PLACE1005850

10 R-PLACE1005851//Homo sapiens clone DJ0789105, WORKING DRAFT SEQUENCE, 2 unordered pieces.//5.5e-06:318:63//AC004887

R-PLACE1005876//B.taurus mRNA for cleavage and polyadenylation specificity factor.//6.7e-28:366:72//X75931

R-PLACE1005884//Human DNA sequence from cosmid V526F1, between markers DXS366 and DXS87 on chromosome X contains STS.//1.0e-06:306:64//Z70281

15 R-PLACE1005898//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.0094:449:59//AC005139

R-PLACE1005921//CITBI-E1-2509N21.TF CITBI-E1 Homo sapiens genomic clone 2509N21, -genomic survey sequence.//4.8e-84:494:89//AQ261347

20 R-PLACE1005923//RPC11-65N9.TJ RPC11 Homo sapiens genomic clone R-65N9, genomic survey sequence.//8.3e-97:520:93//AQ237243

R-PLACE1005925//Human DNA sequence from clone 231L4 on chromosome Xq27.1-27.3 Contains GSS, STS, complete sequence.//5.2e-67:578:78//AL022719

R-PLACE1005932//Caenorhabditis elegans cosmid Y52B11A, complete sequence.//0.0035:176:62//AL032654

R-PLACE1005934

25 R-PLACE1005936//Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5 cM, complete sequence.//0.00021:272:62//AF069716

R-PLACE1005951

R-PLACE1005953//Caenorhabditis elegans cosmid F09E5.//1.3e-07:349:60//U37429

R-PLACE1005955//Human HepG2 3' region MboI cDNA, clone hmd1d01m3.//8.3e-08:128:70//D17131

30 R-PLACE1005966//Pontia protodice large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs.//7.0e-09:549:59//AF044863

R-PLACE1005968//Rattus norvegicus mRNA for p47, complete cds.//1.1e-51:394:81//AB002086

35 R-PLACE1005990//Homo sapiens chromosome 12p13.3 clone RPC111-407G6, WORKING DRAFT SEQUENCE, 51 ordered pieces.//4.4e-63:369:91//AC005866

R-PLACE1006002//Human cosmid CRI-JC2015 at D10S289 in 10sp13.//5.9e-27:299:74//U15177

R-PLACE1006003//Mus musculus clone OST18050, genomic survey sequence.//3.5e-07:164:67//AF046375

R-PLACE1006011//Mus musculus poly-(ADPribosyl)-transferase homolog PARP mRNA, complete cds.//1.1e-32:266:83//AF072521

40 R-PLACE1006017//Homo sapiens Chromosome 22q11.2 Cosmid Clone 31e In DGCR Region, complete sequence.//1.8e-17:164:82//AC000077

R-PLACE1006037//Mus musculus B6D2F1 clone 2C11B mRNA.//2.0e-49:557:72//U01139

R-PLACE1006040//Homo sapiens mRNA for alpha endosulfine.//4.3e-13:128:81//X99906

45 R-PLACE1006076//Homo sapiens clone DJ0781A18, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.3e-18:220:74//AC004885

R-PLACE1006119//Plasmodium berghei (STRAIN ANKA) gamma-GCS gene, complete CDS.//0.0050:271:63//AJ005122

R-PLACE1006129//Drosophila melanogaster, chromosome 2R, region 31C1-31D6, P1 clone DS08879, complete sequence.//0.43:178:65//AC005454

50 R-PLACE1006139//Homo sapiens PAC clone DJ0659J06 from 7q33-q35, complete sequence.//7.5e-13:222:68//AC004849

R-PLACE1006143//Plasmodium falciparum MAL3P6, complete sequence.//0.00019:455:59//Z98551

R-PLACE1006157//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE.//0.00018:351:60//AL034557

55 R-PLACE1006159//Homo sapiens chromosome 10 clone LA10NC01_124_D_3 map 10q25.1 WORKING DRAFT SEQUENCE.//1.1e-10:124:124//U01139

R-PLACE1006164//Human hereditary haemochromatosis region 16p11.3 HFE protein gene, hereditary haemochromatosis (HFE-H) gene, HbRet gene, and sodium phosphate transporter (NPT3) gene, complete cds.//1.0e-

28:342:75//U91328

R-PLACE1006167//Homo sapiens full-length insert cDNA clone ZE14E04.//4.6e-77:426:93//AF086555

R-nnnnnnnnnnnn//Mouse mRNA for alpha-adaptin (C).//3.0e-46:188:82//X14972

R-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds.//1.6e-116:597:95//AF091433

R-PLACE1006195//Homo sapiens chromosome 19, fosmid 39554, complete sequence.//8.8e-11:148:74//AC004410

R-PLACE1006196

R-PLACE1006205//Genomic sequence from Mouse 11, complete sequence.//8.4e-44:332:85//AC000398

R-PLACE1006223//Human DNA sequence from cosmid U74C11, between markers DXS6791 and DXS8038 on chromosome X contains ESTs.//0.041:215:61//Z73362

R-PLACE1006225//Caenorhabditis elegans cosmid Y69H2, complete sequence.//9.7e-13:358:63//Z98877

R-PLACE1006236//Plasmodium falciparum MAL3P4, complete sequence.//0.00019:538:58//AL008970

R-nnnnnnnnnnnn//Homo sapiens BAC clone RG118D07 from 7q31, complete sequence.//3.1e-96:497:95//AC004142

R-PLACE1006246//Homo sapiens clone NH0144M13, WORKING DRAFT SEQUENCE, 1 unordered pieces.//0.029:499:56//AC006034

R-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds.//9.2e-96:499:95//AB014548

R-PLACE1006262//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete sequence.//0.00043:160:66//AC004087

R-PLACE1006288//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 20N2, WORKING DRAFT SEQUENCE.//3.5e-120:611:96//AL031320

R-PLACE1006318

R-PLACE1006325//Plasmodium falciparum MAL3P8, complete sequence.//1.0:426:57//AL034560

R-PLACE1006335//Human DNA sequence from PAC 849L7 on chromosome Xq21.//0.96:173:66//AL008987

R-PLACE1006357//P.falciparum complete gene map of plastid-like DNA (IR-B).//1.9e-07:491:58//X95276

R-PLACE1006360//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//0.25:484:56//AE001398

R-PLACE1006368//Caenorhabditis elegans cosmid Y38H6C, complete sequence.//1.0:240:59//AL031630

R-PLACE1006371//Homo sapiens chromosome 16, cosmid clone 360H6 (LANL), complete sequence.//3.7e-101:574:91//AC004232

R-PLACE1006382

R-PLACE1006385//Mus musculus intersectin-EH binding protein lbp2 mRNA, partial cds.//1.4e-50:350:86//AF057286

R-PLACE1006412//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//5.1e-51:339:82//AC004854

R-PLACE1006414//Homo sapiens 12p13.3 PAC RPCI5-927J10 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.6e-38:297:84//AC004804

R-PLACE1006438//Homo sapiens full-length insert cDNA YH73H06.//7.6e-73:422:90//AF074985

R-PLACE1006445//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018K9, WORKING DRAFT SEQUENCE.//3.0e-07:376:61//AL031726

R-PLACE1006469

R-PLACE1006470//Mouse B1 repetitive sequence DNA.//1.0:96:66//M24152

R-PLACE1006482//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 447C4, WORKING DRAFT SEQUENCE.//3.0e-101:535:94//AL021977

R-PLACE1006492//Homo sapiens chromosome 17, clone hRPK.180_P_8, complete sequence.//0.78:44:95//AC005972

R-PLACE1006506//R.norvegicus BSP gene.//1.0:206:60//X86100

R-PLACE1006521//RPCI11-13L8.TV RPCI-11 Homo sapiens genomic clone RPCI-11-13L8, genomic survey sequence.//9.0e-17:414:61//B75158

R-PLACE1006531//Plasmodium falciparum coronin gene, isolate 3D7.//0.98:186:63//AJ002197

R-PLACE1006534//Anopheles gambiae complete mitochondrial genome.//0.051:412:61//L20934

R-PLACE1006540//Homo sapiens clone UWGC:y55c025 from 6p21, complete sequence.//7.5e-41:470:70//AC004209

R-PLACE1006552//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y47D3, WORKING DRAFT SEQUENCE.//0.57:355:57//Z98865

R-PLACE1006553//Homo sapiens chromosome 1, clone Y47D3, WORKING DRAFT SEQUENCE, 1 unordered pieces.//0.016:291:58//AJ004111

R-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3 p35 subunit mRNA, complete cds.